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Uplift Modeling Using Artificial Immune System

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ABSTRACT

Uplift Modeling aims to detect subgroups in a population with a specific response or reaction to an action taken on the targeted group. In these models, the Treatment set contains objects that have been exposed to some action, such as a marketing campaign or clinical treatment, while in the Control set, they have not. In this study, a novel artificial immune system-based model was designed using an AIRS classifier to solve uplift modeling problems with improved efficiency. In this approach, a predictive model was built for estimating the conditional probability of receiving the desired response from the subpopulation that has taken the action over the relevant probability of the sub-population that has not taken the action. The proposed model was tested on the Hillstorm-visit-w dataset. Experimental results showed a 138 percent improvement in the area under the uplift curve which is a measure to assess an uplift model's performance.

1 Introduction

Using predictive models alone for some clinical or marketing purposes does not lead to desirable outcomes in terms of the effectiveness of the marketing campaign or clinical treatment on the targeted population. The task of these predictive models is to predict, based on several attributes, the class to which an instance belongs, or the conditional probability of it belonging to each of the classes. Consider a direct marketing campaign where potential customers receive a mailing offer [1].

In the context described, a common application of machine learning techniques entails the initial step of selecting a small pilot sample of customers who will be exposed to a marketing campaign. Subsequently, a classifier model is constructed based on the outcomes of this pilot campaign, to identify which customers should receive the campaign offer. The objective here is to target those customers who are most likely to make a purchase following the campaign. Nevertheless, an analysis of customer behavior reveals that relying solely on a predictive model to categorize customers into potential buyers and non-buyers is not yielding satisfactory results.

Some of the customers that were classified as potential buyers would have bought regardless of the campaign; therefore, targeting them will result in unnecessary costs. Other customers were going to make a purchase but were annoyed by the campaign. So not only an extra charge has been paid for sending the email, but the customer has also been lost [2].

The root cause of this occurrence lies in the absence of a clear understanding of why customers opted to make a purchase. It remains ambiguous whether a customer's decision to buy stemmed from a positive response to the marketing campaign or whether they would have made the purchase independently of any influence from said campaign. To execute a genuinely

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effective campaign, our objective should shift towards the identification of customers whose purchases are directly attributable to the campaign's impact—those who are predisposed to buy when targeted but unlikely to do so otherwise. Analogous issues surface in the field of medicine, where certain patients may naturally recover without medical intervention, while others may suffer more from the therapy's side effects than from the ailment itself. Consequently, through the judicious selection of individuals who are likely to respond positively to treatment, we can amplify the treatment's beneficial effects.

Uplift modeling provides a solution to this problem. The approach employs two separate training sets: the treatment set and the control set. The objects in the treatment dataset have been subjected to some action, such as a medical treatment or a marketing campaign. The control dataset contains individuals who have not been subjected to the action. They are used as a background to assess the causal effect of the action. Unlike common predictive modeling approaches that model the probability of the individual belonging to a given class, uplift modeling attempts to model the difference between conditional class probabilities in the treatment and control groups. Thus, the causal influence of the action can be modeled, and the method is able to predict the true gain (with respect to taking no action) from targeting a given individual.

The biological immune system is a system that can detect pathogens invading the body and react to their invasion using cellular signals and interactions. The artificial immune system is a soft computing approach inspired by the biological immune system of mammals. This approach has some interesting features like distributed detection [3], noise tolerance [4], and reinforcement learning [5] the AIRS algorithm is an artificial immune system-based approach that has performed very well in classification and predictive modeling.

