# PRAGUE UNIVERSITY OF ECONOMICS AND BUSINESS

FACULTY OF ACCOUNTING AND FINANCE

Department of Banking and Insurance



# Application of Machine Learning Algorithms within Credit Risk Modelling

## Master's thesis


Author: Bc. Petr Nguyen

Study program: Banking and Insurance | Data Engineering

Supervisor: prof. PhDr. Petr Teplý, Ph.D.



Year of defense: 2023

## Declaration of Authorship

I, as an author, hereby declare that I wrote and compiled the Master's thesis *"Application of Machine Learning Algorithms within Credit Risk Modelling"* independently, using only the resources and literature listed in bibliography.

25h May 2023, Prague

Petr Nguyen

# Abstract

The abstract should concisely summarize the contents of a thesis. Since potential readers should be able to make their decision on the personal relevance based on the abstract, the abstract should clearly tell the reader what information he can expect to find in the thesis. The most essential issue is the problem statement and the actual contribution of described work. The authors should always keep in mind that the abstract is the most frequently read part of a thesis. It should contain at least 70 and at most 120 words (200 when you are writing a thesis). Do not cite anyone in the abstract.

**Keywords:** machine learning, data science, credit risk, probability of default, loans, mortgages

# Abstrakt

Nutnou součástí práce je anotace, která shrnuje význam práce a výsledky v ní dosažené. Anotace práce by neměla být delší než 200 slov a píše se v jazyce práce (tj. česky, slovensky či anglicky) a v překladu (tj. u anglicky psané práce česky či slovensky, u česky či slovensky psané práce anglicky). Anotace práce by neměla být delší než 200 slov a píše se v jazyce práce (tj. česky, slovensky či anglicky) a v překladu (tj. u anglicky psané práce česky či slovensky, u česky či slovensky psané práce anglicky). V abstraktu by se nemělo citovat.

**Klíčová slova:** machine learning, data science, kreditní riziko, pravděpodobnost defaultu, úvery, hypotéky

# Acknowledgments

I, as an author, would like to express my deepest gratitudes and thanks to my supervisor prof. PhDr. Petr Teplý, Ph.D.for his help and significant advices throughout my thesis. Last but not least, I would like to also thank to my family for an enormous support during my studies.

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# Acronyms

**ML** Machine Learning

**PD** Probability of Default

**AUC** Area Under the Curve

**LR** Logistic Regression

**RF** Random Forest

**GB** Gradient Boosting

**MLP** Multi-Layer Perceptron

**DT** Decision Tree

**ADASYN** Adaptive Synthetic Sampling

# Chapter 1

# Introduction

**TBD**

This document serves two purposes. First, it is a template and example for a master's thesis. Second, the text in all sections contains some useful information on structuring and writing your thesis.

The introduction should consist of three parts (as paragraphs, not to be structured into multiple headings): The first part deals with the background of the work and describes the field of research. It should also elaborate on the general problem statement and the relevance. The second part should describe the focus of the thesis, typically the paragraph starts with a phrase like "The objective of this thesis is ...." The last part should describe the structure of the thesis, for instance in the following manner. The thesis is structured as follows: Chapter 2 cites some formal requirements of the faculty and the frequently asked questions about the template, Chapter 3 gives some hints on basic formatting features and covers also acronyms, figures, boxes and tables. **??** gives a recommendation on the usage of hyphens in English language in LaTeX and explains how to use the itemize and quote environments and shows a few enumerate-based environments. **??** presents a checklist of common mistakes to avoid. **??** contains numerous hints. Chapter 4 summarizes our findings.

# Chapter 2

# Theoretical Background

## 2.1 Credit Risk

### 2.1.1 Regulation

**TBD**

## 2.2 Terminology

- **Target variable** - Dependent variable or response variable, which we want to predict or classify ($Y$). In this case we want to predict a defaut status (Yes or No).
- **Feature** - Predictor, independent variable or explanatory variable ($X$), which we want to use to predict the target variable $Y$.
- cross validation
- over fitting

**TBD**

## 2.3 Algorithms

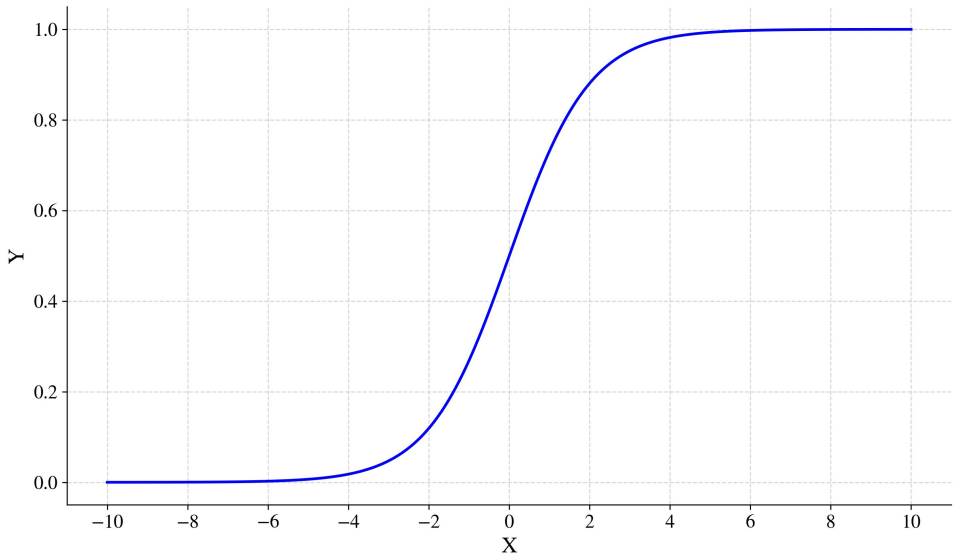
In this section, several algorithms, which are used in the machine learning implementation, are going to be described. Since the goal is to predict whether or

not given client will default, henceforth only (binary) classification algorithms as a part of the supervised learning are described. In other words, regression models and unsupervised learning algorithms are out of the scope of this thesis.

### 2.3.1 Logistic Regression

Despite the algorithm's name, it is actually not a regression but rather a classification model. In contrast, a linear regression's target variable is continuous whereas regarding a logistic regression, the target variable is categorical (or rather dichotomous in case of binary classification) (Wendler & Gröttrup 2021). For the probability estimation it is using a logistic, or so-called sigmoid function, which maps any real value within the range of 0 to 1 and takes a S-shaped curve as can be seen in Figure 2.1.

Figure 2.1: Logistic function




*Source:* Author's simulation in Python

The linear form of the logistic regression with n features can be written as:

$$\ln\left(\frac{P}{1-P}\right) = \beta_0 + \sum_{i=1}^{n} \beta_i X_i \tag{2.1}$$

where $P$ is the probability of the occurred event, conditional on the set of given features. Let us denote $Y = 1$ as an observed target instance where the

event occurred (e.g., default), then:

$$P = \Pr(Y = 1 \mid X) \tag{2.2}$$

Therefore, the term within the natural logarithm are the odds or more particularly, the ratio of the probability of the event with respect to the probability of non-event, both conditional on the same set of given features.

$$\begin{aligned} \frac{P}{1-P} &= \frac{\Pr(Y = 1 \mid X_1, X_2, \ldots, X_n)}{1 - \Pr(Y = 1 \mid X_1, X_2, \ldots, X_n)} \\ &= \frac{\Pr(Y = 1 \mid X_1, X_2, \ldots, X_n)}{\Pr(Y = 0 \mid X_1, X_2, \ldots, X_n)} \end{aligned} \tag{2.3}$$

Referring to the previous equations, solving for $P$, henceforth we get a final equation for computing the probability of occurred event with usage of logistic regression:

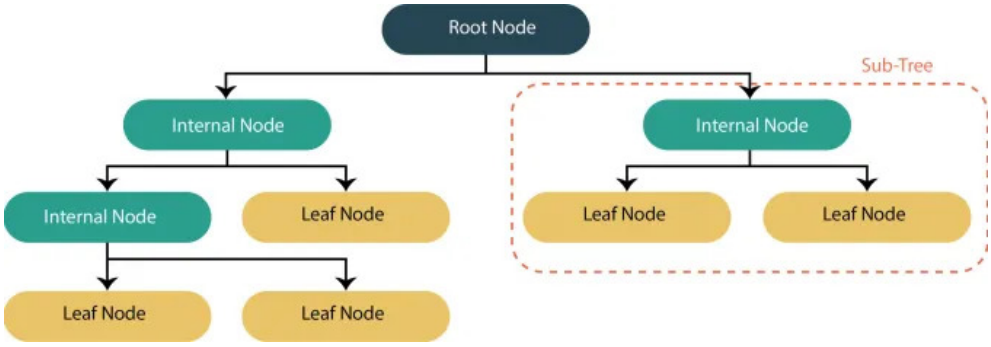
$$P = \frac{1}{1 + e^{-\left(\beta_0 + \sum_{i=1}^{n} \beta_i X_i\right)}} \tag{2.4}$$

### 2.3.2 Decision Tree

Decision tree (DT) is a rule–based algorithm which aims to partition the data into smaller and more homogeneous subsets. Such tree contains nodes, which are also visualized in Figure 2.2, namely:

- Root node - the topmost node of the tree where the splitting begins.
- Internal node - the non–terminal nodes as a result of the split and can be further split into another subsets.
- Leaf node - the terminal nodes as a results of the split and cannot be further split into another subsets.

Figure 2.2: Decision Tree's Nodes




*Source:* (Gauhar 2020)

The splitting process is based on the homogeneity or so called purity of the node with respect to the target variable (Provost & Fawcett 2013). In other words, we want to have the node as pure as possible which means that the node should contain as high proportion of one class as possible. In this case, the node should either contain high proportion of defaulters or non–defaulters, respectively. Such splitting processs starts from the root node and continues until the leaf nodes are pure enough or until the stopping criteria are met. The stopping criteria can be either a maximum depth of the tree, minimum number of observations within the node or minimum number of observations within the leaf node. One way to measure impurity is using Entropy which ranges from 0 to 1 and is defined as:

$$E = -\sum_{i=1}^{n} p_i \log_2 (p_i) \tag{2.5}$$

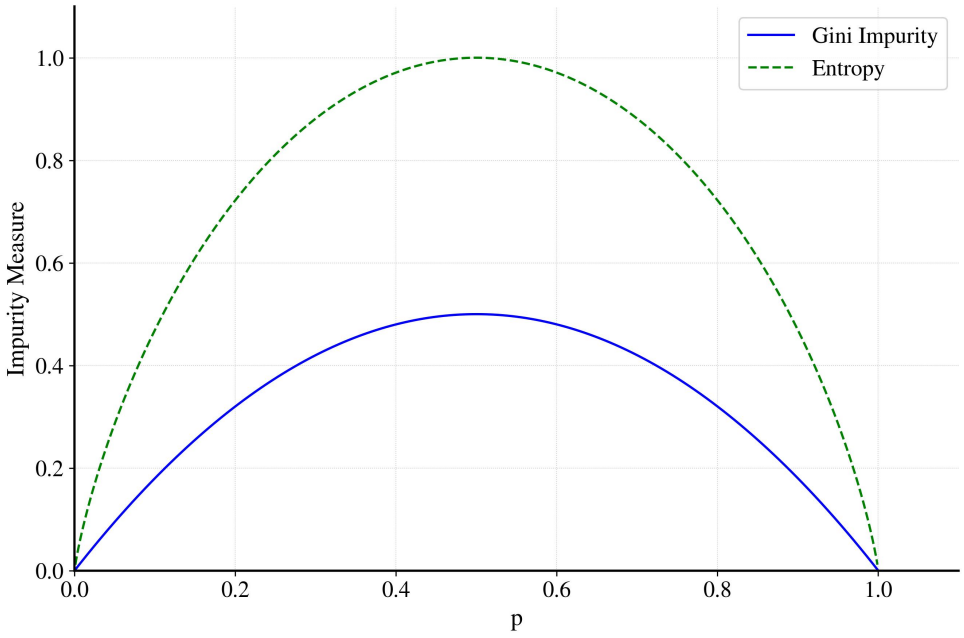
where $p_i$ is the probability of the occurrence of the event $i$, or in other words, it is a fraction of the observations belonging to the class $i$ within given node. In credit risk modelling terms, it is a proportion of defaulters within given node and $1 - p_i$ is a proportion of non–defaulters within given sample. The lower Entropy value, the purer the node is, i.e., the more homogeneous the subset is, where the frequency of one class is dominant to other class. Therefore, the goal is to minimize the Entropy value since we want to have the purest nodes as possible, i.e., the nodes where is either a high proportion of defaulters or non–defaulters. However, the Entropy is not the only way to measure the impurity of the node. Another way is using Gini Impurity which ranges from 0 to 0.5 and is defined as:

$$G = 1 - \sum_{i=1}^{n} p_i^2 \tag{2.6}$$

Both impurity measures are depicted in Figure 2.3 which we want to both of

them minimize. Thus, we choose such feature and such rule which result in the lowest impurity measure. Such process is repeated until the stopping criteria are met or until the leaf nodes are pure enough.

Figure 2.3: Gini Impurity vs. Entropy




*Source:* Author's simulation in Python

After the training, the DT predicts the target variable based on the rules which are stored in the tree. The prediction process starts from the root node and continues until the leaf node is reached. Within the leaf node, the prediction can be either the most frequent class within the node or the probability of the occurrence of the event, i.e., the proportion of defaulters within given node.

### 2.3.3 Naive Bayes

Naive Bayes is a classification and probabilistic machine learning algorithm which is based on the Bayes theorem:

$$\Pr(C = c \mid E) = \frac{\Pr(C = c) \times \Pr(E \mid C = c)}{\Pr(E)} \tag{2.7}$$

where:

- $\Pr(C = c \mid E)$ is the posterior probability which is the probability that

the target variable $C$ takes on the class of interest $c$ after taking the evidence $E$.

- $\Pr(C = c)$ is the prior probability of the class $c$ is the probability we would assign to the class $c$ before seeing any evidence $E$.
- $\Pr(E \mid C = c)$ is the probability of seeing the evidence $E$ conditional on the given class $c$.
- $\Pr(E)$ is the probability of the evidence $E$.

With regards to the binary classification, we can substitute $Y$ as a target variable instead $C$, and set of features $X$ which will refer to the set of evidence $E$., henceforth the probability of $Y$ using the Naive Bayes algorithm can be mathematically expressed as:

$$\Pr(Y \mid X) = \frac{\Pr(Y) \times \Pr(X \mid Y)}{\Pr(X)} \tag{2.8}$$

One of the assumptions of this algorithm is the conditional probabilistic independence among the features. Since all the $X$ features' values combinations do not have to appear at all, we assume their independence (Cichosz 2014). Therefore, instead of computing the probability of all features together, conditional on the class event, for each feature $X$ we the conditional joint probability of $X$ given the class event. Hence:

$$\Pr(X \mid Y) = \prod_{i=1}^{n} \Pr(X_i \mid Y) \tag{2.9}$$

Furthermore, the second adjustment is applied to the denominator of the Bayes theorem, i.e., $\Pr(X)$ - since such probability is constant over all the values of the class event, we can omit it from the equation. Therefore, the probability of the class event $Y$ can be expressed as:

$$\Pr(Y \mid X) = \prod_{i=1}^{n} \Pr(X_i \mid Y) \times \Pr(Y) \tag{2.10}$$

During the training process, the Naive Bayes algorithm computes $\Pr(Y)$ and $\Pr(X \mid Y)$ for each class event $Y$ and each feature $X$. In terms of default status, it calculates the proportion of defaulters $\Pr(Y = 1)$ and non–defaulters $\Pr(Y = 0)$ within given training sample as well as the proportion of defaulters and non–defaulters within given feature $X$.

When it comes to the predictions or classification of new instances, we use the trained Naive Bayes model, i.e., the computed probabilities $\Pr(Y)$ and $\Pr(X \mid Y)$ for both default and non–default class. Specifically, based on the new instance's features $X$, we determine the computed $\Pr(Y)$ and $\Pr(X \mid Y)$ for both classes and aftewards, as a predicted class, we choose such class with the highest posterior probability. In general, the prediction while maximizing posterior probability is given as:

$$\Pr(Y \mid X) = \text{argmax}_{y \in Y} \Pr(X \mid Y = y) \times \Pr(Y = y) \tag{2.11}$$

Specifically, in terms of binary classification for prediction of given class, whether it is default or non–default, we can compute the probability of the default event (1) and non–default event (0) and choose the class with the higher probability.

$$\Pr(Y \mid X) = \max(\Pr(Y = 1 \mid X), \Pr(Y = 0 \mid X)) \tag{2.12}$$

where:

$$\Pr(Y = 0 \mid X) = \Pr(Y = 0) \times \prod_{i=1}^{n} \Pr(X_i \mid Y = 0) \tag{2.13}$$

respectively:

$$\Pr(Y = 1 \mid X) = \Pr(Y = 1) \times \prod_{i=1}^{n} \Pr(X_i \mid Y = 1) \tag{2.14}$$

### 2.3.4 K-Nearest Neighbors

The goal of K-nearest Neighbors algorithm (also known as KNN) is to find $k$ instances that are most similar to particular instances y in the n-dimensional space, where n is the number of features. The principle of this algorithm consists in the similarity between the instances as it assumes that the similar instances are close to each other. Based on the predetermined $k$ neighbors, it will predict the class based on the k nearest instances.

There are several ways how to measure the distance. The most used one is the Euclidean distance. Geometrically, it is a straight line between the two points and within two-dimensional space, it can be derived from the Pythagorean theorem, where the hypotenuse is the straight line measuring the distance. In the n-dimensional space, we take the sum the squared differences between the data points $x$ and $y$, underneath the square root in order to compute the total

Euclidean distance.

$$d_{Euclidean}(x, y) = \sqrt{\sum_{i=1}^{n}(x_i - y_i)^2} \tag{2.15}$$

Other distance measure is the Manhattan distance measure, which is known as a city block distance, referring to the real-life problems, more particularly in order to reach particular destination, we have to take the path in between the blocks. Mathematically, it is similar to the Euclidean distance, but instead of squared differences, it sums the absolute differences between the data points.

$$d_{Manhattan}(x, y) = \sqrt{\sum_{i=1}^{n}|x_i - y_i|} \tag{2.16}$$

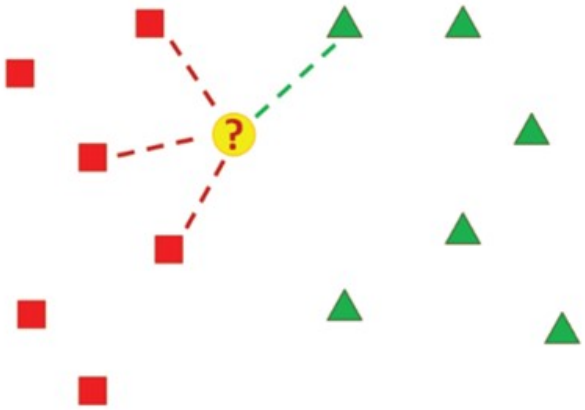
The last measure is the Minkowski distance which is the generalized form Euclidean or Manhattan distance respectively. It depends on p which represents the order of the norm. Hence, the Euclidean distance has the second order of the norm, whereas Manhattan distance has the first order of the norm.

$$d_{Minkowski}(x, y) = \sqrt[p]{\sum_{i=1}^{n}|x_i - y_i|^p} \tag{2.17}$$

Within the training process, KNN memorizes training instances and afterwards when it encounters a new instance, it tries to search for such training instance(s) which most strongly resembles the new instance (Witten *et al.* 2011). Therefore, After the training process, when it comes to the prediction, the KNN compares the new instance to the training instances, calculates the distances between the the new input and the training instances, and predicts the class based on on the majority voting within the $k$ nearest neighbors, or predicts the probability scores as the fraction of positive instances within the $k$ nearest neighbors.

On the following Figure 2.4, let us consider 2–dimensional space and that $k$ is equal to 4, hence we are looking at four nearest neighbors for such new instance. Further, let us consider two classes - red squares and green triangles. By looking at the four nearest neighbors, we can observe that three out of the nearest neighbors are the red triangles. Therefore, when applying majority voting, KNN would predict such instance as a red triangle, or would predict a probability score of 0.75 for the red triangle.

Figure 2.4: K-Nearest Neighbors with $k = 4$




*Source:* (Mucherino *et al.* 2009)

### 2.3.5 Random Forest

Random forest is an ensemble algorithm which is a collection of decision trees where each tree is independently trained on on a bootstrap sample of the training data (Han *et al.* 2011), i.e., on a on a set which is randomly sampled from the training data with replacement which has the same size as the training data. In such way, each bootstrap sample is unique and can contain duplicates of the original data or does not have to contain all the original data. Another aspect of randomness in such algorithm, particularly in the variability within trees, is the number of features considered for the split at each node. Instead of considering all the features of the length $M$, it randomly selects a subset of features of the length $m$ (where $m < M$) and chooses the best split from the subset. The training process of individual decision tree is the same as described in Subsection 2.3.2.

Within classifying new instances, the random forest algorithm predicts the class based on the majority voting of the individual decision trees or predicts a probability as an average of the probabilities of the individual decision trees (Malley *et al.* 2011), thus:

$$\Pr(Y = 1 \mid X) = \frac{1}{B} \sum_{b=1}^{B} \Pr(Y = 1 \mid X, T_b) \tag{2.18}$$

where $B$ is the number of trees and $T_b$ is the $b$-th tree.

**TBD**

### 2.3.6 Gradient Boosting

**TBD**

### 2.3.7 Support Vector Machine

**TBD**

### 2.3.8 Neural Networks

**TBD**

## 2.4 Evaluation Metrics

**TBD**

This section focuses on particular measures through which it is possible to determine a predictive power of model in terms of its performance. The are many ways, how to evaluate the model's performance, therefore, only the most common ones and the most relevant are further described. Note, since default prediction regards classification tasks, therefore regression's evaluation metrics are omitted. If not stated otherwise, the higher metric measure, the better the model's performance is.

### 2.4.1 Confusion Matrix and Derived Metrics

Confusion matrix is a table which summarizes the classification model's performance with respect to the actual classes and predicted classes. It is a square $n \times n$ matrix, where $n$ determines number of classes within the target variable. Let us denote the confusion matrix as $C(f)$ for classification algorithm $f$. Its elements can be denoted as $c_{i,j}$ where $i$ and $j$ refer to the row and column indices, respectively, or more particularly, $i$ refers to the actual class and $j$ to the class predicted by the classifier $f$. Each element of the confusion matrix refers to the number of instances corresponding to actual class $i$ and predicted class $j$ (Japkowicz & Shah 2011). For instance, the element $c_2, 1$ would refer to the number of instances which have the actual class 2 but have been classified as class 1. Mathematically, the confusion matrix can be written as following:

$$C = c_{i,j} = \sum_{l=1}^{m} [(y_l = i) \wedge (f(x_l) = j)] \tag{2.19}$$

Or either in matrix form as:

$$C_{i \times j} = \begin{bmatrix} c_{1,1} & c_{1,2} & \cdots & c_{1,j} \\ c_{2,1} & c_{2,2} & \cdots & c_{2,j} \\ \vdots & \vdots & \ddots & \vdots \\ c_{i,1} & c_{i,2} & \cdots & c_{i,j} \end{bmatrix} \tag{2.20}$$

From the given matrix, the diagonal elements represent the numbers of correctly classified instances, whereas the non-diagonal elements represent the numbers of misclassified instances. Further, let us consider a binary classification - hence, the confusion matrix will have a form of $2 \times 2$.

$$C_{2 \times 2} = \begin{bmatrix} c_{1,1} & c_{1,2} \\ c_{2,1} & c_{2,2} \end{bmatrix} \tag{2.21}$$

We can this rewrite confusion matrix as:

$$C_{2 \times 2} = \begin{bmatrix} TP & FN \\ FP & TN \end{bmatrix} \tag{2.22}$$

where:

- TP is the True Positive which refers to the number of instances which correspond to the actual class $True$ and indeed have been correctly classified as class $True$.
- $FP$ is the False Positive which refers to the number of instances which correspond to the actual class $True$, but have been incorrectly classified as class $False$. In the statistics and hypothesis–testing terms, it can be also called as Type 1 Error.
- $FN$ is the False Negative which refers to the number of instances which correspond to the actual class $False$, but have been incorrectly classified as class $True$. In the statistics and hypothesis–testing terms, it can be also called as Type 2 Error.
- $TN$ is the True Negative which refers to the number of instances which

correspond to the actual class $False$ and indeed have been correctly classified as class $False$.

### Accuracy

Such metric ranges from 0 to 1 and it describes in relatives terms how many instances the model has correctly predicted. Thus, the goal is to minimize the number of False Positives and False Negatives, or in credit risk modelling terms, number of defaulters which the model has classified as non–defaulters and number of non–defaulters which the model has classified as defaulters. However, accuracy is inappropriate metric for evaluation when having imbalanced class, i.e., where the distribution of the target variable is skewed. In such case, the model can achieve a relatively high accuracy even though it is not able to predict the minority class correctly (Brownlee 2021), thus it would lead to the misleading results. This is the case of the credit risk modelling, when the loan portfolio oftenly have a lot of non–defaults and few defaults. Therefore, it is deemed appropriate to consider other metrics when having imbalanced class.

$$Accuracy = \frac{TP + FN}{TP + TN + FP + FN} \tag{2.23}$$

### Recall

Such metric is also known as True Positive Rate (TPR) or Sensitivity, which also ranges from 0 to 1, and it describes in relative terms how many actual *True* instances the model has correctly predicted out of all the *True* instances. Thus, the goal is to minimize the number of False Negatives, i.e., number of defaulters which the model has classified as non–defaulters. A lower value of recall could therefore indicates that either the model is not able to predict correctly the $True$ classes resulting in low number of True Positives and/or high number of False Negatives. Recall metris is useful when having imbalanced class and should be used instead of accuracy metric as it measures the model's ability to correctly identify instances of the minority class (i.e., defaults). Mathematically based on the confusion matrix elements, it can be computed as:

$$Recall = \frac{TP}{TP + FN} \tag{2.24}$$

### Precision

This metric describes in relative terms how many predicted *True* instances are actually *True*. Thus, the goal is to minimize the number of False Positives, i.e., number of non–defaulters which the model has classified as defaulters. A lower value of precision could therefore indicates that either the model is not able to predict correctly the $True$ classes (low number of True Positives) or its prediction of $True$ classes is noisy (high number of False Positives). Precision is another metric which should be used instead of accuracy when having imbalanced class as it tt measures the model's ability to correctly identify instances of the minority class while minimizing false positives (i.e., non–default instances which the model has classified as default). Similarly, Precision also ranges from 0 to 1 and can be derived from the confusion matrix as follows:

$$Precision = \frac{TP}{TP + FP} \tag{2.25}$$

### F1 Score

F1 score incorporates both Recall and Precision into a single value and takes on values between 0 and 1 as well. Is it defined as a weighted harmonic mean of these two metrics (Brabec *et al.* 2020) (where both Recall and Precision have uniform weights), and the goal is to minimize False Positives and False Negatives at the same time as within accuracy. Nevertheless, F1 score is deemed as more appropriate metric when dealing with imbalanced class as it provides more balanced evaluation of model's performance in imbalanced datasets compared to accuracy.

$$F1 = \frac{2 \times Precision \times Recall}{Precision + Recall} = \frac{2 \times TP}{2 \times TP + FP + FN} \tag{2.26}$$

### Matthews Correlation Coefficient

The drawback of Recall, Precision and F1 score is they are asymmetric measures, i.e., they do not take into account the True Negatives. Therefore, such metrics' values will differ if we swap the positive and negative classes (Chicco & Jurman 2020), e.g., 1 would indicate non–default and vice versa. In order to overcome such drawback, Matthews Correlation Coefficient can be used as it is symmetric and it takes into account all the four elements of the confusion ma-

trix as well as it captures imbalanced class issue. Methodologically, Matthews Correlation Coefficient is defined as a discretization of Pearson correlation for the case of binary variables (Boughorbel *et al.* 2017). Pearson correlation coefficient is defined as:

$$r(x,y) = \frac{\sum_{i=1}^{n}(x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum_{i=1}^{n}(x_i - \bar{x})^2}\sqrt{\sum_{i=1}^{n}(y_i - \bar{y})^2}} \tag{2.27}$$

Thus, assuming that $x$ is the vector of True labels and $y$ is the vector of predictions, the Matthews Correlation Coefficient can be defined as:

$$MCC = \frac{TP \times TN - FP \times FN}{\sqrt{(TP + FP)(TP + FN)(TN + FP)(TN + FN)}} \tag{2.28}$$

Matthews correlation coefficient ranges from -1 to 1, where 1 indicates perfect model's predictions, -1 indicates that model misclassifies all the instances and 0 indicates that model's predictions are not better than random guessing.

### 2.4.2 AUC

In order to derive Area Under the Curve ($AUC$), first we need to define Receiver Operating Characteristics ($ROC$) curve. ROC curve is two-dimensional visualization of the model performance as a probability curve in terms of True Positive Rate ($TPR$) and False Positive Rate ($FPR$) based on varying the given threshold.

Briefly, it can be construct as following: First, we need to sort the instances by the predicted probability and based on the given probability, we set a threshold - what will be above the threshold will be classified as $True$ instance and what is below the threshold will be classified as $False$ instance. Based on these classified instances, the confusion matrix can be constructed and via which we can compute the $TPR$ and $FPR$ values. Thus, if the probability is 1, the threshold will be 1 as well and hence:

- $TPR$ will be 0 because there is no probability which is higher than 1 and hence, everything will be classified as $False$ which will result into $TP$ of 0, and subsequently into $TPR$ of 0 as well.

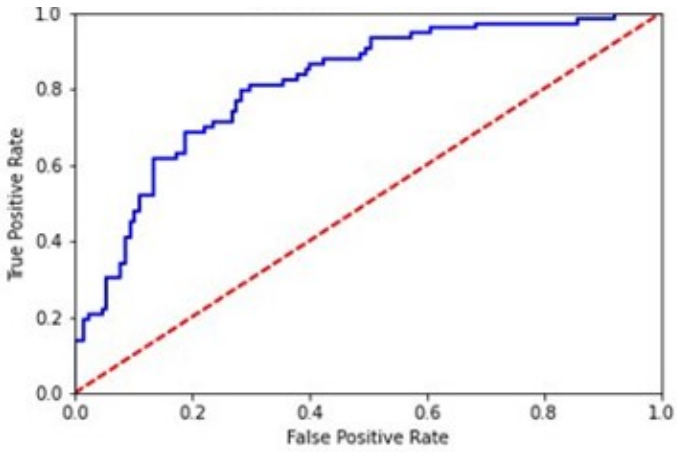
- $FPR$ will be 0, too â€“ since everything will be classified as $False$, therefore $FP$ will be 0 which implies $FPR$ to be 0, too.

On the other hand, if the probability is 0, the threshold will be 0 as well and hence:

- $TPR$ will be 1 because there is no probability which is lower than 0 and hence, everything will be classified as $True$ which will result into $FN$ of 0, and subsequently into $TPR$ of 1.
- $FPR$ will be 1, too â€“ since everything will be classified as $True$, therefore $TN$ will be 0 which implies $FPR$ to be 1.

Thus, based on each threshold, the $TPR$ and $FPR$ will be to coordinates for single point within the graph and based on such points, we can construct the ROC curve. Such visualization on the following Figure 2.5. Note the diagonal line represents a random model which randomly and correctly predicts the $True$ and $False$ classes in such way, that $FPR$ and $TPR$ are the same. Logically, a decent model should perform better than the random model, thus it the ROC curve should be above the diagonal line. Intuitively, the best possible theoretical model would have $TPR$ of 1 and $FPR$ of 0, meaning that all the $True$ actual classes should be predicted as $True$ and all the $False$ actual classes should not be classified as $True$ Within the ROC curve, the given curve reaches the left top corner which corresponds to the coordinates of $TPR$ and $FPR$.

Figure 2.5: ROC Curve




*Source:* Author's results in Python.

$AUC$ is basically the representation of ROC curve as a single number as it aggregates the performance on all possible thresholds. $AUC$ can be inter-

preted as the probability that the randomly chosen actual $True$ instance is ranked higher than the randomly chosen actual $False$ instance. Since ROC curve is a probability curve, thus it is considering distribution curve of $TP$ and distribution class of $TN$, separated by particular threshold â€“ hence, $TP$ would have probability scores above the given thresholds, whereas $TN$ would have probability scores below the threshold. If these curves do not overlap, meaning the model can perfectly distinguish between the $True$ and $False$ values, therefore the $AUC$ would be 1 and the ROC curve would reach the left top corner. However, this idealistic situation does not occur in the practice at all, but rather the two distributions are overlapping since the misclassification of the classes takes the place. The bigger overlap, the lower $AUC$ is. If the distributions are completely overlapping, it implies the $AUC$ of 0.5, meaning that the model cannot distinguish between the $True$ and $False$ classes, which is the worst scenario. On the other hand, if the distributions are totally opposite (meaning that the $TP$ instances would have probability scores below the given threshold, whereas the $TN$ instances would have probability scores above the given threshold), the $AUC$ would be 0 since the model is predicting the $True$ actual classes instead of $False$ and vice versa.

As the $AUC$ is an area present underneath the ROC curve, mathematically, it can be computed with the definite integral where $x$ is the given threshold:

$$AUC = \int_0^1 TPR\left(FPR^{-1}(x)\right) dx \tag{2.29}$$

### 2.4.3 Kolmogorov-Smirnov

The Kolmogorov-Smirnov (KS) is non–parametric metric for assessing discriminant power of a model as it measures distance between the cumulative distribution functions (CDF) between two classes, and is quantified as a maximum vertical absolute difference between such two CDF's (Adeodato & Melo 2016). In credit risk modelling terms, we can express KS as follows:

$$\text{Kolmogorov Smirnov} = \max_{0 \leq j \leq 1} |F_D(j) - F_{ND}(j)| \tag{2.30}$$

where $F_D$ and $F_{ND}$ are the cumulative distribution functions of default and non-default cases, respectively, and $j$ is the probability score threshold which ranges between 0 and 1.

### 2.4.4 Somer's D

The Somers' D is a metric which is part of the Kendall family of ranking measures. Particularly, assuming X-Y pairs, a Kendall's $\tau_a$ is defined as:

$$\tau\left(X, Y\right) = \mathrm{E}\left[\mathrm{sign}(X_i - X_j)\mathrm{sign}(Y_i - Y_j)\right] \tag{2.31}$$

Equivalently, Kendall's $\tau_a$ can be defined as the difference between the probability that the two X-Y pairs are *concordant* and the probability that they are *discordant*. X-Y pair is concordant if the larger of the $X$ values is paired with with larger of the $Y$ values, i.e, $X_i < X_j$ and $Y_i < Y_j$. In contrast, X-Y pair is discordant if the larger of $X$ values is associated with smaller of $Y$ values or vice versa, i.e, $X_i < X_j$ and $Y_i > Y_j$, or $X_i > X_j$ and $Y_i < Y_j$ (Newson 2002). Therefore, Somers' D can be defined as the difference between the two conditional probabilities of concordance and discordance, given that the two $X$ values are unequal (Newson 2014) as follows:

$$D\left(Y \mid X\right) = \frac{\tau\left(X, Y\right)}{\tau\left(X, X\right)} \tag{2.32}$$

In case of a binary classification, $X$ values would represent *True* labels and $Y$ values would represent predicted probability scores as rank vectors. Such metric ranges from -1 to +1 (likewise as Matthews correlation coefficient +1). Thus, the higher value of Somers' D, the model's better ability to distinguish between borrowers who are likely to default and those who are not.

### 2.4.5 Brier Score Loss

Methodologically, Brier Score Loss is calculated in the same way as Mean Squared Error (MSE). However, Brier Score Loss is applied to the predicted probabilities (i.e., assumes that the target variable is dichotomous) (Comotto 2022), whereas MSE is rather used in regression tasks where is no assumption regarding the continuous target variable. Henceforth, Brier Score Loss is defined as a mean squared error between the $True$ labels ($y$) and the predicted probabilities ($\hat{y}$) as follows:

$$\text{Brier Score Loss} = \frac{1}{n}\sum_{i=1}^{n}(y_i - \hat{y}_i)^2 \tag{2.33}$$

Brier Score Loss ranges from 0 to 1, where the the ideal scenario would be Brier Score Loss of 0 - in such case, the model would be perfect predictive power.

### 2.4.6 Jaccard Score

Jaccard Score which is also known as Jaccard Index is a similarity metric as it measures similarity between the *True* labels and predicted classes (0 or 1). Let us denote $y$ as a vector of *True* labels and $\hat{y}$ as a vector of predicted classes. Hence, we can define Jaccard Score as the ratio of the size of intersection of $y$ and $\hat{y}$ to the size of union of $y$ and $\hat{y}$ (Leskovec *et al.* 2020). Thus:

$$\text{Jaccard Score} = \frac{|y \cap \hat{y}|}{|y \cup \hat{y}|} \tag{2.34}$$

Likewise, Jaccard score ranges from 0 to 1 where the higher value indicates the higher similarity between the *True* labels and predicted classes, hence the better model's performance.

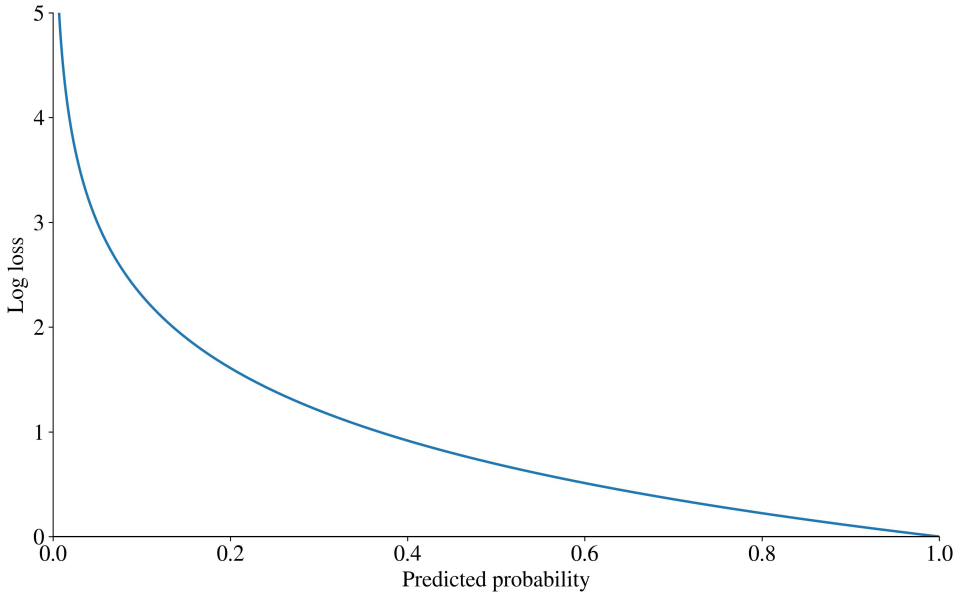
### 2.4.7 Log Loss

Log loss, also know as logistic loss or cross–entropy loss, is a loss function metric which takes *True* labels and predicted probabilities as an input and the minimize the difference between these two in a logarithmic function's form. Particularly, it indicates how close the predicted probabilities are to the corresponding $True$ labels. The more predicted probabilities diverges from the actual value, the more the log loss function penalizes the model's performance (Dembla 2020).

$$\text{Log Loss} = -\frac{1}{N}\sum_{i=1}^{N} y_i \ln(p_i) + (1 - y_i)\ln(1 - p_i) \tag{2.35}$$

Logically, the lower Log loss value, the better performance of the model is. As depicted in Figure 2.6, we can observe the closer the predicted probability is closer to 1 with respect to the $True$ label being equal to 1, the more is the log loss function closer to 0 which is desired in terms of model's performance.