Until today, various approaches have been employed for constructing uplift models. This research endeavors to enhance the performance of uplift modeling by leveraging features derived from artificial immune systems, including their evolutionary nature, learning capability, and swarm intelligence. The goal was to exploit population-based methods inspired by the immune system to improve the efficiency and effectiveness of uplift modeling in capturing intricate patterns and optimizing uplift models. The integration of the AIS algorithm presented promising prospects for enhancing decision-making and targeted interventions, particularly in the context of large-scale datasets with dynamic environments. The performance measure used in this research is the Area Under the Uplift Curve, a widely adopted metric in uplift modeling. In this regard, the AIRS algorithm, one of the most practical approaches within the artificial immune system domain, was employed to develop an uplift model based on an artificial immune system framework that can address uplift modeling problems with a credible value for the Area Under the Uplift Curve. This study establishes the model architecture based on AIRS as a foundation for designing the model, exemplifying how population-based approaches can be employed and framed to tackle uplift modeling problems and evaluate the efficacy of such a model architecture.

The rest of this paper is organized as follows: Section 2 provides more details about uplift modeling and AIRS, Section 3 is dedicated to previous and related works, Section 4 describes the proposed method in detail, Section 5 provides the experimental results and Section 6 summarizes and concludes the work.

2 Research Literature

Uplift modeling comprises a range of techniques utilized to model the incremental impact of an action or treatment on a population and to gauge the response of that population in reaction to the action or treatment. To build an uplift model, first, the population should be divided into two subpopulations named C and T. Objects of the T group were exposed to some action like a marketing campaign or clinical treatment but the objects of the C group were not. The T group is called the Treatment population and the C group Control Population. In the binary case, the outcome variable is in the form of $Response \in \{0, 1\}$, in which the $Response = 1$ is considered as a desirable outcome. A conventional response model tries to model the probability $P_x(\text{Response} = 1|T)$. It's the probability of an individual, described by the variables x, returning the desirable outcome given that they are in subpopulation T. Notice that this technique ignores the subpopulation C. Contrary to a response model, an uplift model tries to perform modeling according to 1 [6].

$$U_x = P_x(\text{Response} = 1|T) - P_x(\text{Response} = 1|C) \tag{1}$$

This equation models the increase in the probability that an individual will return the desired response given that they are in subpopulation T over the relevant probability where they are in subpopulation C.

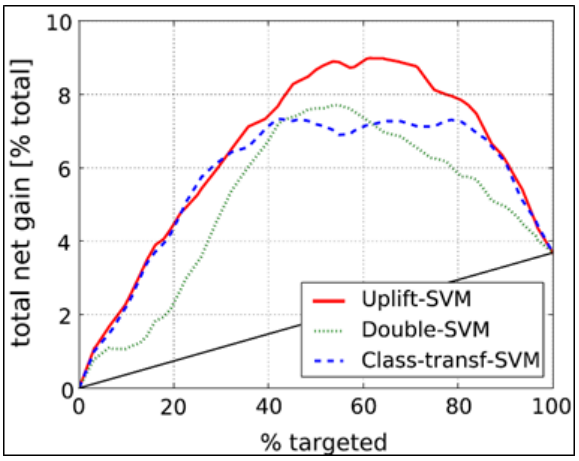

Figure 1. Uplift Curves for the Breast Cancer Dataset for Three Different Approaches [7].

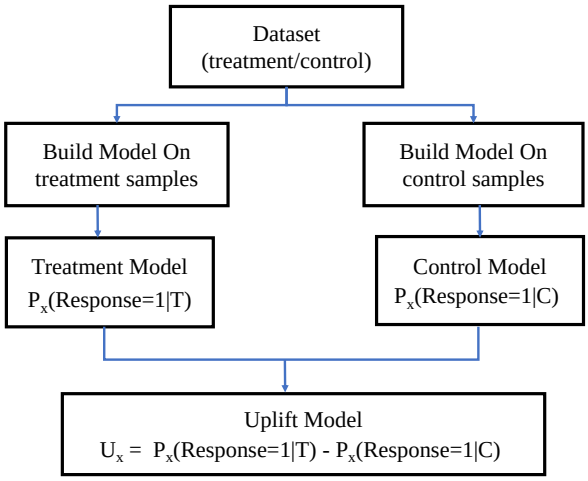

Figure 2. Uplift Model Building Procedure.