Figure 2.6: Log Loss Function when $Y = 1$




*Source:* Author's simulation in Python

# Chapter 3

# Empirical Analysis - Machine Learning Implementation

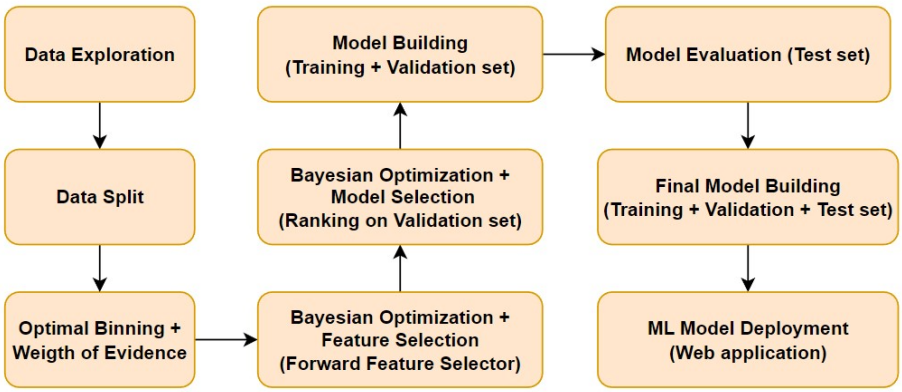
This chapter focuses on the main part of this thesis, particularly on the practical example of machine learning implementation. The machine learning framework deployed in this thesis is shown in Figure 3.1.

- **Data Exploration** - this part of the framework is focused on the exploration of the data in order to infer some insights about the data quality, distribution of the variables, statistical testing or association analysis.
- **Data Split** - this part of the framework is focused on the splitting of the data which are used separaterly in diferrent tasks such as model training, model selection and model evaluation.
- **Optimal Binning and WoE Encoding** - this part of the framework is focused on the optimal binning and the WoE encoding of the features as the main part of the feature preprocessing.
- **Feature Selection** - this part of the framework is focused on the feature selection in order to reduce the dimensionality of the data and to improve the performance of the machine learning models - each input model estimator is tuned with Bayesian Optimization.
- **Model Selection** - this part of the framework is focused on the model selection in order to find the best model based on the ranking - each input model is tuned with Bayesian Optimization on the subsets of selected features.
- **Model Building (Evaluation)** - this part of the framework is focused

on the recalibration of the final model by re-training it on the joined training and validation sets, which will be further evaluated.

- **Model Evaluation** - this part of the framework is focused on the evaluation of the final model on the unseen data from test set.
- **Model Building (Deployment)** - this part of the framework is focused on the final recalibration of the final model by re-training it on the joined training, validation and test sets, which will be further deployed into a production.
- **Model Deployment** - this part of the framework is focused on the deployment of the final model into a production as a web application.

Figure 3.1: Machine Learning Framework




*Source:* Author's results

## 3.1 Repository and Environment Structure

The whole machine learning implmenetation as the scope of this thesis is done mainly using Python Programming Language and further with collaboration of Git and HTML. The whole repository can be found in the separate appendix or is available on the GitHub repository `https://github.com/petr-ngn/FFU_VSE_Masters_Thesis_ML_Credit_Risk_Modelling`. The repository structure is shown in Figure 3.2.

Figure 3.2: Repository Structure

```
|--- data
|  |--- interim_dat.csv
|  |--- preprocessed_data.csv
|  |--- raw_data.csv
|
|--- flask_app
|  |--- inputs
|  |  |--- inputs_flask_app_dict.pkl
|  |
|  |--- templates
|  |  |--- index.html
|  |  |--- results.html
|  |
|  |--- static
|  |
|  |--- app.py
|
|--- models
|  |--- feature_preprocessing
|  |--- feature_selection
|  |--- model_selection
|  |--- objects_FINAL
|
|--- plots
|--- Masters_Thesis.ipynb
|--- README.md
|--- requirements.yml
```

*Source:* Author's results at GitHub

- `data` - directory containing the raw data, partially preprocessed data (`interim`) and the final preprocessed data.
- `flask_app` - directory containing the Flask application which is used for the deployment of the model. Particularly, it contains the `app.py` file which is the main back-end file of the application, the `templates` and `static` subdirectories which contain the front-end HTML files for the application, and the `inputs` subdirectory which contains the input dictionary for the application (such as the trained model, threshold, final features etc.).
- `models` - directory containing the the subdirectories of the trained and fitted objects for features preprocessing, feature selection and model selection, including the final objects used in deployment.
- `plots` - directory containing the plots generated within the main Python notebook.

- `Masters_Thesis.ipynb` - main Python notebook containing the main part of the machine learning Implementation, such as exploratory analysis, data preprocessing, training and evaluation of the models.
- `README.md` - README file containing the description of the repository.
- `requirements.yml` - file containing the list of the required packages and their specific versions used in this project.

This particular solution is developed in Python version 3.10.9 and these are the main packages and modules used in this project:

- `NumPy`, `Pandas` - for data manipulation and analysis.
- `Matplotlib`, `Seaborn` - for data visualization.
- `Scipy` - for statistical analysis.
- `OptBinning` - for optimal binning of features with respect to the target.
- `ImbLearn` - for handling imbalanced data using oversampling.
- Scikit-learn - for feature selection, model selection and model evaluation.
- Scikit-optimize - for more advanced hyperparameter optimization.
- Flask - for deployment of the model as web application.

To replicate this solution, one may download this repository as a zip file or either can clone this repository using Git to the local repository. Before running any files or scripts, it is important to set the environment for such project using the file `requirements.yml`. This can be done by running the following command in the Anaconda terminal which will create the new environment with the name `FFU_VSE_Masters_Thesis` and install all the required packages:

```
>> conda env create -n FFU_VSE_Masters_Thesis -f requirements.yml
```

Be aware of your current path directory in your terminal. In order to install the file `requirements.yml`, you need to define a path to the directory, where such file is located. To achieve this, the user has to either change the path in the terminal using `cd` command, insert the path directory before the `requirements.yml` in terminal, or to copy the file `requirements.yml` to the current path directory. The following code shows the former approach:

```
>> cd C:\Users\ngnpe\FFU_VSE_Masters_Thesis_ML_Credit_Risk_Modelling
>> conda env create -n FFU_VSE_Masters_Thesis -f requirements.yml
```

To preserve the reproducibility of this solution and conistency of the results, the random seed is instantiated to `42`, so for instance data split, model optimization or training would be deterministic and not totally random everytime when replicating the solution.

Some `Scikit-learn` or `Scikit-optimize` objects have optional argument `n_jobs` which utilizes the number of CPU cores used during the parallelizing computation. Such argument was set to `-1`, hence all the processors are used in order to speed up the training or optimization process.

## 3.2 Data Exploration

This section is focused on exploration of the analyzed loan dataset, particularly on dataset description, distribution analysis and association analysis, in order to infer potential valuable insights and hypotheses which can be used in the preprocessing or modelling part.

### 3.2.1 Dataset Description

The analyzed dataset pertains to the HMEQ dataset which contains loan application information and default status of 5,960 US home equity loans. Such dataset was acquired from Credit Risk Analytics platform. Since this dataset regards the loan application scoring data, using macroeconomic or other external data is omitted due to the dataset characteristics as well as modelling with behavioral scoring. Thus our goal is to predict whether the loan applicant will or would default based on provided information from the loan application.

As can be seen in Table 3.1, the dataset contains 13 columns, 12 features and 1 target variable `BAD` indicating whether the loan was in default (`1`) or not (`0`). Amongst the 12 features, there are 10 numeric features and 2 categorical features, namely `REASON` which contains 2 categories - Debt consolidation (`DebtCon`) and Home improvement (`HomeImp`), and `JOB` which fontains following categories - Administration (`Office`), Sales, Manager (`Mgr`), Professional Executive (`ProfExe`), Self-employed (`Self`), and Other.

Table 3.1: Dataset columns

| Columns | Description | Data type |
|---|---|---|
| BAD | Default status | Boolean |
| LOAN | Requested loan amount | numeric |
| MORTDUE | Loan amount due on existing mortgage | numeric |
| VALUE | Value of current underlying collateral property | numeric |
| REASON | Reason of loan application | categorical |
| JOB | Job occupancy category | categorical |
| YOJ | Years of employment at present job | numeric |
| DEROG | Number of derogatory public reports | numeric |
| DELINQ | Number of delinquent credit lines | numeric |
| CLAGE | Age of the oldest credit line in months | numeric |
| NINQ | Number of recent credit inquiries | numeric |
| CLNO | Number of credit lines | numeric |
| DEBTINC | Debt-to-income ratio | numeric |

*Source:* `http://www.creditriskanalytics.net/datasets-private2.html`

After the initial data inspection, data does not contain any duplicates but does contain missing values, which are summarized in Table 3.2. Most of the missing values contains the feature `DEBTINC` with 1,267 missing observations, whereas columns indicating default status (`BAD`) or requested loan amount (`LOAN`) do not contain any missing values, which is expected as the bank should have the available information about their loans whether they have defaulted or not, and since this dataset pertains to the application scoring, when applying for a loan, an applicant should always fill out the requested loan amount.

Table 3.2: Missing Values Summary

| Columns | # NA's | % NA's |
|---|---|---|
| BAD | 0 | 0.00 % |
| LOAN | 0 | 0.00 % |
| MORTDUE | 518 | 8.69 % |
| VALUE | 112 | 1.88 % |
| REASON | 252 | 4.23 % |
| JOB | 279 | 4.68 % |
| YOJ | 515 | 8.64 % |
| DEROG | 708 | 11.88 % |
| DELINQ | 580 | 9.73 % |
| CLAGE | 308 | 5.17 % |
| NINQ | 510 | 8.56 % |
| CLNO | 222 | 3.72 % |
| DEBTINC | 1267 | 21.26 % |

*Source:* Author's results in Python

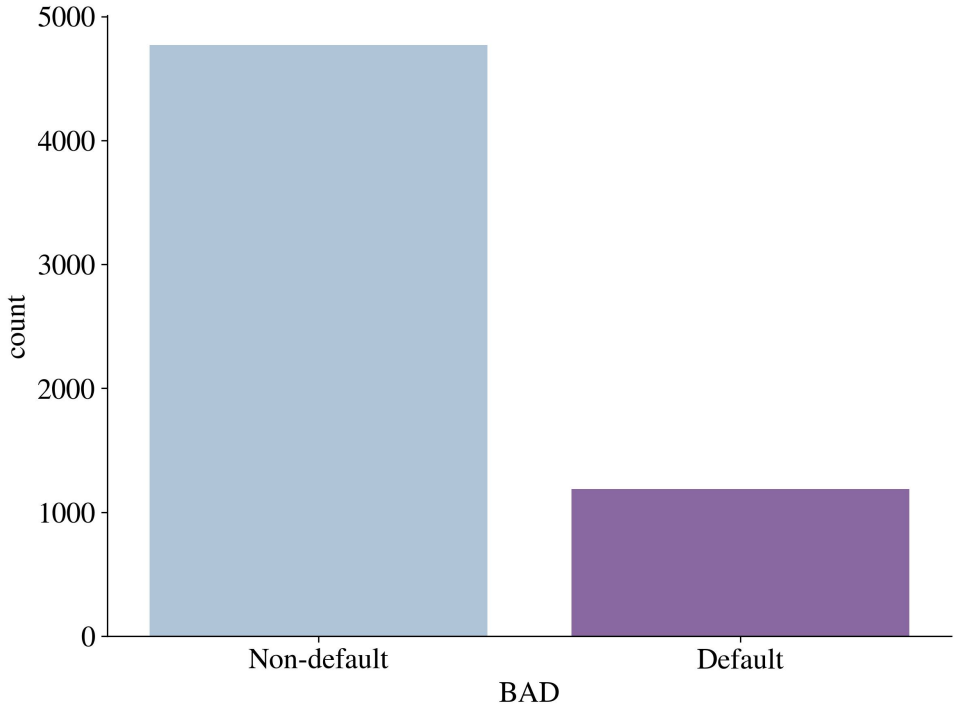
### 3.2.2 Distribution Analysis

In this subsection, we inspect the distribution of our variables, including the target variable and the features. Such distribution inspection may help us to identify potential outliers, missing values, and other potential issues with the dataset.

#### Default Distribution

Regarding the the target variable distribution, from the Figure 3.3 we can observe that the default status distribution is heavily imbalanced, as most of the loans have not defaulted yet. Particularly, 80.05% of the observations have been labelled as non-default (4,771 observations) and 19.95% observations labelled as default (1,189 observations). This may cause problems in the modelling part, as the model may be biased towards the majority class, i.e., the non-default class. Such imbalanced class issue will be further treated in Subsection 3.3.1.

Figure 3.3: Default status distribution




*Source:* Author's results in Python

### Numeric Features' Distribution

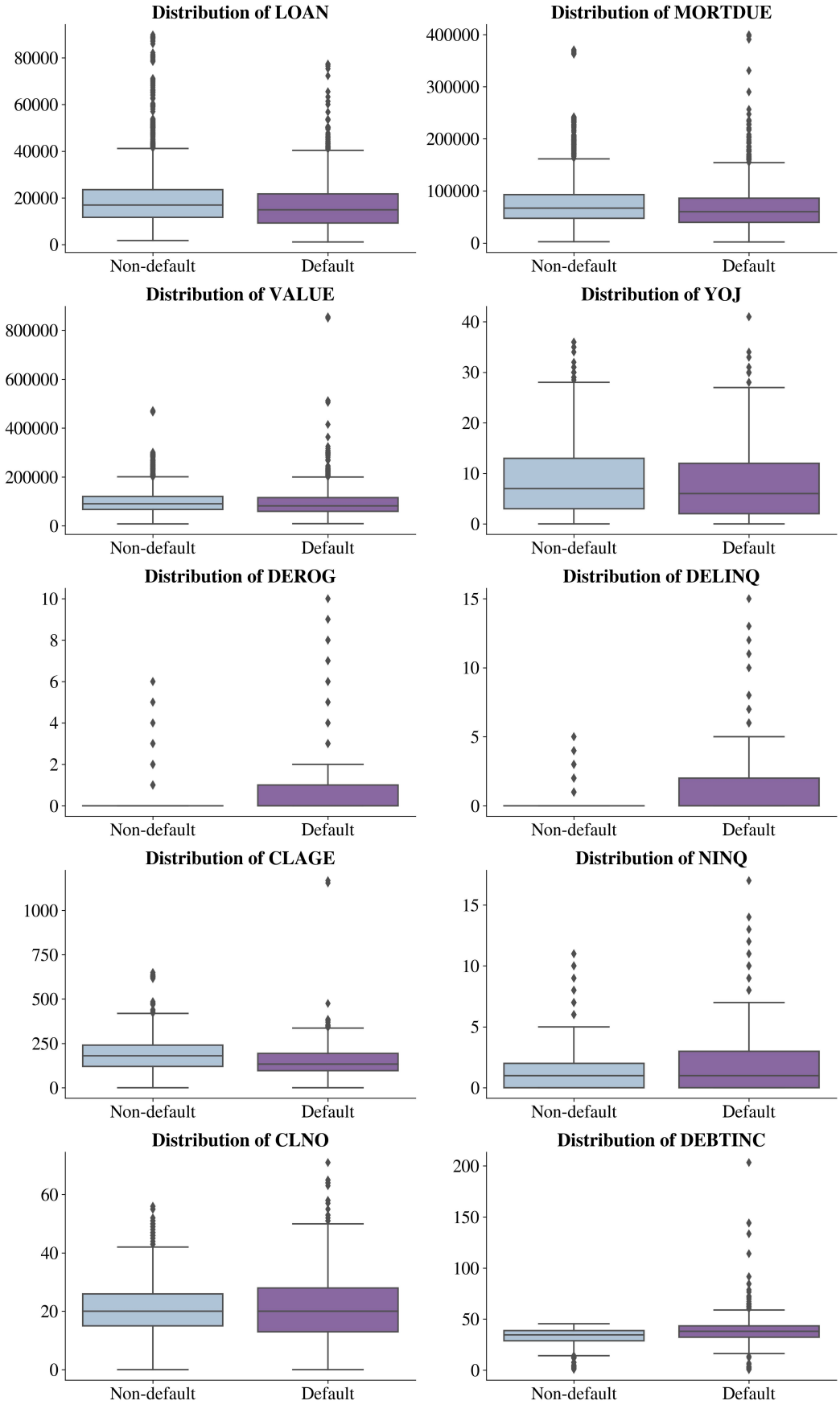
Regarding the numeric features, it can be observed that most of them exhibit a positive skewness and contain outliers, as illustrated in Figure 3.4, which depicts the conditional distribution of the numeric features with respect to the default status via boxplots.

All the outliers appear to be valid, indicating that they have not arisen due to data entry errors. This can be attributed to the non-negative nature of all the numeric features, which makes it impossible to have negative values for features such as the number of years at present job or the number of delinquent credit lines, among others. Additionally, the maximum values of the given features are not unrealistically high, further corroborating the validity of the outliers. However, it is necessary to treat these outliers as they can bias a model's weights or coefficients, particularly in the case of logistic regression or neural networks. Outliers can also jeopardize distance calculations in the case of KNN, or in general, affect the position and orientation of the decision boundary. Such factors can lead to overfitting and inaccurate and biased predictions. A detailed explanation of the outlier treatment is provided in Subsection 3.3.2.

Concerning the target variable, it can be observed that there are some dif-

ferences in the distribution shapes of DEROG and DELINQ, which exhibit less skewness and lower dispersion for non-default cases as compared to default cases. Since both features indicate negative information about delinquency, it is expected that a higher value for these features would increase the likelihood of loan default. Referring to the feature DEBTINC, it does not exhibit any extreme values for non-default cases, but some extreme values are present for default cases. From this, it can be inferred that if the debt-to-income ratio is too high, indicating that the applicant's income is not sufficient to cover their debt, the loan is more likely to end in default. The association between the default status and the numeric features is further investigated in Section 3.2.3.

Figure 3.4: Conditional distribution of numeric features




*Source:* Author's results in Python

Due to the fact that the boxplots do not capture the missing values occurred in given features, it is also important to inspect the numbers and proportions of missing values in each feature, conditional on the default status. As can be seen in Table 3.3, $n_0$ refers to the number of missing values in given feature for non-default cases, $n_1$ refers to the number of missing values in given feature for default cases. $N_0$ and $N_1$ refer to the total number non–default cases and default cases respectively, therefore $n_0/N_0$ refers to the proportion of missing values in given feature for non-default cases, and $n_1/N_1$ refers to the proportion of missing values in given feature for default cases.

Pertaining to the feature `DEBTINC`, we can observe a significant difference in the number of missing values between the default and non-default cases. Out of all defaulted loans, 66.11 % had missing debt–to–income ratio, whereas only 10.08 % out of all non-defaulted loans had missing debt–to–income ratio. Therefore, there could be a strong association between the missing debt–to–income ratio and the default.

Similarly, the table depicts a significant difference with respect to `VALUE` as 0.15 % had missing collateral property value out of all non–defaulted loan, and 8.92 % defaulted loans had missing collateral property value. It can be inferred that loan applicants who withhold information on their collateral property value or debt-to-income ratio are more likely to default on their loans. This may be due to negative information that they are trying to conceal, such as an excessively high debt or low income, or a low collateral property value. Such associations are further investigated in Section 3.2.3.

Table 3.3: Numeric features NA's table

| **Feature** | $n_0$ | $n_1$ | $n_0/N_0$ | $n_1/N_1$ |
|---|---|---|---|---|
| LOAN | 0 | 0 | 0 % | 0 % |
| MORTDUE | 412 | 106 | 8.64 % | 8.92 % |
| VALUE | 7 | 105 | 0.15 % | 8.83 % |
| YOJ | 450 | 65 | 9.43 % | 5.47 % |
| DEROG | 621 | 87 | 13.02 % | 7.32 % |
| DELINQ | 508 | 72 | 10.65 % | 6.06 % |
| CLAGE | 230 | 78 | 4.82 % | 6.56 % |
| NINQ | 435 | 75 | 9.12 % | 6.31 % |
| CLNO | 169 | 53 | 3.54 % | 4.46 % |
| DEBTINC | 481 | 786 | 10.08 % | 66.11 % |

*Source:* Author's results in Python

### Categorical Features' Distribution

Regarding the distribution of categorical features, the dataset includes 2 nominal features, namely `REASON` and `JOB`. The conditional distribution of categorical features on the default status is visualized using barplots in Figure 3.5. The plot indicates that most loan applicants applied for debt consolidation, while most job occupancies were labeled as `Other`.