2.1 Development of an Uplift Model

To assess the effect of the action taken on any individual in a dataset like X, the effect of action should be measured at the level of that individual. For every individual in the dataset, this effect will be determined by the value of the uplift score and symbolized by U_x. In order to estimate the value of the uplift score for any individual, the success probability of being affected by the action should be calculated for that individual. One method for building an uplift model is to build two separate predictive models on Treatment and Control datasets. This method of building the uplift model is known as the Two Model Approach in the literature. The amount of uplift is calculated by placing the value of predicted scores by both models in Equation 1 [6]. Figure 1 shows the uplift curves created by different models.

The performance of an uplift model can be determined by estimating the area under the uplift curve [8]. In this kind of curve, the X-axis represents the number of samples that have been affected by a specific action. The Y-axis represents the model success rate for every targeted percentage of the population. For creating an uplift curve, an uplift model should be utilized to score both treatment and control groups. The mentioned scoring should be done by the model created using equation 1. After scoring every object presented in the validation set, the difference between the incremental curve of the control and treatment groups will be calculated. Consider the number of data samples that have been exposed to take some action in dataset D would be symbolized by N_T and those not subjected to the action would be symbolized by N_C. Lift represents the number of true positives detected by model m amongst the top-ranked fraction f. Varying $f \in [0, 1]$ produces a lift curve. The area under the lift curve (AUL) for a given model and data is calculated using equation 2 [8].

$$\begin{aligned} AUL &= \int Lift(D, f)\mathrm{d}f \\ &\approx \frac{1}{2} \sum_{k=1}^{N_t+N_c} (f_{k+1} - f_k) + Lift(D, f_k) \end{aligned} \tag{2}$$

By having the area under the lift curves for control and treatment groups, the area under the uplift curve can be achieved using equation 3 [8].

$$AUUC = AUL_t - AUL_c \tag{3}$$

2.2 Artificial Immune Recognition System

The biological immune system functions as a surveillance and defense mechanism that identifies and responds to the presence of invading pathogens within the organism through intricate cellular signaling and interactions. An essential component of this process is the antigen, a specific portion of a pathogen that serves as a recognizable target for the immune system. Upon the recognition of an antigen, the immune response is triggered, initiating a series of events. When antigens bind to receptors located on the surface of B cells, it initiates a stimulation process that leads to the proliferation and differentiation of these B cells. This phenomenon is referred to as clonal selection, as it involves the preferential expansion of B cells responsive to the specific antigen encountered. Consequently, the generated B cells can follow one of two paths: becoming memory cells or differentiating into plasma cells. Memory cells are integral for ensuring a more rapid and efficient immune response during subsequent encounters with the same pathogen, while plasma cells play a crucial role by secreting copious amounts of antigen-specific antibodies to neutralize

the invading pathogen [9].

In many Artificial Immune System (AIS) techniques, including the Artificial Immune Recognition System (AIRS), as discussed by Watkins et al. [10], the concept of antigen-antibody binding is referred to as "antigenic presentation." This concept serves as the foundation for matching training data, represented by antigens, with potential solutions, embodied by B-Cells. An Artificial Recognition Ball (ARB), as proposed by Timmis et al. [11], can be viewed as a representation of multiple identical B-Cells, serving to minimize redundancy and regulate the survival of these elements within the population. Upon determining the affinity between a B-Cell and an antigen, the involved B-Cell transforms a plasma cell, triggering a process known as clonal expansion. During clonal expansion, the B-Cell undergoes rapid proliferation (cloning) proportional to its degree of match with the antigen, resulting in an antigen-specific response. Subsequently, these clones undergo affinity maturation, a process that involves B-cell clones undergoing genetic changes known as somatic hypermutation, resulting in the development of antibodies with improved specificity for a particular antigen. Eventually, they undergo a selection process, from which certain cells may transition into memory cells. These memory cells are retained to enable a swifter response to the same or similar antigens in case of a host re-infection, a phenomenon recognized as the secondary immune response. Within the framework of AIRS, the principles of clonal expansion and affinity maturation are harnessed to encourage the generation of potential memory cells, which are later utilized for classification purposes.