With respect to the default status, there appears to be no significant difference between the default and non-default cases in terms of the relative distribution of the `REASON` feature. However, a slight difference is observed between the default and non-default cases in terms of the relative distribution of the `JOB` feature. Specifically, the categories `Office`, `ProfExe`, and `N/A` exhibit a relatively higher proportion of non-default cases than default cases. Hence, a moderate association between the `JOB` feature and the default status is possible, as further investigated in Section 3.2.3.

Figure 3.5: Conditional distribution of categorical features


*Source:* Author's results in Python

### 3.2.3 Association Analysis

In this subsection, we aim to examine potential relationships between the variables by analyzing their associations. Firstly, we investigate the association between the default status and the features. Subsequently, we explore the association among the features themselves.

#### Association between default status and numeric features

To measure the association between the target variable and the numeric features, we use the Point-Biserial correlation coefficient, which is the Pearson's product moment correlation coefficient between a continuous variable and a dichotomous variable (Kornbrot 2014). This coefficient ranges from -1 to +1

and can be used to assess the strength and direction of the relationship between a continuous variable and a binary variable. The formula for computing this coefficient is as follows:

$$r_{pb,X} = \frac{\mu\left(X|Y=1\right) - \mu\left(X|Y=0\right)}{\sigma_X} \sqrt{\frac{N\left(Y=1\right) \times N\left(Y=0\right)}{N\left(N-1\right)}} \tag{3.1}$$

Here, $\mu\left(X|Y=1\right)$ and $\mu\left(X|Y=0\right)$ represent the means of the given numeric feature $X$ conditional on the default status and non-default status, respectively, while $\sigma_X$ denotes the standard deviation of $X$. The values of $N\left(Y=1\right)$ and $N\left(Y=0\right)$ indicate the number of observations with default status and non-default status, respectively, and $N$ represents the total number of observations within the feature $X$.

The following Table 3.4 displays the computed Point-Biserial coefficient for each numeric feature with respect to the default status, along with its statistical significance. The results show that features such as `DEROG`, `DELINQ`, and `DEBTINC` are moderately and positively associated with the default status at the 1% statistical significance level. These findings support the observations made in Section 3.2.2 regarding the positive associations of these features with the default status. It can be inferred that these features may serve as important predictors in the model.

Table 3.4: Point–Biserial Correlation table

| **Feature** | **Coefficient** | **Significance** |
|---|---|---|
| LOAN | -0.075 | *** |
| MORTDUE | -0.048 | *** |
| VALUE | -0.030 | ** |
| YOJ | -0.060 | *** |
| DEROG | 0.276 | *** |
| DELINQ | 0.354 | *** |
| CLAGE | -0.170 | *** |
| NINQ | 0.175 | *** |
| CLNO | -0.004 | |
| DEBTINC | 0.200 | *** |

*: $p < 0.10$, **: $p < 0.05$, ***: $p < 0.01$

*Source:* Author's results in Python

### Association between default status and categorical features

In order to measure the strength of the relationship between the dichotomous default status and categorical variables, we employ Cramer's V, which ranges from 0 to 1 and is defined as:

$$CV_X = \sqrt{\frac{\chi^2}{N\,(k-1)}} \tag{3.2}$$

As noted in Section 3.2.2, the association between the default status and `REASON` is weak, as evidenced by the Cramer's V value being close to zero. Conversely, the association between the default status and `JOB` is slightly stronger, as the categories `Office`, `ProfExe`, and `N/A` exhibit a higher proportion of non-default cases than default cases. Both `REASON`'s and `JOB`'s associations with default status are statistically significant at the 1% significance level.

While statistical significance is important, it does not necessarily indicate that a feature is a strong predictor of the target variable. Ultimately, the usefulness of a feature in predicting the target variable is determined by the performance metrics of the model.

Table 3.5: Cramer's V Association table

| **Feature** | **Coefficient** | **Significance** |
|---|---|---|
| REASON | 0.038 | *** |
| JOB | 0.120 | *** |

*: $p < 0.10$, **: $p < 0.05$, ***: $p < 0.01$

*Source:* Author's results in Python

### Association between default status and missing values

Given that the loan dataset contains missing values, it is necessary to examine whether the missingness is associated with the default status. One possible approach is to encode the feature with missing values as a binary variable, where 1 indicates the presence of a missing value and 0 otherwise.

To quantify the strength of association between the two binary variables, the Phi coefficient is used, which is defined as:

$$\phi_X = \sqrt{\frac{\chi^2}{n}} \tag{3.3}$$

In line with the finding regarding the `DEBTINC` and `VALUE` in Section 3.2.2, there is a strong and statistically significant association between the missing debt-to-income ratio and default status, and a moderate and statistically significant association between the missing collateral property value and default status, as shown in Table 3.6. Therefore, we can anticipate that these features will be crucial indicators in default prediction. Further details on feature selection are presented in Subsection 3.4.2.

Table 3.6: Phi Correlation Coefficient table

| **Feature** | **Coefficient** | **Significance** |
|---|---|---|
| LOAN | 0.000 | |
| MORTDUE | 0.003 | |
| VALUE | 0.254 | *** |
| REASON | 0.004 | |
| JOB | 0.064 | *** |
| YOJ | 0.056 | *** |
| DEROG | 0.070 | *** |
| DELINQ | 0.061 | *** |
| CLAGE | 0.030 | ** |
| NINQ | 0.039 | *** |
| CLNO | 0.018 | |
| DEBTINC | 0.547 | *** |

*: $p < 0.10$, **: $p < 0.05$, ***: $p < 0.01$

*Source:* Author's results in Python

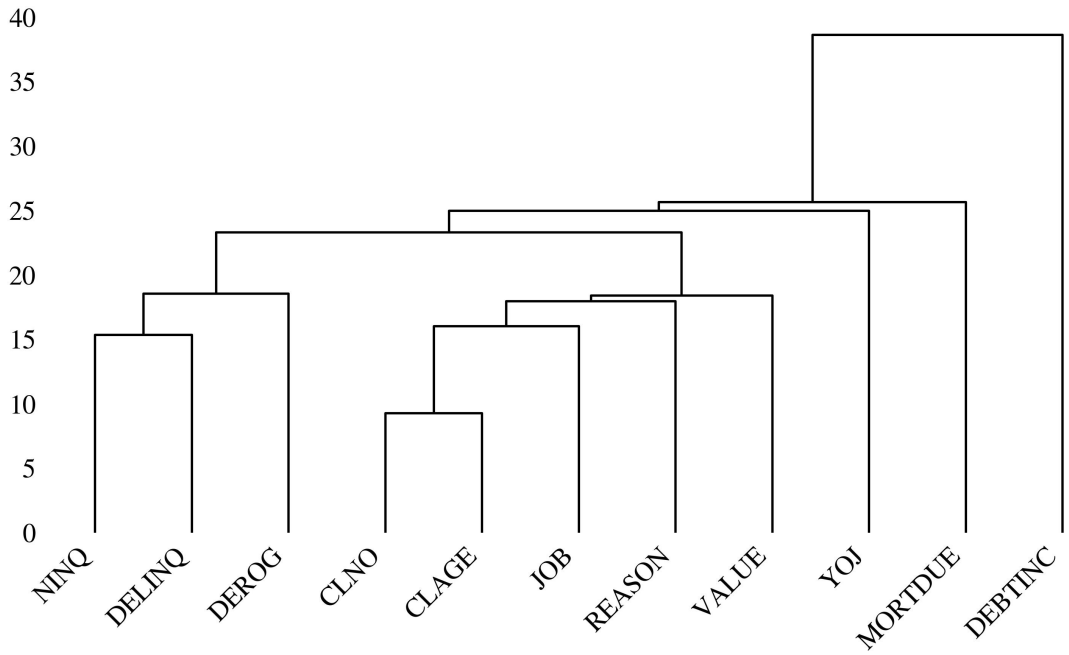
### Missing Values Association

Additionally, it is imperative to investigate the relationship between missing values and default status, as well as the interrelationship between the missing values themselves. A common approach to identifying patterns of missing data in a dataset is through the use of a dendrogram, which clusters variables hierarchically based on the occurrence of missing values. This method groups variables into clusters based on the similarity of their missing value patterns, such that variables with comparable patterns of missingness are clustered to-

gether. Conversely, variables with dissimilar patterns of missingness are placed in separate clusters. The dendrogram is constructed by merging the two closest clusters iteratively until all variables are in the same cluster. The distance between the clusters at each step of the merging process is shown on the y-axis of the dendrogram, and the order in which the variables are merged is displayed on the x-axis.

In Figure 3.6, the hierarchical clustering of the dataset's variables is illustrated, excluding the default status and requested loan amount feature `LOAN`, as these variables do not contain any missing values. As depicted in the dendrogram, the `CLNO` and `CLAGE` features have the most similar patterns of missing values occurrences. Therefore, it can be inferred that a significant number of loan applicants tend to omit information regarding their number of credit lines (`CLNO`) and the age of their most recent credit line (`CLAGE`) when submitting their loan applications.

Figure 3.6: Nullity dendrogram




*Source:* Author's results in Python

### Multicolinearity Analysis

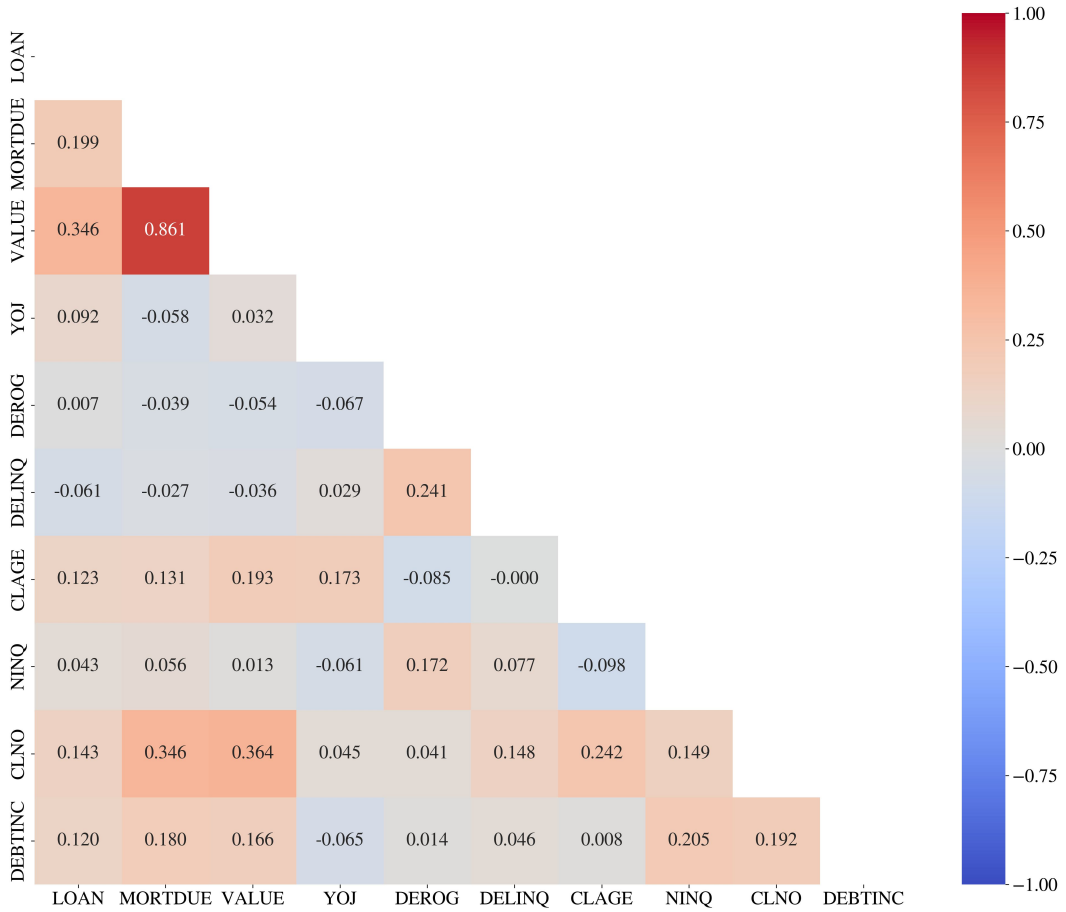
To quantify the association between the numerical features, Pearson correlation coefficient is often used. However, it is highly sensitive to outliers and makes assumptions regarding the normal distribution and linear relationship

between variables. Consequently, Spearman correlation coefficient is utilized as an alternative, as it is a non-parametric measure that does not make any assumptions regarding the distribution of variables or the linearity of their relationship. The Spearman correlation coefficient is defined as follows:

$$\rho_{spearman} = 1 - \frac{6 \sum_{i=1}^{n} d_i^2}{n\left(n^2 - 1\right)} \tag{3.4}$$

In the Figure 3.7, we can observe a very strong correlation between the `MORTDUE` and `VALUE` features. Such multicolinearity can cause problem in predictions na model's overfitting. Therefore, a feature selection is recommended - such selection is further described in Subsection 3.4.2.

Figure 3.7: Spearman Correlation Matrix




*Source:* Author's results in Python

## 3.3 Data Preprocessing

In this section, the process of preprocessing data is described as the crucial step in the machine learning modelling. Particularly, the following is described:

- Splitting the data
- oversampling,
- discretization,
- Weight–of–Evidence encoding.

### 3.3.1 Data Split and ADASYN Oversampling

To ensure appropriate model training and unbiased evaluation, it is necessary to split data into separate sets for various purposes. Specifically, the data was split into three sets with the ratio of 70:15:15:

- Training set for model training, feature selection, and hyperparameter tuning;
- Validation set for selecting the best final model;
- Test set for the final evaluation of the best final model.

The data is split using stratified split to preserve the default status distribution, which was highly imbalanced. Stratification ensures that the distribution of defaults and non-defaults remains the same across all sets, thereby avoiding overfitting and data leakage. Using stratification, each set had 80 % non-defaults and 20 % defaults. This method enables accurate prediction since the model is trained and evaluated on the same population (Igareta 2021).

#### ADASYN Oversampling

However, stratification alone may not be sufficient for dealing with imbalanced classes. One would use random undersampling or random oversampling to deal with the class imbalanced issue. The former randomly eliminates majority class instances whereas the latter randomly duplicates minority class instances. However, both have particular drawbacks, as the random undersampling may lead to a a significant loss of information, and random oversampling is lead to the high degree of repetation of minority instances. Both

then could lead to model's overfitting and detoriation in model's performance (Ma & He 2013). This might be a significant issue when the target variable distribution is heavily imbalanced - assume that we have a dataset of 1,000 instances where 990 instances belongs to majority class and 10 instances to minority class. If we perform random undersampling in order to balance the target variable distribution, we would have to remove 980 instances and end up with undersampled dataset of 20 instances, which is not acceptable for model training. On the other hand, if we perform random oversampling, we would end up with 1,980 instances, where 980 instances would be the same as in the original dataset, which would lead to the model's overfitting.

Therefore, the Adaptive Synthetic Sampling (henceforth ADASYN) technique is used for oversampling the minority class. ADASYN generates synthetic instances of the minority class based on the nearest neighbors of the minority class instances. Such approach is more effective than Synthetic Minority Oversampling Technique (henceforth SMOTE) which also uses nearest neighbors to generate synthetic instances of minority class, as it generates more synthetic instances which are hard–to–learn by K-Nearest Neighbors given the density distributtions, whereby SMOTE generates synthetic instances uniformly for each minority instance. (He *et al.* 2008). In other words, ADASYN generates more synthetic instances in regions where the density of the majority class within $K$ nearest neighbors of minority instance is higher and fewer synthetic instances in regions where the density is lower, thereby ADASYN focuses on generating more hard–to–learn minority instances. Thereby, it makes easier for the machine learning model to learn the decision boundary between the minority and majority classes and boost the model's performance by focusing on hard–to–learn instances (He *et al.* 2008). The oversampling is performed on the training set only after the split to avoid data leakage and biased evaluation.

Before oversampling algorithm's execution, first we need to calculate the number of instances of minority class to be synthetically generated in order to balance the target variable distribution. The number of instances to be generated $G$ is calculated as follows:

$$G = (m_l - m_s) \times \beta \tag{3.5}$$

where $m_l$ is the number of majority class instances, $m_s$ is the number of minority class instances and $\beta$ indicates the desired ratio between the numbers of

majority and minority class instances after oversampling.

Then for each minority class instance $x_i$, using K-nearest Neighbors with Euclidean distance calculate the ratio $r_i$ as:

$$r_i = \frac{\delta_i}{K} \tag{3.6}$$

where $\delta_i$ is the number of majority class instances within the $K$ nearest neighbors of $x_i$. In such case, higher $r_i$ indicates dominance of the majority class in given specific neighbourhood of $x_i$ (Nian 2018). Subsequently, all the $r_i$ ratios are normalized as:

$$\hat{r}_i = \frac{ri}{\sum_{i=1}^{m_s} r_i} \tag{3.7}$$

In such way that sum of all the normalized $\hat{r}_i$ ratios is equal to 1. Hence, we can denote $\hat{r}_i$ as the density distribution.

$$\sum_{i=1}^{m_s} \hat{r}_i = 1 \tag{3.8}$$

Finally, the oversampling process is initialized. For each minority class instance $x_i$, calculate the number of instances to be synthetically generated based on the respective density distribution $\hat{r}_i$ and the total number of instances to be synthetically generated $G$. Thus, for the minority classes with higher density, it generates more synthetic instances, since those instances are hard–to–classify by the K-Nearest Neighbors.

$$G_i = G \times \hat{r}_i \tag{3.9}$$

Further, for each minority class instance $x$, generate $G_i$ synthetic instances $s_i$ as follows:

$$s_i = x_i + (x_{zi} - x_i) \times \lambda \tag{3.10}$$

where $x_{zi}$ represents the radnomly chosen minority class instance within the $K$ nearest neares neighbors for $x_i$, and $\lambda \in [0, 1]$ is a random number.

The following Table 3.7 shows the default distribution of the individual sets before and after oversampling. The training set after ADASYN oversampling was balanced, while the default distribution remained the same across the validation and test sets before and after oversampling, which is desirable due to

stratification.

Table 3.7: WoE distribution

| Set | # instances | % defaults | % non–defaults |
|---|---|---|---|
| Training | 4,171 | 19.95 % | 80.05 % |
| Training (oversampled) | 6,437 | 48.13 % | 51.87 % |
| Validation | 895 | 20.00 % | 80.00 % |
| Test | 894 | 20.00 % | 80.00 % |

*Source:* Author's results in Python

In Python, the data are divided and oversampled using a custom function `data_split()`. This function first employs the `train_test_split()` function from the `scikit-learn` module to split the data into training, validation, and test sets with a stratification technique. Next, the `ADASYN()` class from the `imblearn` module is used to oversample the training set. This is achieved by generating synthetic instances of the minority class based on the five nearest neighbors and Euclidean distance.

However, the `ADASYN()` class from `imblearn` is not designed to handle missing values or categorical features encoded as character. To overcome this limitation, the following approach is taken:

1. Separate the categorical and numeric features;
2. Impute the missing values with arbitrary values:
   - Categorical features: string `'N/A'`;
   - Numeric features: number `99999999999999` - such value is chosen since it is highly unlikely to be present in the dataset.
3. Convert the categorical features into dummy variables;
4. Join the numeric features with the dummy variables;
5. Perform the oversampling on the joined dataset;
6. Convert the dummy variables back into categorical features;
7. Retrieve back the missing values:
   - Categorical features: replace string `'N/A'` with `np.nan`;

- Numeric features: for each feature $X$ if its value exceeds the original maximum value, then replace it with `np.nan`;[1]

**ADD IMPACT OF OVERSAMPLING ON FEATURES DISTRIBUTION**

### 3.3.2 Optimal Binning and Weight–of–Evidence

In the context of data preprocessing, it is crucial to consider the most appropriate feature transformation method that optimizes the performance of machine learning models. Although common approaches such as dummy encoding, standardization, logarithmic transformation, and normalization are widely used, they may not always be suitable for a given dataset due to the presence of certain characteristics. For instance, dummy encoding may not be suitable for categorical features with a large number of categories as it could lead to the curse of dimensionality. Standardization may not be appropriate for features with a large number of outliers as it may result in a loss of information. Similarly, logarithmic transformation may not be appropriate for features with a large number of zeros, and normalization may not be suitable for features with a significant number of outliers.