In AIRS, ARBs experience a form of clonal expansion after being presented with training data (analogous to antigens). When new ARBs were created, they were subjected to a process of random mutation with a certain probability and were then incorporated into the memory set of cells should their affinity have met certain criteria. Within the AIRS system, ARBs competed for survival based on the idea of a resource-limited system [11]. A predefined number of resources existed, for which ARBs competed based on their stimulation level: the higher the stimulation value of an ARB the more resources it could claim. ARBs that could not successfully compete for resources were removed from the system. The term metadynamics of the immune system refers to the constant changing of the B-cell population through cell proliferation and death. This was present in AIRS with the continual production and removal of ARBs from the population. Table 1 summarizes the mapping between the immune system and AIRS. In the following, some of the key terms and concepts that are used in this paper are discussed [10].

Table 1. Mapping Between the Immune System and AIRS [10].

Immune System	AIRS
Antibody	Feature Vector
Recognition Ball	Combination of feature vector and vector class
Shape-Space	Type and possible values of the data vector
Clonal Expansion	reproduction of ARBs that are well matched with antigens
Antigens	Training data
Affinity Maturation	Random mutation of ARB and removal of the least stimulated ARBs
Immune Memory	Memory set of mutated ARBs
Metadynamics	Continual removal and creation of ARBs and memory cells

- **Affinity:** a measure of similarity between two antibodies or antigens. This value is guaranteed to be between 0 and 1 and is calculated as the distance between two feature vectors.
- **Antibody:** a feature vector coupled with its associated class; the combination of a feature vector and its class is referred to as an antibody when it's part of an ARB or memory cell.
- **Antigen:** a feature vector coupled with its associated class; the combination of feature vector and its class is referred to as an antigen when it's being presented to the ARBS for stimulation and/or response.
- **Artificial Recognition Ball (ARB):** also known as a B-Cell. It consists of an antibody, a count of the number of resources held by the cell, and the current stimulation value of the cell.
- **Class:** the category of a given feature vector.
- **Clonal rate:** an integer value used to determine the number of mutated clones a given ARB is allowed to produce. An ARB is allowed to produce up to ($clonal\ rate \times stimulation\ value$) mutated clones after responding to a given antigen.
- **Feature vector:** An array that represents different features associated with the data. Each feature has its range of legitimate values.
- **K value:** the parameter that indicates how many memory cells should be used to determine the classification of a given test item.
- **Memory cell (mc):** the antibody of an ARB that was the most stimulated by a given training antigen at the end of exposure to that antigen. Memory cells are used in the classification stage to determine the class of a given antigen.
- **Mutation rate:** a parameter between 0 and 1 that indicates the probability that any given feature or class variable of an ARB will be mutated.

- **Seed cell:** an antibody, drawn from the training set, used to initialize Memory Cell and ARB populations at the beginning of training.
- **Stimulation function:** a function used to measure the response of an ARB to an antigen or another ARB. The stimulation function is inversely proportional to the distance between the feature vectors of the ARB and the antigen. the value returned by the stimulation function is called the stimulation value.
- **Stimulation threshold:** a parameter between 0 and 1 used as a stopping criterion for the training on a specific antigen. When the average stimulation value of the ARBs of each class is above the stimulation threshold does training in reaction to the particular antigen stop.

3 Previous Works

In this section, we present an overview of previous works that have applied artificial immune systems (AIS) to various problem domains, highlighting their contributions and achievements. We then shift our focus to the realm of uplift modeling, exploring the existing literature on uplift modeling techniques and their respective advantages and disadvantages. By examining the advancements made in both AIS applications and uplift modeling, we aim to identify the gaps and challenges that motivate our research endeavor of leveraging AIS for improving uplift modeling performance.