Therefore, alternative approaches such as discretization or binning are increasingly being used. This approach enables the identification of outliers within bins, which is not feasible with standardization or normalization. Additionally, discretization can capture missing values without requiring the removal or imputation of such values. As a result, binning is a more flexible and versatile feature transformation method that can effectively handle different types of datasets and is particularly useful in cases where other methods may not be appropriate.

In this thesis, we employ the `BinningProcess` from the `optbinning` module in Python for an optimal binning of both numeric and categorical features. This approach involves grouping the values of a continuous variable into discrete intervals, or "bins", based on their relationship with the target variable. Similarly, for categorical features, the approach involves grouping the categories based on their relationship with the target variable. The optimal binning is performed with the objective of achieving maximum separation between the

[1]The theory behind this ADASYN will be described later.

classes of the target variable within each bin. This is done to ensure that the bins are highly informative with respect to the target variable, and that each bin contains a meaningful range of values. Furthermore, the resulting bins are encoded into numeric values using the Weight-of-Evidence (WoE) approach. The WoE is a commonly used measure of the strength of association between a binary target variable and an independent variable. It is calculated as

$$WoE_{X,b} = \ln\left(\frac{\Pr\left(X = b \mid Y = 0\right)}{\Pr\left(X = b \mid Y = 1\right)}\right) \tag{3.11}$$

he following Figure 3.8 depicts the distribution of Weight-of-Evidence (WoE) bins for each feature. It can be observed that binning captures either linear, non-linear, monotonic, or non-monotonic relationships between the default status and the numeric features in terms of WoE. Regarding the `DELINQ` feature, a monotonic relationship can be observed, where the higher number of delinquent credit lines, the lower the WoE coefficient, indicating a larger distribution of defaults with respect to non-defaults in the given bin. Thus, the higher the number of delinquent credit lines, the higher the likelihood of defaulting in terms of WoE.

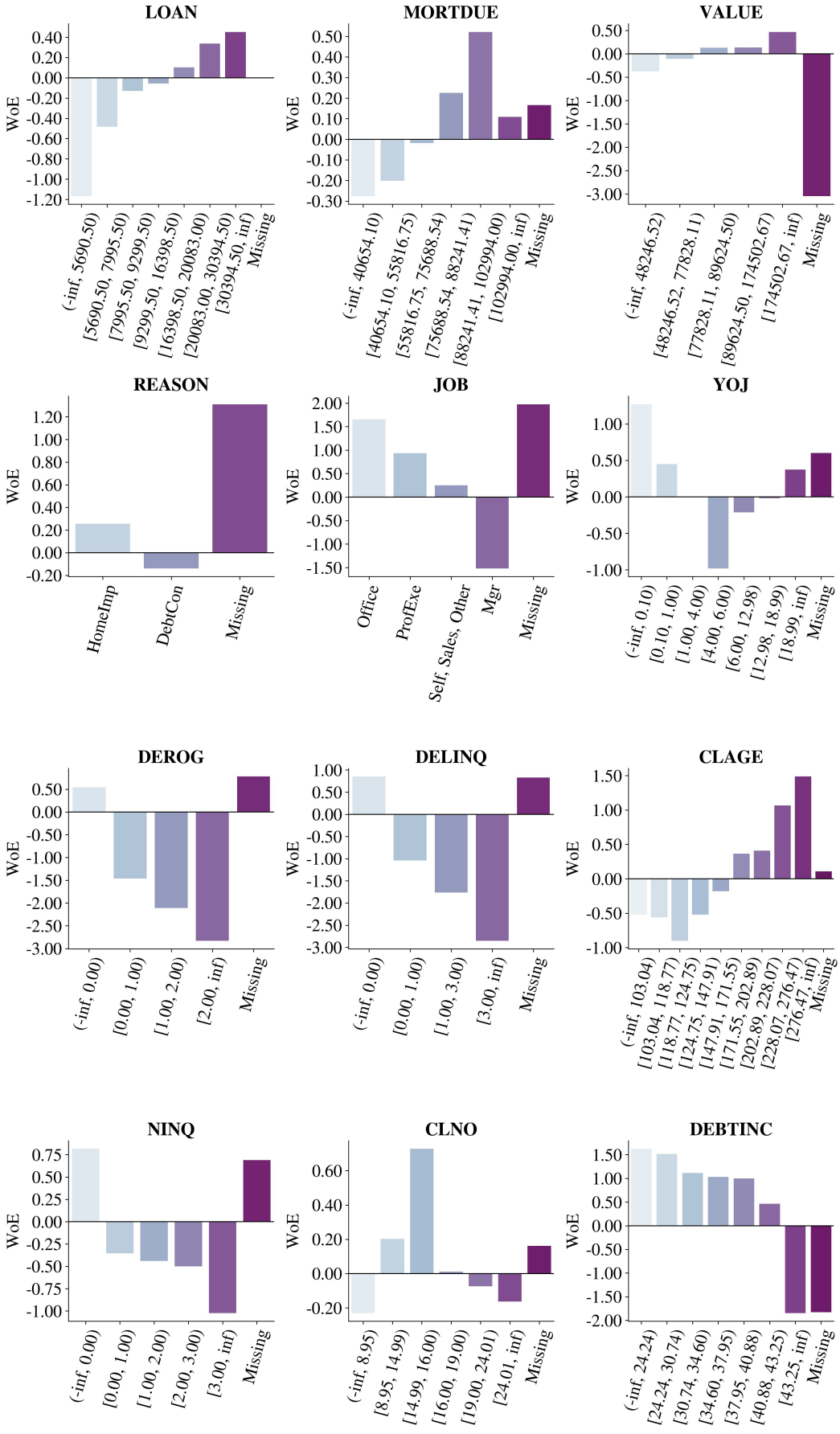
A non-linear relationship can be observed with respect to the `YOJ` feature, where the WoE coefficient is positive for applicants who have recently started working at their new job (i.e., number of years at the present job is less than 1) and for applicants who have been working at their current job for a relatively long time (i.e., number of years at the present job is higher than 19). Thus, applicants who have been working for a longer time have stable income and are more creditworthy and less likely to default. Regarding applicants who have recently started working at their new job, it is possible that they are less likely to default since the `YOJ` feature does not capture the applicant's total number of years of work experience, but only the number of years at the present job. Thus, in the given dataset, applicants who have recently started working at their new job have a relatively higher total number of years of work experience, making them more creditworthy and less likely to default. On the other hand, for applicants who have been working at their present job between 1 and 19 years, the WoE coefficient is negative. This relationship seems to be complex and can be influenced by other factors not present in the dataset, such as the applicant's age, total number of years of work experience, education, etc.

Both numeric and categorical features contain a separate bin capturing miss-

ing values, which can be a useful indicator when training a model. This is evident in the DEBTINC feature, where the bin capturing missing values has the most negative WoE coefficient, indicating that there is a larger distribution of defaulters compared to non-defaulters. This finding was already raised in Section 3.2.3 in terms of the strong and statistically significant association between the default status and the missing values in DEBTINC.

However, inconsistencies can also be observed in terms of distributions from exploratory analysis and the WoE coefficient distributions. One example pertains to the Mgr category in the JOB feature, where the WoE coefficient is substantially negative, indicating that among managers, there is a larger distribution of defaulters compared to non-defaulters. However, this was not observed in the distribution analysis of categorical features (Section 3.2.2), where the relative distributions conditional on the default status do not differ too much in terms of the Mgr category. This is a result of ADASYN oversampling, which synthetically replicates minority instances, especially those instances that are hard-to-learn. Hence defaulted loans that managers have applied for are difficult to learn, and ADASYN balances default distribution by generating default instances having JOB equal to Mgr, which results in an increase in the number of instances having JOB equal to Mgr, i.e., a larger distribution of defaulters in the Mgr bin, and therefore a negative WoE coefficient.

Figure 3.8: WoE Bins Distribution




*Source:* Author's results in Python

## 3.4 Modelling

Once the data are finally preprocessed, the next step regards the modelling part which includes hyperparameter tuning, feature selection, model selection and model building.

In Python, 8 different machine learning models from `Scikit-learn` module are used for the default status prediction, which are:

- Logistic Regression - `LogisticRegression()`,
- Decision Tree - `DecisionTreeClassifier()`,
- Gaussian Naive Bayes - `GaussianNB()`,
- K-Nearest Neighbors - `KNeighborsClassifier()`,
- Random Forest - `RandomForestClassifier()`,
- Gradient Boosting - `GradientBoostingClassifier()`,
- Support Vector Machine - `SVC()`,
- Neural Network - `MLPClassifier()`.

### 3.4.1 Hyperparameter Bayesian Optimization

In order to enhance a model's performance, it is recommended to select optimal hyperparameter values instead of relying on default hyperparameters. Grid Search and Random Search are commonly used methods for hyperparameter tuning, however, they are computationally expensive and do not guarantee to find the global optimum. Additionally, they do not consider any information from previous iterations and rather check all possible hyperparameter combinations or randomly select hyperparameter combinations, respectively.

To overcome these limitations, Bayesian Optimization is used as a hyperparameter tuning approach. This method employs a probabilistic model using a Gaussian Process to approximate the objective function of interest. By utilizing Bayesian inference, the approach updates the prior distribution over hyperparameter values based on the results of previous iterations and uses the resulting posterior distribution to guide the selection of the next set of hyperparameters to evaluate. In summary, Bayesian Optimization provides a more efficient and effective approach to hyperparameter tuning compared to Grid Search and Random Search, by utilizing prior information and Bayesian inference to guide the

selection of hyperparameters to evaluate. *Theory behind Bayesian Optimization will be described later.*

In Python, a custom function, `bayesian_optimization()`, is implemented to perform hyperparameter tuning using Bayesian Optimization. This function utilizes `BayesSearchCV` class from the `Scikit-optimize` module, with a 10-fold stratified cross-validation scheme and 50 iterations, while maximizing the F1 score. For each model, the Bayesian Optimization algorithm performs 50 iterations, searching for the best hyperparameters values that maximize the F1 score. Within each iteration, a 10-fold stratified cross-validation is conducted to evaluate the model's F1 score.

The use of `BayesSearchCV` with stratified cross-validation in the hyperparameter tuning process provides a robust and reliable approach to selecting the optimal hyperparameters for the model, while the incorporation of Bayesian Optimization enables the efficient exploration of the hyperparameter space. By maximizing the F1 score, the hyperparameters selected through this process will result in a model with improved performance for the classification task at hand.

The hyperparameter space is defined for each model as follows( *The individual hyperparameters will be later described in the theory part*):

### Logistic Regression

Table 3.8: Logistic Regression - Hyperparameter Space

| **Hyperparameter** | **Space** |
|---|---|
| Intercept | True, False |
| $C$ factor | $<1 \times 10^{-6}$, 5> |
| Penalty | L1, L2, Elastic Net, None |
| Solver | lbfgs, liblinear, newton-cg, sag, saga |
| Class weight | None, balanced |
| L1 ratio | <0, 1> |
| Intercept scaling | True, False |

*Source:* Author's results in Python

### Decision Tree

Table 3.9: Decision Tree - Hyperparameter Space

| **Hyperparameter** | **Space** |
|---|---|
| Criterion | Gini, Entropy |
| Max depth | <1, 10> |
| Max features | <1, `len(X.columns)`> |

*Source:* Author's results in Python

### Gaussian Naive Bayes

Table 3.10: Gaussian Naive Bayes - Hyperparameter Space

| **Hyperparameter** | **Space** |
|---|---|
| Variance smoothing | $<1 \times 10^{-9}, 1 \times 10^{-6}>$ |

*Source:* Author's results in Python

### K-Nearest Neighbors

Table 3.11: K–Nearest Neighbors - Hyperparameter Space

| **Hyperparameter** | **Space** |
|---|---|
| # neighbors | <5, 20> |
| Weights | Uniform, Distance |
| Algorithm | Ball Tree, KD Tree, Brute, Auto |
| Metric | Euclidean, Manhattan, Minkowski |

*Source:* Author's results in Python

### Random Forest

Table 3.12: Random Forest - Hyperparameter Space

| **Hyperparameter** | **Space** |
|---|---|
| # estimators | <100, 1000> |
| Criterion | Gini, Entropy, Log Loss |
| Max depth | <1, 10> |
| Max features | <1, `len(X.columns)`> |
| Class weight | None, balanced, subsample balanced |
| Bootstrap | True, False |
| CCP alpha | $<1 \times 10^{-12}$, 0.5> |

*Source:* Author's results in Python

### Gradient Boosting

Table 3.13: Gradient Boosting - Hyperparameter Space

| **Hyperparameter** | **Space** |
|---|---|
| # estimators | <100, 1000> |
| Criterion | Friedman MSE, Squared Error |
| Max depth | <1, 10> |
| Max features | <1, `len(X.columns)`> |
| Loss | Log Loss, Exponential |
| Learning rate | <0.0001, 0.2> |

*Source:* Author's results in Python

**Support Vector Machine**

Table 3.14: Support Vector Machine - Hyperparameter Space

| Hyperparameter | Space |
|---|---|
| C factor | $<1 \times 10^{-6}$, 5> |
| Kernel | Linear, Poly, RBF, Sigmoid |
| Degree | <1, 10> |
| Gamma | scale, auto |
| Shrinking | True, False |
| Decision function shape | OVR, OVO |
| tol | $<1 \times 10^{-9}$, $1 \times 10^{-3}$> |
| Class weight | balanced, None |

*Source:* Author's results in Python

**Neural Network**

Table 3.15: Multi Layer Percepton - Hyperparameter Space

| Hyperparameter | Space |
|---|---|
| Hidden layer size | <5, 500> |
| Activation function | Identity, Logistic, Tanh, ReLU |
| Solver | Adam, SGD, LBFGS |
| Learning rate | Constant, Adaptive, Invscaling |

*Source:* Author's results in Python

### 3.4.2 Feature Selection

In subsection, the process of selecting optimal features is described. Such process is called feature selection and can be defined as the process of detecting the most relevant features and discarding the noisy redundant ones. Instead of using all the features in dataset, we use only the subset of the most relevant ones, which can further reduce the dimensionality of dataset, boost model performance, save computational resources and reduce overfitting (Bolón-Canedo *et al.* 2015).

With respect to the target variable, we distinguish 2 most common types of feature selection approaches: (1) filter methods and (2) warapper methods.

Using the former approach, the feature selection is independent on a machine learning model itself, but rather is performed using univariate statistical tests, such as correlation measures, Chi–square test, Fisher score and others (Kaushik 2016), and chooses those ones with the highest or lowest values. This approach is used when we prefer lower computational cost and faster feature selection process, but since it does no take into account the model itself, it does not have to able to select the features which would be optimal for particular model. Regarding the latter approach, the feature selection is based on a specific machine learning model and follows a greedy search approach by evaluating all the possible combinations of features against the evaluation metric criteria (Verma 2020). Although, such approach is very computationally expensive, it is able to select the optimal features for a particular model.

The most common wrapper method for feature selection is Recursive Feature Elimination (henceforth RFE). Such method takes a machine learning model as an base estimator, fit the model on whole set of features, computes and ranks their coefficients or feature importances, eliminates the least important features and repeats the process until the desired number of features is reached (Brownlee 2020) or until the stop criteria is met. However, the drawback of RFE is that it always requires feature importances or coefficients to compute, which is not suitable for models which do not produce any coefficients nor feature importances, such as KNN or Naive Bayes. Therefore, this approach is not implemented in this thesis.

Instead, the feature selection is performed with Sequential Feature Selection (henceforth SFS). Such method is iteratively adding (or removes) features the set sequentially. Hence, there are two approaches, Forward SFS and Backward SFS. The former approach keeps adding features to the set until the desired number of features is reached, while the latter approach starts with the whole set of features and removes them until the desired number of features is reached. In this thesis, Forward SFS is used since it was way more computationally efficient than Backward SFS within author's analysis. Forward SFS starts with an empty set of features and afterwards, variant features are sequentially added until the desired number of features is reached or until the addition of extra features does not reduce the criterion (Verma 2021). According to Scikit-learn's documentation (scikit-learn n.d.), at each stage, SFS chooses the best feature to add based on the cross–validation score.

Within machine learning implemenation, instead of fitting Forward SFS only

with one model, Forward SFS is fitted for each input model in order to obtain the best subsets of features for each model, assuming the importance of each features varies across the models. Instead of using input models with default hyperparameters, each model is tuned with Bayesian Optimization in order to obtain the optimal hyperparameters for each model, which would further improve the performance of each model within SFS and therefore, it would lead to the more optimal selection of features. The custom feature selection algorithm is stated in Algorithm 1, thus, when having $n$ input models, it returns $n$ subsets of optimal features, one per each model:

**Algorithm 1** Feature Selection Algorithm

1: **for** *model* $\in$ *models* **do**
2: *optimized_model* $\leftarrow$ BayesianOptimization(*model*)
3: *best_features* $\leftarrow$ ForwardSFS(*optimized_model*)
4: **end for**

Particularly, each input model is first tuned on the training set with Bayesian Optimization with 50 iterations and 10–fold stratified cross validation (in order to preserve the target variable distribution across the folds) while maximizing the F1 score - within author's machine learning implemenation, his custom function `bayesian_optimization()` is used. Once the model is tuned, the Forward SFS is fitted with such tuned model on the same training set with 10–fold stratified cross validation while maximizing the F1 score. Instead of selecting the fixed number of features, Scikit-learn's `SequentialFeatureSelector` class allows to set a stop criterion (`tol` parameter) which stops adding features if the objective score function is not increasing between two consecutive feature additions (scikit-learn n.d.).

Such feature selection algorithm is wrapped into author's custom function `SFS_feature_selection()`. This function iteratively prints the process of the feature selection as can be seen in Figure 3.9, including the current step (Bayesian Optimization or Feature Selection), the execution time in muntes, and the selected features for each model. Since we have 8 input models, we get 8 optimal subset of features.

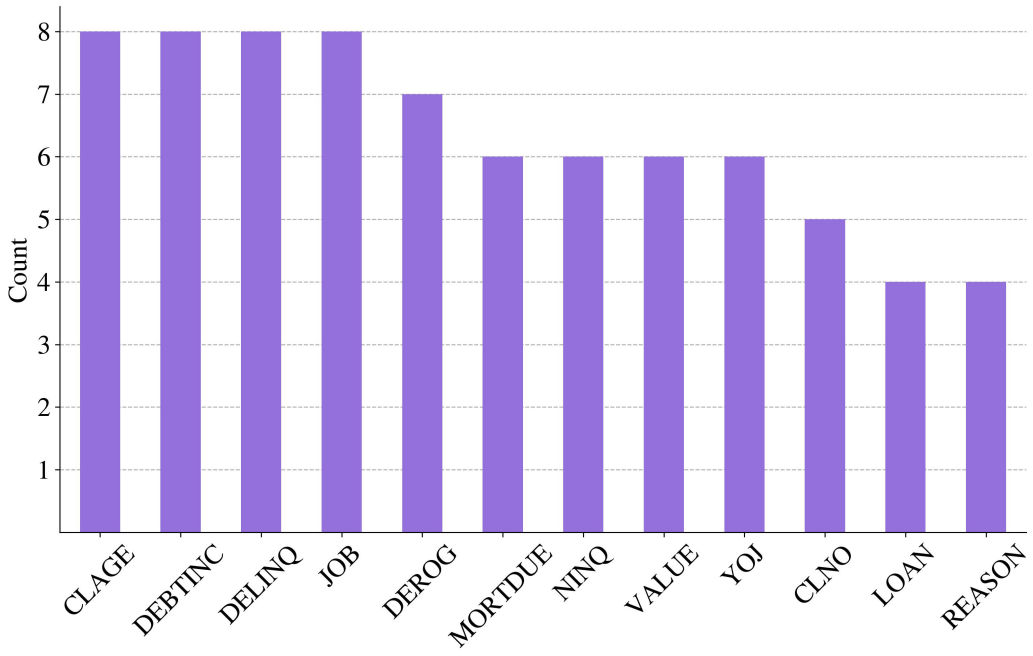
Figure 3.9: Feature Selection Print Statement

```
--------------------------------------------------------------------------------
---------------------------------------- 2/8 -----------------------------------
--------------------------------------------------------------------------------
------------------------------ FEATURE SELECTION WITH DT -------------------------
--------------------------------------------------------------------------------
--------------------------------------------------------------------------------

1/4 ... Starting Bayesian Optimization on the whole set of features
2/4 ... Bayesian Optimization finished
3/4 ... Starting Forward Sequential Feature Selection
4/4 ... Forward Sequential Feature Selection with finished

Execution time: 0.8622 minutes

9 features selected: VALUE, JOB, YOJ, DEROG, DELINQ, CLAGE, NINQ, CLNO, DEBTINC

--------------------------------------------------------------------------------
--------------------------------------------------------------------------------


--------------------------------------------------------------------------------
---------------------------------------- 3/8 -----------------------------------
--------------------------------------------------------------------------------
------------------------------ FEATURE SELECTION WITH GNB -------------------------
--------------------------------------------------------------------------------
--------------------------------------------------------------------------------

1/4 ... Starting Bayesian Optimization on the whole set of features
2/4 ... Bayesian Optimization finished
3/4 ... Starting Forward Sequential Feature Selection
4/4 ... Forward Sequential Feature Selection with finished

Execution time: 0.4152 minutes

6 features selected: MORTDUE, JOB, DELINQ, CLAGE, NINQ, DEBTINC

--------------------------------------------------------------------------------
--------------------------------------------------------------------------------
```

*Source:* Author's results in Python

The following Figure 3.10 depicts the reccurrence of the selected features. As can be seen, features such as `CLAGE`, `DEBTINC`, `DELINQ` and `JOB` were selected by each model. On the other hand, features such as `LOAN` and `REASON` were selected by only four times. Therefore, it can be expected that such features which were selected every time will have significant impact in predictions.

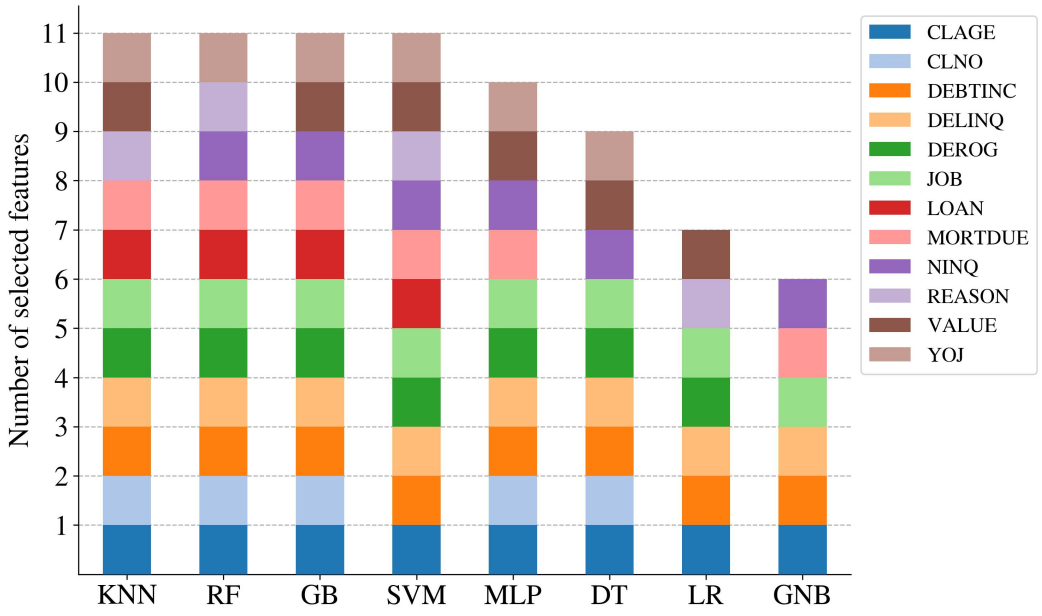
Figure 3.10: Reccurrence of Selected Features




*Source:* Author's results in Python

According to Figure 3.11, models such as K–Nearest Neighbors, Random Forest, Gradient Boosting and Support Vector Machine chose almost all the features as one feature feature was eliminated. On the other hand, Gaussian Naive Bayes chose only 6. It seems to be that most of the features are important as each model has selected a higher amount of features. It is evident the more comples and/or black–box models require more features in contrast to transparant models such as Logistic Regression or Gaussian Naive Bayes.

Figure 3.11: Distribution of Selected Features per Model




*Source:* Author's results in Python

### 3.4.3 Model Selection

In combination with the pre–selected subsets of features, the next step regards the selection of the final model. The algorithm process is described in Algorithm 2 below:

**Algorithm 2** Model Selection Algorithm

```
for model ∈ models do
    for F ⊆ features_subsets do
        optimized_model ← BayesianOptimization(model, F)
        for metric ∈ evaluation_metrics do
            performance ← Evaluation(optimized_model, metric)
        end for
    end for
end for
```

Therefore, each input model is tuned on each subset of features selected within feature selection on the training set and subsequently, the optimized model is evaluated on the validation set. Thus, when having $n$ input models and $m$ subsets of selected features, we get $n \times m$ tuned models. $m \leq n$ because we exclude duplicated subset of selected features which can occur when more than one model choose the same subset(s) of features. Since there are 8 input

models and 8 unique subsets of selected features, the total number of tuned models is 64.

When evaluating classification models using class-based metrics such as F1 score, Precision, Recall, Accuracy, Matthews Correlation Coefficient and Jaccard Score, a default classification threshold of 0.5 is often used. This threshold separates predicted classes based on whether the predicted probability score is higher or lower than 0.5. However, in real-world use cases, the 0.5 classification threshold may not be appropriate. Therefore, it is recommended to calculate an optimal threshold rather than relying on the default one. One approach to finding the optimal threshold is to use the Younden index, which is derived from the Receiver Operating Characteristic (ROC) curve. The Younden index searches for the threshold that maximizes the sum of True Positive Rate and True Negative Rate, decreased by 1, thus:

$$J = TPR + TNR - 1 \tag{3.12}$$

Mathematically, the optimal threshold using Youden index is derived as follows:

$$T_{opt} = \text{argmax}_{t\in[0,1]}\,(J) \tag{3.13}$$

In Python, the `roc_curve` function from `Scikit-learn` returns False Positive Rate instead of the True Negative Rate. Nevertheless, we can derive the True Negative Rate from False Positive Rate as follows:

$$TNR = 1 - FPR \tag{3.14}$$

Therefore:

$$T_{opt} = \text{argmax}_{t\in[0,1]}\,(TPR + (1 - FPR) - 1) \tag{3.15}$$

In order to ensure a more comprehensive and unbiased evaluation of a model's performance, it is recommended to consider multiple metrics rather than relying on a single metric alone. This approach provides a more generalized overview of the model's performance across different aspects and helps to prevent any bias towards a single metric. To accomplish this, models can be ranked based on their performance on each individual metric, where a higher score or a lower loss indicates a better model, resulting in a higher rank for that metric. Subsequently, for each metric, the ranking of the models is determined, and the final ranking is calculated as a weighted average of these individual rankings.

The weights have been set expertly and are summarized in Table 3.16.

Specifically, the highest weight (1.5) is assigned to the F1 score, which provides a balanced measure of a model's performance with respect to both False Positives and False Negatives. This metric is commonly used in classification tasks, particularly in imbalanced datasets, such as the validation set in our case, which has not been oversampled. In addition to the F1 score, higher weight is assigned to the Recall score as well (1.2), which is a metric that penalizes False Negatives. False Negatives occur when the model predicts a negative result (i.e., no default) for an instance that is actually positive (i.e., default). In the context of loan applications, one may prefer to reject a loan applicant who would not have defaulted (False Positive) rather than approving the application of a client who would have defaulted (False Negative). Therefore, it is appropriate to give higher weight to Recall in order to reduce the likelihood of False Negatives. Henceforth, the weights are assigned to different metrics based on their relevance to the models' ranking, with the highest weight given to F1 score and additional weight given to Recall to ensure that False Negatives are minimized.

Table 3.16: Model Ranking Weights table

| Metric | Weight |
|---:|---|
| F1 score | 1.5 |
| Recall | 1.2 |
| Precision | 1 |
| Accuracy | 1 |
| AUC | 1 |
| Somers' D | 1 |
| Kolmogorov Smirnov Distance | 1 |
| Matthews Correlation Coefficient | 1 |
| Jaccard Score | 1 |
| Brier Score Loss | 1 |

*Source:* Author's results in Python

The custom function `model_selection()` iteratively prints the process of the model tuning and evaluation on each subset of features, in order to keep the track of such process as it is depicted in Figure 3.12. Particularly, it prints which model on which features is being tuned and evaluated, exeuction time, optimal threshold, F1 score on the validation set and the best hyperparameters.

Figure 3.12: Model Selection Print Statement

```
--------------------------------------------------------------------------------
------------------------------------ 56/64 -------------------------------------
--------------------------------------------------------------------------------
--------------------------- BAYESIAN OPTIMIZATION OF SVM ------------------------
-------------------------- WITH FEATURES SELECTED BY MLP -------------------------
--------------------------------------------------------------------------------
--------------------------------------------------------------------------------

1/2 ... Starting Bayesian Optimization on the subset of features (10 features):
        MORTDUE, VALUE, JOB, YOJ, DEROG, DELINQ, CLAGE, NINQ, CLNO, DEBTINC
2/2... Bayesian Optimization finished

Execution time: 22.0695 minutes

F1 Score on Validation set: 0.7102272727272726

Optimal classification threshold: 0.6477

Tuned hyperparameters of SVM:

    C: 4.999999999999999
    break_ties: False
    cache_size: 200
    class_weight: balanced
    coef0: 0.0
    decision_function_shape: ovr
    degree: 1
    gamma: scale
    kernel: rbf
    max_iter: -1
    probability: True
    random_state: 42
    shrinking: False
    tol: 1.102507160381566e-09
    verbose: False

--------------------------------------------------------------------------------
--------------------------------------------------------------------------------
```

*Source:* Author's results in Python

The final output of the function `model_selection()` is table which summarizes the model's computed metrics as depicted in Table 3.17. As can be seen, the best models in terms of ranking are the Gradient Boosting models which in general have the highest score metrics and the lowest loss metrics. On the other hand, the worst-performing models are Gaussian Naive Bayes models.

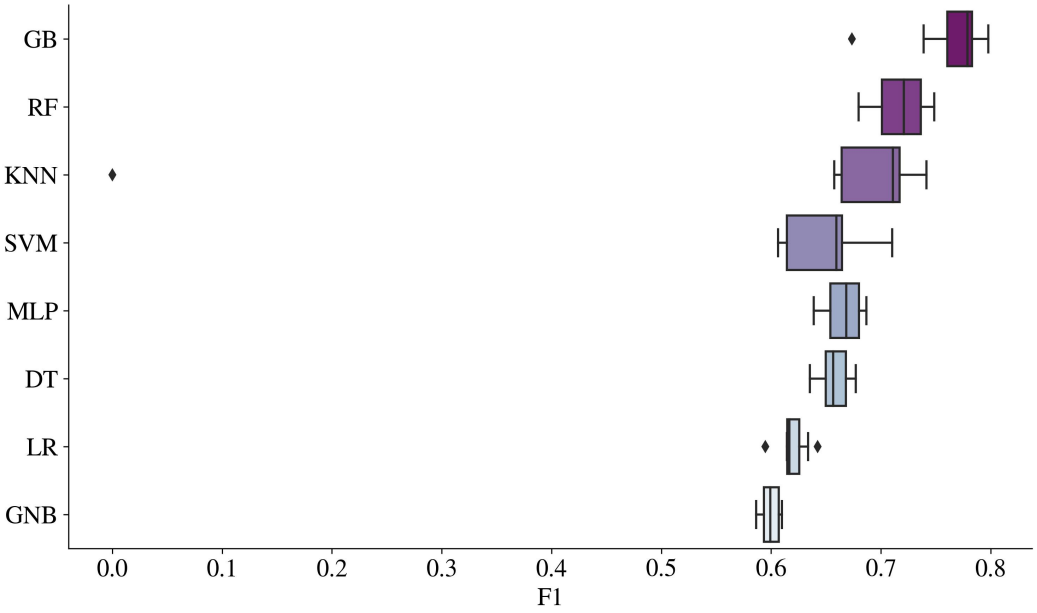
Table 3.17: Model Selection table

| **Tuned model** | **FS model** | # Features | Time | Thres | F1 | Prec | Rec | Acc | AUC | SD | KS | MCC | JC | BSL | Log Loss | rank |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| GB | MLP | 10 | 12.30 | 0.4955 | 0.7809 | 0.7853 | 0.7765 | 0.9128 | 0.9515 | 0.9030 | 0.7751 | 0.7265 | 0.6406 | 0.0666 | 0.2487 | 1 |
| GB | KNN | 11 | 12.80 | 0.5072 | 0.7978 | 0.7912 | 0.8045 | 0.9184 | 0.9587 | 0.9175 | 0.7989 | 0.7467 | 0.6636 | 0.0687 | 0.4135 | 2 |
| GB | SVM | 11 | 15.08 | 0.5053 | 0.7896 | 0.8155 | 0.7654 | 0.9184 | 0.9555 | 0.9109 | 0.7961 | 0.7397 | 0.6524 | 0.0718 | 0.3486 | 3 |
| GB | GB | 11 | 11.44 | 0.4132 | 0.7799 | 0.7778 | 0.7821 | 0.9117 | 0.9543 | 0.9086 | 0.7989 | 0.7247 | 0.6393 | 0.0703 | 0.3372 | 4 |
| GB | RF | 11 | 13.38 | 0.4973 | 0.7775 | 0.7841 | 0.7709 | 0.9117 | 0.9541 | 0.9081 | 0.7961 | 0.7225 | 0.6359 | 0.0669 | 0.2803 | 5 |
| RF | KNN | 11 | 5.94 | 0.4725 | 0.7486 | 0.7326 | 0.7654 | 0.8972 | 0.9226 | 0.8452 | 0.7109 | 0.6843 | 0.5983 | 0.0923 | 0.3232 | 6 |
| GB | DT | 9 | 12.00 | 0.4729 | 0.7675 | 0.7697 | 0.7654 | 0.9073 | 0.9407 | 0.8814 | 0.7556 | 0.7096 | 0.6227 | 0.0808 | 0.4693 | 7 |
| RF | GB | 11 | 5.18 | 0.4517 | 0.7385 | 0.7135 | 0.7654 | 0.8916 | 0.9200 | 0.8400 | 0.7123 | 0.6709 | 0.5855 | 0.0886 | 0.3135 | 8 |
| RF | MLP | 10 | 6.62 | 0.4761 | 0.7357 | 0.7181 | 0.7542 | 0.8916 | 0.9179 | 0.8358 | 0.7081 | 0.6679 | 0.5819 | 0.0879 | 0.3084 | 9 |
| GB | LR | 7 | 16.81 | 0.4362 | 0.7388 | 0.7000 | 0.7821 | 0.8894 | 0.9219 | 0.8438 | 0.7081 | 0.6706 | 0.5858 | 0.0886 | 0.3925 | 10 |
| ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| GNB | LR | 7 | 0.39 | 0.2990 | 0.6099 | 0.5094 | 0.7598 | 0.8056 | 0.8420 | 0.6840 | 0.5866 | 0.5043 | 0.4387 | 0.1340 | 0.6458 | 55 |
| DT | GNB | 6 | 0.89 | 0.5000 | 0.6354 | 0.6284 | 0.6425 | 0.8525 | 0.8187 | 0.6375 | 0.5838 | 0.5430 | 0.4656 | 0.1251 | 2.1679 | 56 |
| GNB | KNN | 11 | 0.38 | 0.3588 | 0.6093 | 0.5219 | 0.7318 | 0.8123 | 0.8479 | 0.6957 | 0.5698 | 0.5024 | 0.4381 | 0.1367 | 0.6686 | 57 |
| GNB | DT | 9 | 0.39 | 0.2241 | 0.6063 | 0.5095 | 0.7486 | 0.8056 | 0.8467 | 0.6935 | 0.5768 | 0.4991 | 0.4351 | 0.1316 | 0.6370 | 58 |
| GNB | GB | 11 | 0.38 | 0.1829 | 0.5969 | 0.4893 | 0.7654 | 0.7933 | 0.8531 | 0.7063 | 0.5810 | 0.4880 | 0.4255 | 0.1310 | 0.6461 | 59 |
| GNB | MLP | 10 | 0.39 | 0.2194 | 0.6013 | 0.5000 | 0.7542 | 0.8000 | 0.8493 | 0.6986 | 0.5768 | 0.4930 | 0.4299 | 0.1319 | 0.6360 | 60 |
| GNB | GNB | 6 | 0.38 | 0.4787 | 0.5950 | 0.5039 | 0.7263 | 0.8022 | 0.8356 | 0.6711 | 0.5559 | 0.4835 | 0.4235 | 0.1470 | 0.5280 | 61 |
| LR | GNB | 6 | 1.59 | 0.4561 | 0.5948 | 0.5121 | 0.7095 | 0.8067 | 0.8379 | 0.6758 | 0.5531 | 0.4831 | 0.4233 | 0.1319 | 0.4180 | 62 |
| GNB | SVM | 11 | 0.38 | 0.1991 | 0.5885 | 0.4872 | 0.7430 | 0.7922 | 0.8425 | 0.6850 | 0.5712 | 0.4756 | 0.4169 | 0.1345 | 0.6721 | 63 |
| GNB | RF | 11 | 0.39 | 0.3413 | 0.5864 | 0.4943 | 0.7207 | 0.7966 | 0.8288 | 0.6577 | 0.5545 | 0.4720 | 0.4148 | 0.1486 | 0.7040 | 64 |

*Source:* Author's results in Python

In order to gain a more detailed understanding of the model selection results, the distribution of computed metrics is plotted. In Figure 3.13, the F1 score distribution is visualized for each input model. An outlier can be observed in KNN where the F1 score is 0.

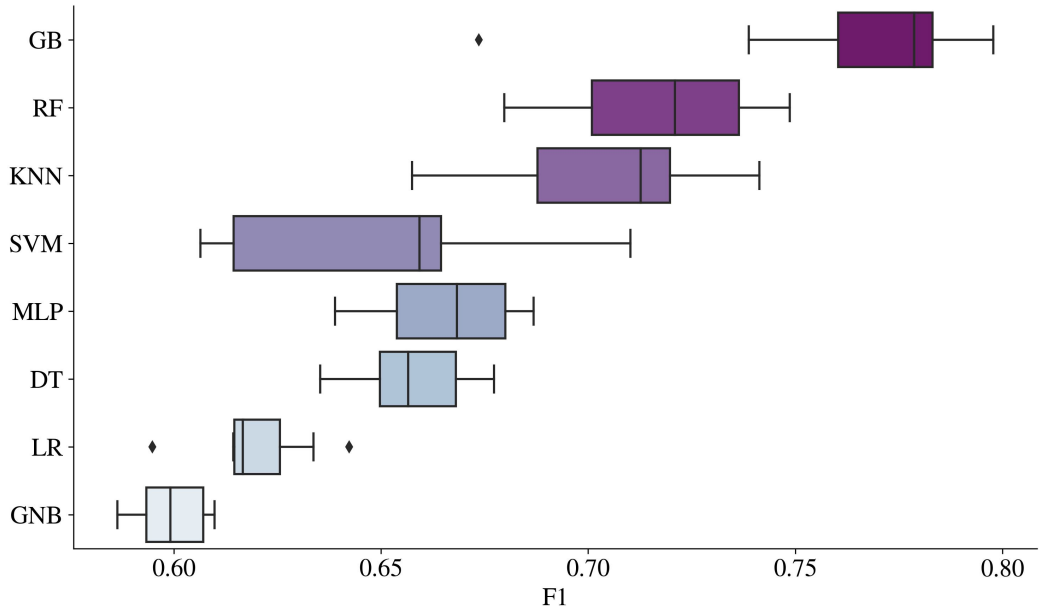
Figure 3.13: F1 score distribution




*Source:* Author's results in Python

Such outlier is removed in Figure 3.14 to gain a more general insight into the F1 score distribution. It can be observed that Gradient Boosting models have the highest F1 scores of around 80 %. Another tree ensemble model, Random Forest, is performing well as the second best. However, more transparent models such as Logistic Regression and Naive Bayes are performing poorly, having F1 scores around 60 %. Surprisingly, black box models such as Support Vector Machine and Neural Network are outperformed by the less complex KNN model. Nonetheless, given the relatively small sample size, KNN performs better than Neural Network and non-linear SVM on small datasets, whereas NN or non-linear SVM generally outperform KNN when it comes to large datasets.