3.1 AIS Previous Works

The AIS algorithms have a wide range of capabilities that can be applied to a diverse range of problems. For instance, [12] enhanced a Mobile Ad Hoc Network security by using a danger theory-based AIS system. Their method relies on an artificial immune system to distinguish between a genuine node and a selfish node within a Mobile Ad Hoc Network. Their proposed scheme performed better in terms of packet delivery ratio and detection rate when misbehaving nodes were presented compared to other well-known approaches. However, classification is not the only application of AIS.

This method can also be used to perform optimization tasks. An example of this is the research conducted by [13] for accurately detecting satellite faults by applying an AIS-based optimization to a Support Vector Machine (SVM). Through the dynamic measurements of the spacecraft, the proposed system was used to monitor spacecraft health throughout the mission. Another application that faces several challenges in optimization is Image steganography. The reason for this is that in image steganography various heuristic cost functions ensure undetectability due to their heuristic design. In difficult problems like this, AIS's optimization capability can be leveraged. As a result, [14] proposed a cost adjustment algorithm for adaptive steganography based on AIS. Through the immunity-based information masking model, they dynamically optimize the adjustment mode by reassigning the cost based on the modification probability distribution of the cost function. Consequently, modified pixels are more concentrated in difficult-to-detect regions.

AIRS is one of the AIS algorithms that is capable of solving various detection, classification, and optimization problems. It has been successfully applied to a range of applications. In 2022, Jagadeeshwaran et.al. proposed an AIRS-based solution for detecting brake system faults in cars by vibration analysis [15]. This was accomplished by collecting vibration signals under various brake faults and classifying the extracted statistical data using the AIRS. Then, a diagnostic module based on this classifier is proposed for categorizing and displaying brake faults in the car infotainment system.

It was also shown that AIRS performed very well when it came to predicting air quality. Lasisi et.al. [16] proposed a high detection rate (96.40%) and low false alarm rate air quality prediction strategy based on AIRS. By using their selected strategy, they demonstrated that estimates of air quality can be made accurately and control measures can be implemented quickly.

AIRS can also be used for feature selection. In 2021, a hybrid feature selection method based on AIRS was proposed by Ridok et al. for rapid and accurate identification of the cancer cell pattern from the cell biopsy [17]. Their method achieved an accuracy of 98% in identifying cancer cells.

3.2 Uplift Modelling Previous Works

Improving the performance of uplift models proved to be a challenging research problem. In 2010 Piotr Rzepakowskiand and his co-researcher [18] proposed a decision tree-based approach in which they used two distribution divergence measures as splitting criteria, the Kullback-Leibler divergence [19, 20] and the squared Euclidean distance. They also designed a tree pruning method specifically for uplift modeling. Their idea was to look at the differences between treatment and control probabilities at the root of the subtree and in its leaves and prune if, overall, the differences in leaves are not greater than the difference in the root. Their experimental results were competitive regarding previous uplift modeling approaches. In 2012 they extended their approach to use uplift decision

trees not only for a two-class classification problem but a multi-class classification approach that can be used in multiple treatment cases [21]. Additionally, splitting criteria based on chi-squared divergence were introduced and analyzed.

A Statistical Relational Learning algorithm was proposed for building uplift models in 2013. This algorithm was applied to diagnose breast cancer [22]. This method is named Score As You Lift (SAYL). It combines Statistical Relational Learning with the marketing concept of uplift modeling. The area under the uplift curve is used to direct clause construction and evaluation of the theory. Experimental results showed that SAYL performed better than other previous approaches on a mammography application, while still generating human interpretable models. One of the major disadvantages of the proposed work is the lack of comparability with other methods in the Uplift modeling literature. The author has compared only his proposed method which is a kind of uplift modeling, with methods other than those related to uplift modeling.

In 2015, an ensemble-based approach was introduced by Soltys et al. [23] to investigate the application of ensemble techniques, such as bagging and random forests, in the context of uplift modeling. Through a series of experiments, this research sought to assess the efficacy of these ensemble methods in uplift modeling. The experimental results consistently demonstrated that the utilization of ensemble techniques often led to substantial improvements in model performance, effectively transforming initially ineffective single models into highly proficient uplift ensembles. These improvements exceeded those achievable through standard classification methods. The proposed approach attributed these gains primarily to the considerable diversity within the ensembles, a diversity arising from the inherent difficulty in modeling differences between class probabilities in treatment and control groups, as opposed to modeling class probabilities themselves. However, it is important to note that employing ensemble methods also entails increased time and computational complexity. Furthermore, when treatment assignments are non-random and exhibit bias, estimating the true effect of the action becomes challenging. Consider, for example, a medical treatment with potentially severe side effects, where doctors may opt not to administer it to patients in critical condition, thus placing them in the control group. Consequently, these patients may have lower chances of recovery, making the control group outcomes appear worse and the treatment's effectiveness seemingly greater than it is in reality.

Szymon Jaroszewicz and Łukasz Zaniewicz presented an Uplift Support Vector Machine approach with an additional penalty term [24]. They called this penalty term Székely regularizer which is based on the energy distance between probability distributions proposed by Székely and Rizzo [25, 26]. The distance has the property that it is zero if and only if the distributions are identical; therefore, it can be used to enforce similar distributions of model scores in the treatment and control groups. As a result, uplift models that can be obtained are additionally forced to make similar predictions on the treatment and control groups. This helps to reduce the effect of treatment assignment bias. In their experiments on biased datasets, an increase in the Székely penalty term resulted in decreasing the differences between scores the model assigns to treatment and control records accompanied by large improvements in model performance.

In 2017 they extended L p-SVMs to the case of uplift modeling. and demonstrate that they allow for a more stable selection of the size of negative, neutral, and positive groups [7]. They also presented quadratic and convex optimization methods for efficiently solving the two proposed optimization tasks. They assessed the performance of their approach on 28 different datasets and the results showed that their approach performed better in 19 out of 28 datasets compared to other investigated approaches.

Yan Zhao and his co-researchers proposed a new tree-based ensemble algorithm for uplift modeling in 2017 [27]. They took advantage of the fact that the Contextual Treatment Selection (CTS) algorithm which generates tree-based ensembles also leads to significant performance improvement for uplift modeling problems [28]. They described a modified version of CTS called the Unbiased Contextual Treatment Selection (UCTS) which eliminates the estimation bias of leaf responses by using separate data sets for partition generation and leaf estimation. Their experiments showed that the presented approach achieves competitive results on both synthetic and industry-provided data. In addition, they showed that by properly tuning the "node size" parameter, the algorithm is proved to be consistent under mild regularity conditions.

Previous methods in uplift modeling, such as decision tree-based [18, 21, 27], Statistical Relational Learning [22], ensemble approaches [23, 27], and SVM-based models [7, 24], have certain shortcomings that hinder their effectiveness in solving uplift modeling challenges.

Decision tree-based methods often struggle to capture intricate interactions and complex patterns in data, limiting their predictive power for uplift modeling [29]. Statistical Relational Learning approaches may face challenges in scaling to large datasets and

handling dynamic environments due to their computational complexity [30]. Ensemble approaches, while effective in improving predictive performance, may lack interpretability [31], making it difficult to gain insights into the underlying factors driving uplift. SVM-based methods, on the other hand, may suffer from limited scalability and struggles in handling high-dimensional feature spaces [32].

To address these shortcomings, Artificial Immune System (AIS) approaches offer promising solutions. AIS algorithms, with their evolutionary nature and learning capabilities, can effectively capture complex patterns and interactions in data [3]. They provide an adaptive framework that can handle large-scale datasets and dynamic environments by dynamically adjusting their parameters and strategies [11].