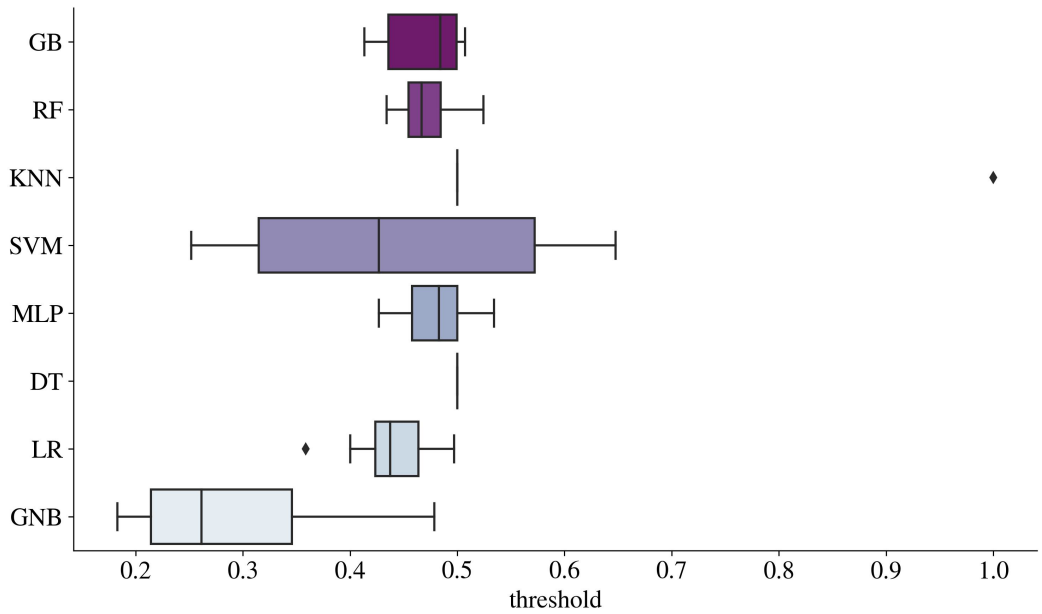
Figure 3.14: F1 score distribution - without outliers




*Source:* Author's results in Python

The optimal threshold distribution for each base model is presented in Figure 3.15. We can observe an outlier in KNN having a threshold value of 1, which explains the F1 score outlier found previously in Figure 3.13.

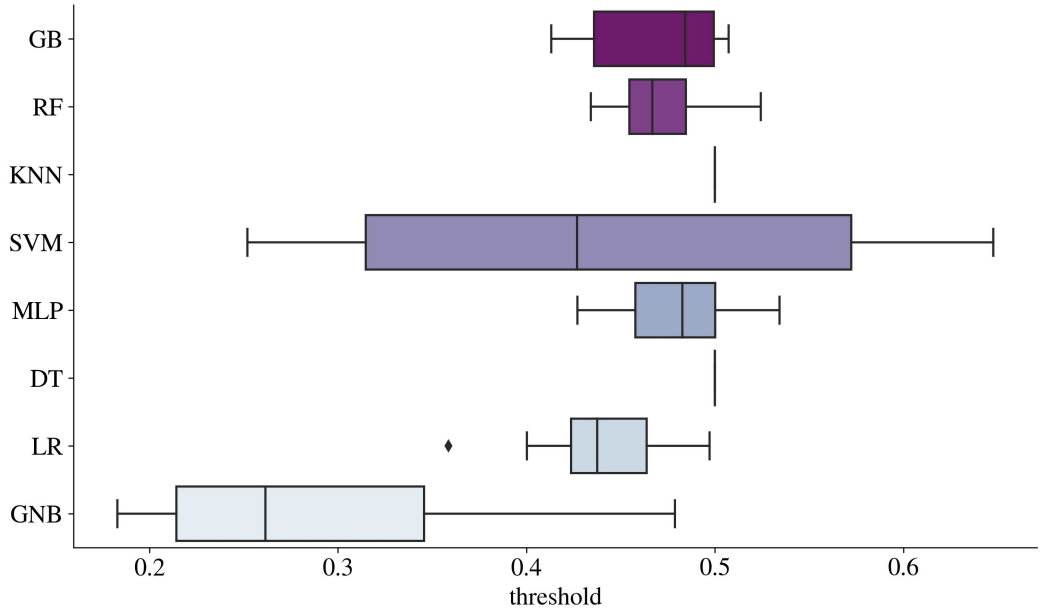
Figure 3.15: Threshold distribution




*Source:* Author's results in Python

In order to obtain a better insight into the distribution of optimal thresholds, the outlier in KNN is excluded, resulting in the threshold distribution depicted in Figure 3.16. The optimal threshold values are mostly distributed below 0.5, indicating that the models are generally more conservative. The most conservative model is Gaussian Naive Bayes, which has a median threshold value around 0.25.

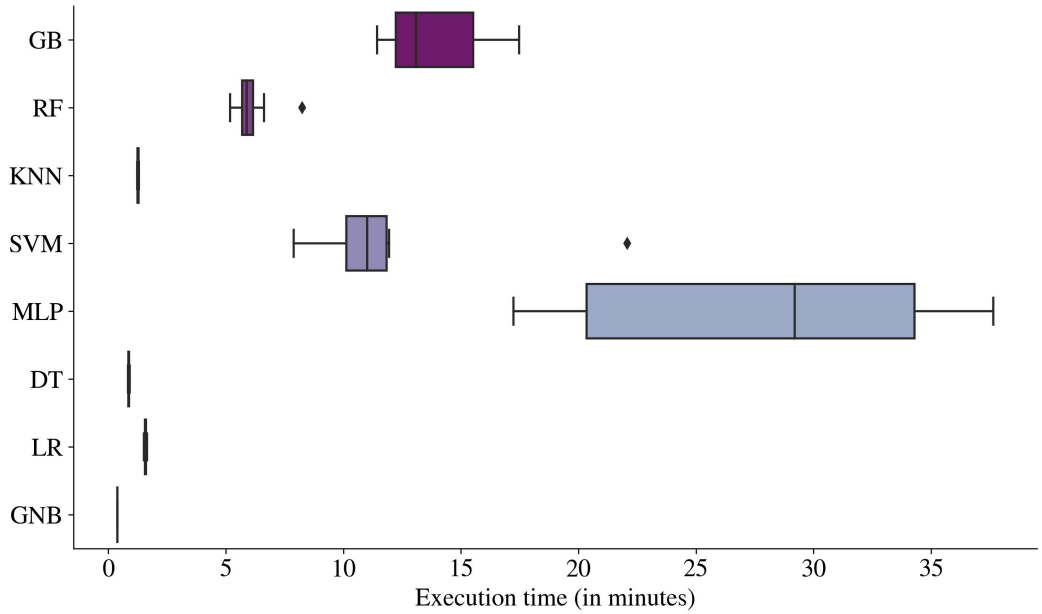
Figure 3.16: Threshold distribution - without outliers




*Source:* Author's results in Python

Upon examining the optimization time of each model, it can be observed that the transparent and non-complex models such as Logistic Regression, Gaussian Naive Bayes, or even Decision Tree, which take around only 1 minute to optimize themselves, also perform poorly, as already inspected in Figure 3.14. Conversely, the most time-consuming models are undoubtedly the Neural Network models, which take around 30 minutes to optimize themselves. Other time-consuming models include Gradient Boosting and Support Vector Machine, which take around 13 and 11 minutes to optimize themselves, respectively. This finding suggests that longer optimization time does not necessarily lead to better performance, as the Neural Network models are significantly outperformed by several other models.

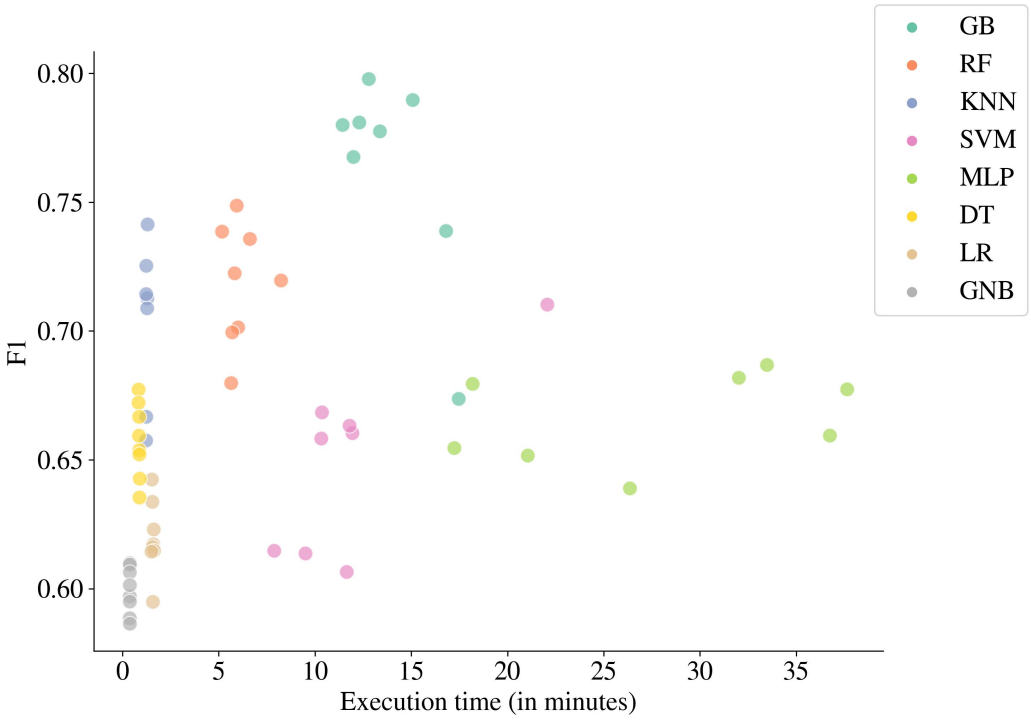
Figure 3.17: Execution time distribution




*Source:* Author's results in Python

The execution time and the F1 score were inspected together using a scatterplot, as shown in Figure 3.18. A cluster of non-complex and transparent models, such as Logistic Regression, Gaussian Naive Bayes, Decision Tree, and KNN, can be observed around the vertical line near 0 execution time. These models are quick to optimize, but their F1 scores are generally low, except for KNN. Further, their variance in execution time is quite low, regardless of the feature subset they are optimized on. On the other hand, the Neural Network models always perform poorly, regardless of the length of the execution time. Furthermore, the variance of the F1 scores is quite low for these models, indicating that the execution time does not have a significant impact on the F1 score in the case of Neural Networks.

Figure 3.18: Execution time vs. F1 Scatterplot




*Source:* Author's results in Python

To summarize this subsection, the best and final model is the Gradient Boosting Classifier which was optimized on the subset of features selected by Multi-Layer Percepton - both the model information and its final hyperparameters' values are described in Table 3.18. Such model is then used in the next modelling steps, including the recalibration, evaluation and deployment.

Table 3.18: Final Model Information

| | |
|---|---|
| **Final Model** | Gradient Boosting |
| **FS Model** | Multi–Layer Percepton |
| **Final Features** | MORTDUE, VALUE, JOB, YOJ, DEROG, DELINQ, CLAGE, NINQ, CLNO, DEBTINC |
| **Threshold** | 0.4955 |
| **F1** | 0.7809 |
| *# estimators* | 1,000 |
| *Criterion* | Friedman MSE |
| *Max depth* | 10 |
| *Max features* | 1 |
| *Loss* | Log loss |
| *Learning rate* | 0.0150 |

*Source:* Author's results in Python

### 3.4.4 Model Building

In order to ensure that the final model performs well on unseen data, it is common practice to employ the recalibration approach, which involves retraining the model on both the training and validation sets. By doing so, the sample size used for training is increased, resulting in improved model performance. The recalibrated model is then used to evaluate the performance of the final model on the test set, which is the ultimate measure of a model's performance.

In addition to recalibrating the final model, it is crucial to recalibrate the threshold value for assigning class labels based on predicted probabilities. The optimal threshold value can be determined using the training and validation sets. In this thesis, the optimal threshold value is found to be **0.4955**, which is then used for evaluating the final model's performance on the test set. By recalibrating the threshold value, the model's performance is further improved, resulting in more accurate predictions.

Moreover, the recalibration process helps to mitigate overfitting issues, which occur when the model is only trained on the training set. By incorporating

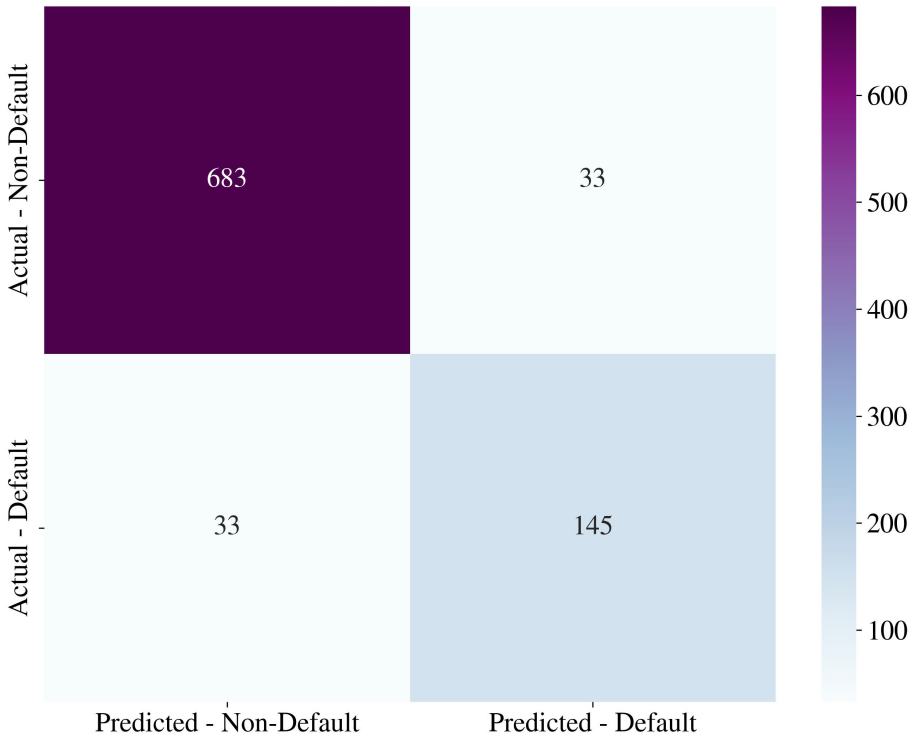
the validation set into the training process, the recalibrated model can better generalize to new data and improve its overall performance on the test set. The inclusion of the validation set during the recalibration process does not cause any data leakage issues since this set was already used during model selection to evaluate each model's performance. Therefore, using the validation data for recalibration is a sound practice that helps to ensure the reliability and accuracy of the final model.

## 3.5 Model Evaluation

After recalibrating the model and threshold, the final step in evaluating the model's performance is to test it on previously unseen data, specifically the test set. This evaluation is critical to determine whether the model can generalize well to new data beyond the training, feature selection, and model selection phases. During the evaluation, the recalibrated classification threshold of 0.4511, determined in the model recalibration process, is also used.

In Figure 3.19, the confusion matrix for the final model, based on the test set and using the recalibrated threshold, is presented. The matrix shows that the model is generalizing well, having correctly predicted 140 defaults and misclassified only 38 defaults and further, correctly predicted 686 non–defaults and misclassified only 30 non–defaults. Such a result indicates that the model is a good fit for the data and can provide useful predictions for the problem at hand.

Figure 3.19: Confusion Matrix




*Source:* Author's results in Python

In order to obtain a better understanding of the model's performance on previously unseen data, we computed several metrics that were used during the model selection process. These metrics are presented in Table 3.19. The results indicate that the model performs well on the unseen data, with most of the scores metrics around 80 % to 90 %. Furthermore, the loss metrics are relatively low, indicating that the model can effectively distinguish between defaults and non-defaults. Overall, these results suggest that the model is performing well and is suitable for predicting defaults. The results suggest that the model has a good balance between correctly identifying defaults and non-defaults, as well as minimizing false positives and false negatives. This further confirms the model's ability to accurately predict defaults.

Table 3.19: Metrics Evaluation

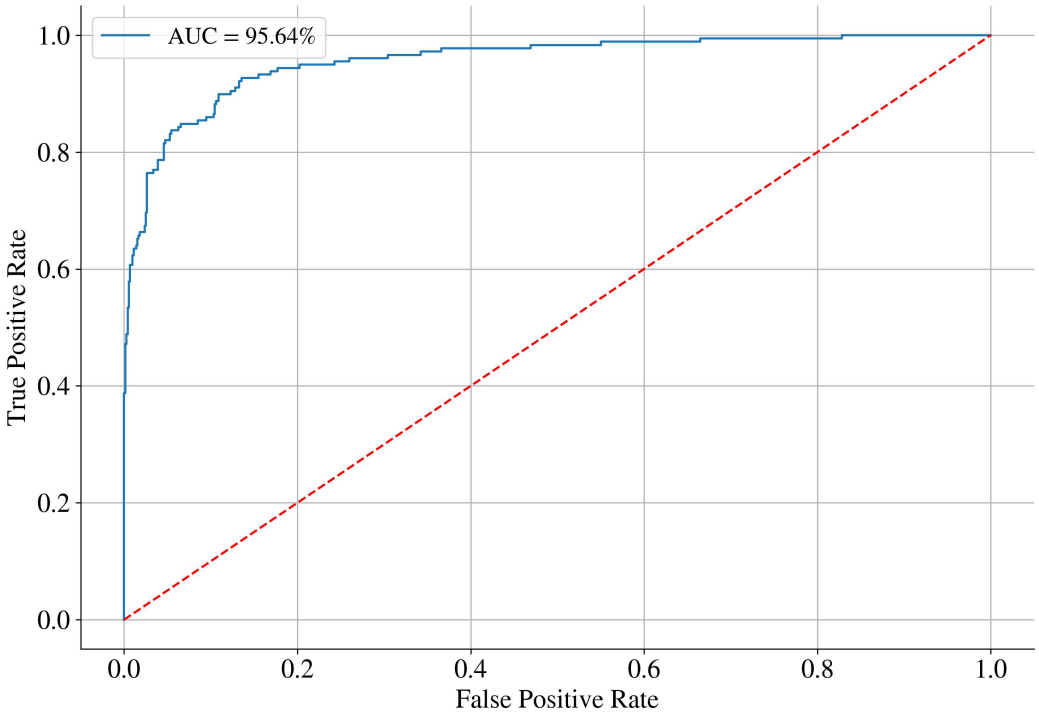
| Metric | Value |
|---|---|
| F1 | 0.8146 |
| Precision | 0.8146 |
| Recall | 0.8146 |
| Accuracy | 0.9262 |
| AUC | 0.9564 |
| Somers D | 0.9128 |
| KS | 0.7915 |
| MCC | 0.7685 |
| Jaccard Score | 0.6872 |
| Brier Score Loss | 0.0594 |
| Log Loss | 0.2163 |

*Source:* Author's results in Python

To further evaluate the performance of the model, we can visualize the Receiver Operating Characteristic (ROC) curve, as presented in Figure 3.20. The curve illustrates the trade-off between the true positive rate and the false positive rate at various classification thresholds. An ideal ROC curve should have an area under the curve (AUC) value of 100 %, indicating a perfect classifier, while a random classifier would have an AUC of 50 %.

From the curve, we observe that the AUC value of the model is 95.55 %, indicating a high degree of accuracy in distinguishing between defaults and non-defaults. The curve covers most of the area under the diagonal line, indicating that the model is performing well in differentiating the two classes. Therefore, the results suggest that the model is performing well and is capable of accurately identifying potential defaulters.

Figure 3.20: ROC Curve



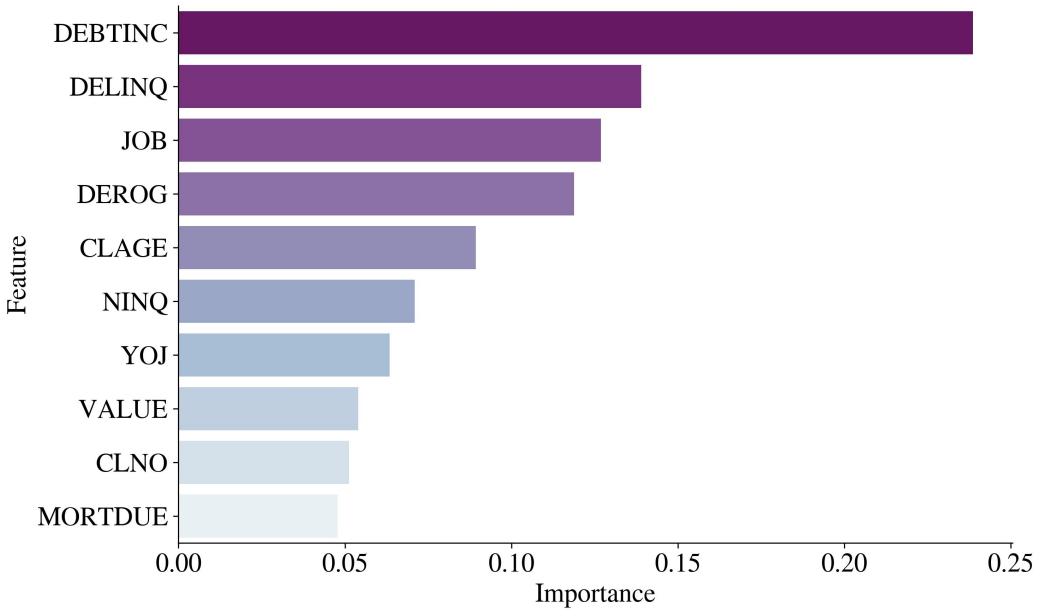

*Source:* Author's results in Python

To gain insights into the impact of the features used in the final model, a feature importance graph was visualized and is presented in Figure 3.21. Feature importance is a measure of how much a feature contributes to the overall performance of the model, and it is based on the reduction in impurity achieved by splitting the data on that feature. The higher the reduction in impurity, the more important the feature is considered to be. Overall, the feature importance plot provides valuable insights into the factors that are most important in predicting loan defaults. It can be used to identify which features are contributing the most to the model's accuracy and to guide future feature selection efforts. The two most important features used in the final model are `DEBTINC` and `DEROG`, which are crucial delinquency indicators in determining whether a borrower would be able to repay their loan. These two features have a significant impact on the model's ability to accurately predict loan defaults, with high feature importance scores.

Understanding the impact of individual features on model performance can be useful in identifying areas for improvement, as well as in identifying the most significant factors that drive loan defaults. By focusing on these important features, lenders and policymakers can better understand and address the

underlying factors that contribute to default risk, ultimately leading to better lending decisions and improved outcomes for borrowers and lenders alike.

Figure 3.21: Feature Importance




*Source:* Author's results in Python

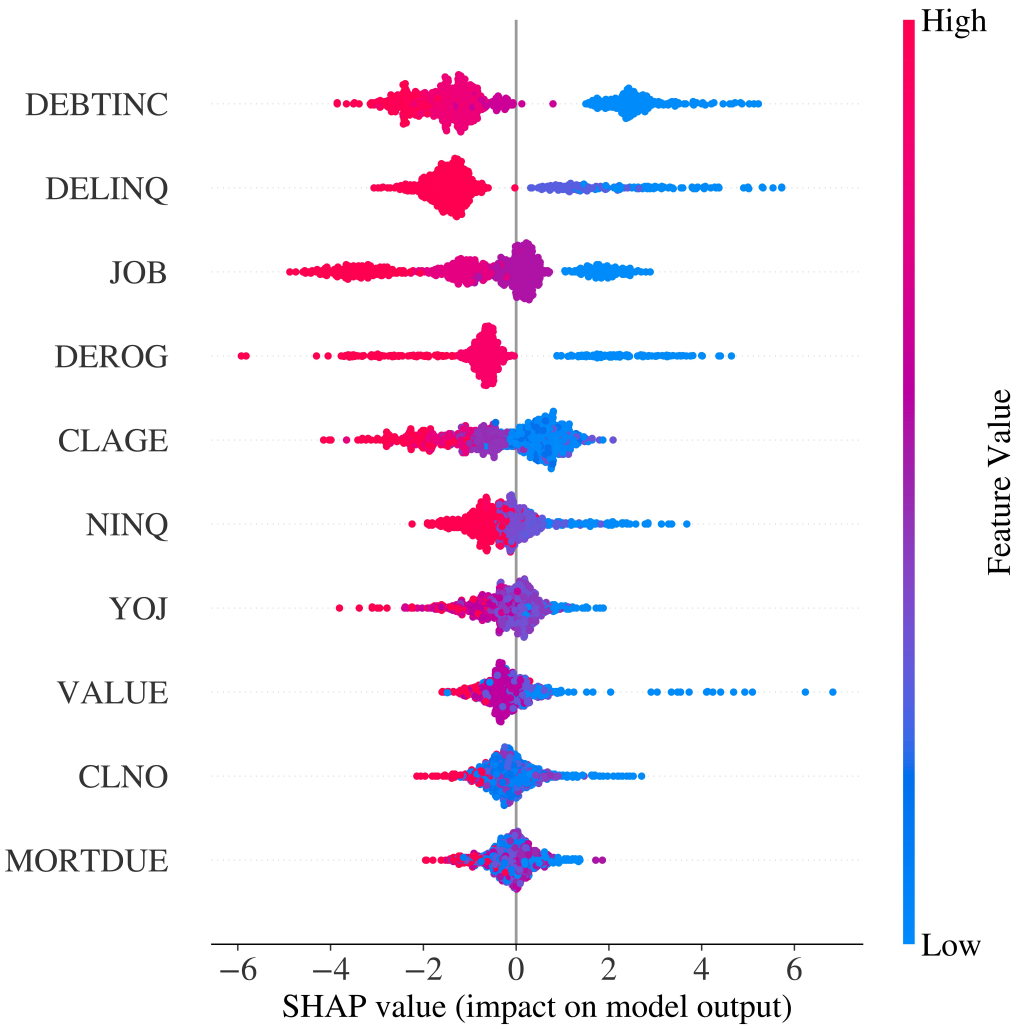
To gain further insights into the impact of the features on the final model's predictions, the SHAP (SHapley Additive exPlanations) summary plot is displayed in Figure 3.22. The SHAP summary plot provides a clear visualization of the contribution each feature makes to a prediction and is used for a black box model explainability. Each dot in the plot represents a feature and its corresponding SHAP value. The color of the dot represents the feature's value, with red indicating high values and blue indicating low values. The position of the dot on the x-axis represents the impact of the feature on the prediction, with features on the right-hand side contributing more positively to the prediction, and features on the left-hand side contributing more negatively.

Since our data points are encoded in WoE values, the higher (the more positive) value, the larger distribution of non-defaulters compared to defaulters, and vice versa, the lower (the more negative) value, the larger distribution of defaulters compared to non-defaulters. For the most important features, we can observe that the blue values (negative WoE values) and red values (positive WoE values) are quite separable. Negative WoE values are positively contributing to the predictions, and the positive WoE values are negatively

contributing to the predictions. This means that the more negative the WoE value, the more likely the borrower is to default, and vice versa.

Overall, the SHAP summary plot provides a valuable tool for interpreting and understanding the complex decision-making process of the final model. The plot enables us to examine the impact of individual features on the model's output and helps us to identify which features are most influential in the model's decision-making process. By understanding the relative importance of each feature, we can gain deeper insights into the creditworthiness assessment process and make more informed decisions in the lending industry.

Figure 3.22: SHAP Summary Plot




*Source:* Author's results in Python

## 3.6 Machine Learning Deployment

This section describes the process of taking a trained machine learning model and making it available for use in the real world. It involves taking the model from a development environment and integrating it into a production environment where it can be used to make predictions or decisions based on new data. In this thesis, the machine learning model is deployed as web application using Flask and HTML.

### 3.6.1 Final Model Building

Before deploying the model in a production setting, a meticulous process is undertaken to ensure optimal performance. This involves conducting a final recalibration of the model using the entire dataset, comprising the training, validation, and test sets. The purpose of this recalibration is to fine-tune the model parameters, thereby maximizing its ability to generalize and yield accurate predictions.

The test set, which has been employed previously during the model evaluation phase, is incorporated into the recalibration process without any risk of data leakage. By including the test set, the sample size for training is expanded, thereby increasing the model's capacity to generalize effectively.

Upon completion of the recalibration, the final classification threshold for deployment is determined to be **0.3358**. This value is derived from a comprehensive analysis of the training, validation, and test sets, which ensures that the model's generalization capabilities are further enhanced for optimal performance in real-world applications.

### 3.6.2 Flask and HTML Web Application

In this case, the machine learning model was deployed into a web application using Flask and HTML. The application is temporarily deployed on the Cloud server on the **PythonAnywhere** platform and is accessible here: `http://ml-credit-risk-app-petrngn.pythonanywhere.com/`. However, the application will be shut down after the thesis defense and will not be available online anymore due to the budget reasons. Nevertheless, the code for the ap-

plication is available in the GitHub repository, and the application can be run locally using any Python compiler.

Furthermore, prior to deployment, we need to prepare several Python inputs for the web application, including:

- Model - the final model recalibrated on the training, validation and test set.
- Threshold - the final classification threshold recalibrated on the training, validation and test set.
- Features - the final features used in the final model.
- Data Frame - he input data frame used in the web application to store the loan applicant's inputs.
- Optimal Binning Transformator - fitted `BinningProcess` object for binning and WoE-encoding of the loan applicant's inputs.
- WoE Bins - a set of bins and WoE values used for mapping the WoE values to missing values.

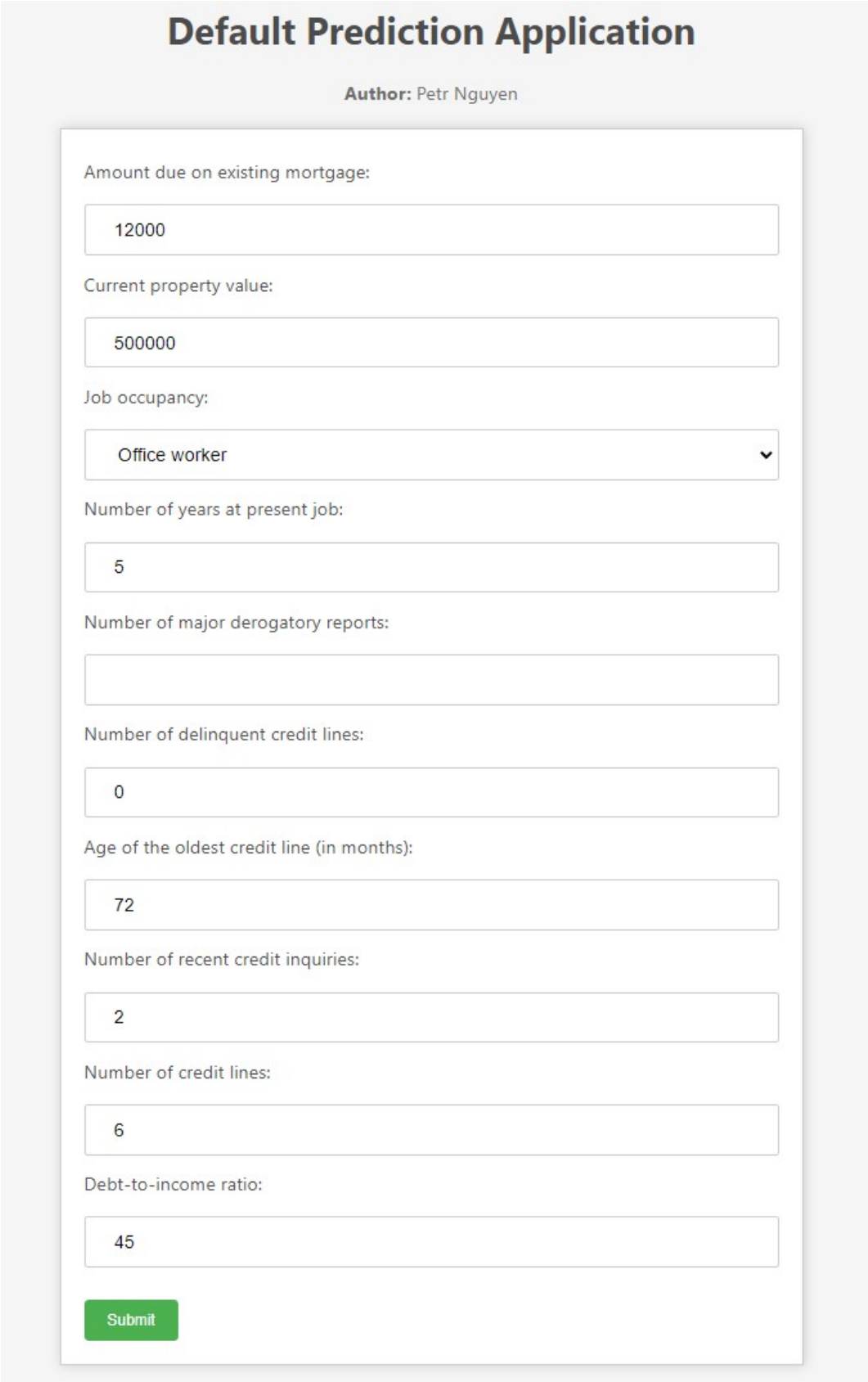
Such inputs required for the machine learning application are exported in the `.pkl` format using the `pickle` module. This format allows for efficient and easy-to-use serialization and deserialization of the inputs. The pickled file is then loaded directly into the Flask application.

For the back-end of the web application, Flask is used to deploy the machine learning model. The Flask application is coded in the `app.py` file, which is stored in the `flask_app` repository. The front-end of the web application is coded in HTML, with CSS and JavaScript elements used to enhance the user interface.

The web application first renders an HTML page, as shown in Figure 3.23. This page contains a loan application form, in which the user or the loan applicant fills in the respective field values that correspond to the features on which the machine learning model was trained. The form is designed to capture the necessary information required for the model to make a prediction about the loan applicant's application. Note that not all fields in the loan application form need to be filled out, except for the requested loan amount. This is because missing values in certain features may indicate a higher risk of defaulting. Conversely, one may choose to impose a restriction on the form,

requiring all fields to be filled out. However, this could result in a lower number of received applications from delinquent clients, as they may not have all the necessary information to complete the form.

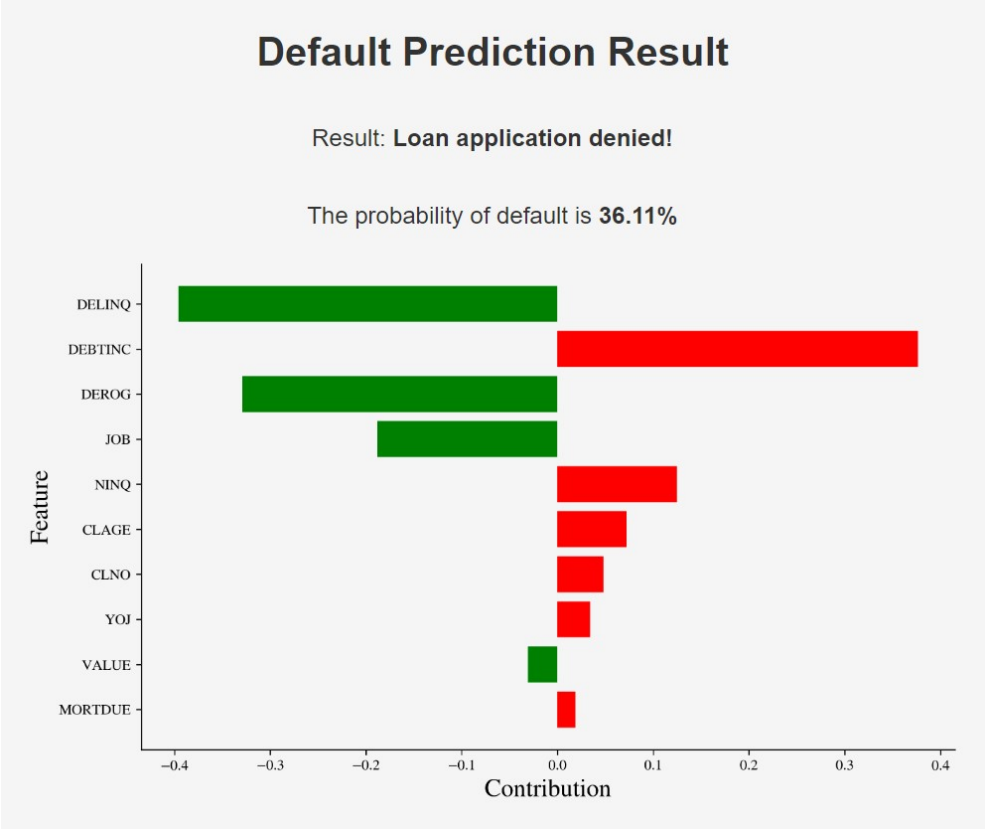
Figure 3.23: Flask Web Application Form




*Source:* Author's results in Python

Once, the loan application form is submitted, the web application uses the pickled input to transform the data from the loan application form and use it in the recalibrated model in order to get the result, whether the given loan applicant would repay his loan based on predetermined threshold. The result is then displayed in the web application, as shown in Figure 3.24. Particularly, the web application returns whether the loan application would be denied or approved and also the probability score of default.

Figure 3.24: Flask Web Application - Prediction Result




*Source:* Author's results in Python

Besides the prediction results, it also displays the Local Interpretable Model-Agnostic Explanations (LIME) of the black–box model (Gradient Boosting) with respect to the inputs submitted within the form. LIME focuses on the local explainability of the black box model around the black–box prediction as it generates a new dataset consisting of perturbed samples around the given prediction and then trains a surrogate linear model on the new dataset. Such local interpretable, surrogate model should be a good approximation of the black box model in the vicinity of the given prediction, i.e., the local inter-

pretable model is then used to explain the prediction of the black box model (Ribeiro *et al.* 2016).

The LIME explanation of input instances $x$ is given as follows:

$$\xi(x) = \arg\min_{g \in G} L(f, g, \pi_x) + \Omega(g) \tag{3.16}$$

where $f$ is the original black–box model, $g$ is the surrogate model, $L$ is the loss functions measuring how far is the explanation $\xi(x)$ far from the prediction produced by black–box model $f$, and $\Omega(g)$ is the complexity of the surrogate model $g$.

The explanation is given in terms of the feature importance, which is represented by the magnitude of the feature's coefficient in the local interpretable model. The higher the magnitude of the coefficient, the more important the feature is in the prediction of the black box model. Therefore, as it is shown in Figure 3.24, the red bars indicate positive contribution to the probability of default whereas green bars indicate negative contribution to the probability of default. In other words, The features with red bars indicates that the client would not probably repay his loan and vice versa. The contributions' magnitudes are in line with the findings from feature imporance or SHAP values which is focused on the global explainability of the black–box model (not local explainability), that features such as debt–to–income ratio (`DEBTINC`) or number of deliquent credit lines (`DELINQ`) have the largest impact of the probability default. Particularly, a high value of debt–to–income ratio causes higher probability default, whereas no delinquent credit lines leads to the lower probability default.

# Chapter 4

# Conclusion

The conclusion should briefly summarize the problem statement and the general content of the work and the emphasize on the main contribution of the work.

When writing the conclusion keep in mind that some readers may not have gone through the whole thesis, but have jumped directly to the conclusion after having read the abstract in order the decide on the personal relevance of the thesis. Therefore, the conclusion should be self contained, which means that a reader should be able to understand the essence of the conclusion without having to read the whole thesis.

The conclusion typically ends with an outlook that describes possible extensions of the presented approaches and of planned future work.

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# Appendix A

# Title of Appendix A

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# Appendix B

# Project's website

You can create a special website for your project which contains empirical data and MatLab/R/Stata source codes, see meta-analysis.cz/sigma, for example. Stating in your thesis that the data and source codes are available upon request is enough but please, have them prepared for such requests. The faculty does not allow enclosed DVD.

- File 1: Master's thesis
- File 2: Empirical data
- File 3: Source codes