Additionally, the rule-based nature of AIS algorithms enables interpretability and explainability [33], allowing practitioners to gain insights into the uplift model's decision-making process. By leveraging these features, AIS-based uplift modeling approaches can overcome the limitations of previous methods and provide improved performance, scalability, interpretability, and adaptability in the context of uplift modeling.

4 Proposed Method: Artificial Immune System-based Uplift Modeling

In this research, an algorithm based on artificial immune system is presented for building uplift models. The input of the algorithm is a list of validation set antigens and the output is the predicted uplift score for each antigen. Once the antigens are prepared, the algorithm proceeds by utilizing a specific method to calculate the Area Under the Uplift Curve. This measurement helps evaluate the performance of the uplift model. In Figure 3 the pseudo-code of the suggested method is shown. The detailed description of pseudo code will be discussed step by step.

4.1 Data Pre-processing

The first step of the algorithm is to preprocess the data. At the beginning of this stage, a binary variable called Action is added to the dataset as a predictive variable. The reason behind adding the Action variable is that in the binary case, for analyzing the effect of the action on the objects of the dataset, the action can only have two distinct values: "took action" and "took no action". If a dataset lacks this variable by default, it should be added in the preprocessing stage. The value of this variable in the feature vector for a given record of the dataset would be considered "false" if no action is taken on the object representing this

Input: Dataset DS containing Treatment and Control records
Output: Area Under Uplift Curve

```
1. Preprocess the data
2.     Introduce an Action Variable as follows:
3.     If (Action is taken)
4.       Action = true;
5.     else
6.       Action = false;
7.    Create a list of Antigens using each record of DS and call it the Antigen population
8.       Partition the Antigen Population into two subsets: Training Set and Validation Set
9. Build a prediction model PM using AIRS classifier on the training set
10. Calculate the uplift for the Validation Set using the Uplift Calculation Unit
11.      Score the validation set using PM (Stage 1 classification)
12.      For each Antigen Ag in the validation set
13.                    Ag.Stage1PredictedScore = PM.predictedScore(Ag)
14.      For each Antigen Ag in the validation set
15.        Reverse the value of the Action variable
16.       Score the validation set using PM (Stage 2 classification)
17.       For each Antigen Ag in the validation set
18.                    Ag.Stage2PredictedScore = PM.predictedScore(Ag)
19.      For each Antigen Ag in the Validation Set
20.      If (Stage1Action value is 1 for the current AG)
21.         Ag.upliftScore = Ag.Stage1PredictedScore - Ag.Stage2PredictedScore
22.       else
23.         Ag.upliftScore = Ag.Stage2PredictedScore - Ag.Stage1PredictedScore
24. Produce the Uplift Curve for the Validation Set Antigen List using the Uplift Curve Creator Unit
25.    Sort the Antigen list in the validation set
26.    Build an uplift curve UC using Uplift Curve Creator Unit
27.    Calculate the area under the uplift curve AUUC for UC
28. Return AUUC
```

Figure 3. Algorithm for Calculating Area Under Uplift Curve.

record, and "true" if the object is subjected to the action. This procedure is done in lines 2-6 of Figure 3 pseudo-code.

In the next two steps of preprocessing, requirements for using datasets in artificial immune system-based algorithms are prepared. The process begins with building antigens and forming a list of antigens to be used as input to the algorithm. This is done in line 7 of Figure 3 pseudocode. Antigens at the start are

utilized for building the AIRS classifier and then for creating the uplift curve so that the area under this curve can be estimated. Therefore, for each record of the dataset, an antigen will be created representing that record of the dataset. These antigens form a list of antigens that can be used as input to the presented approach. The suggested structure for the antigen is shown in Figure 4. Antigen's constituent elements are as follows:

Uplift Score	Predictive Score (Stage2)	Predictive Score (Stage1)	Action State	Class	Feature Vector

Figure 4. Antigen Structure.

- **Feature Vector:** An array that can contain different types of attributes such as nominal, binary, or numeric attributes. These attributes act as predictor variables in the classification stage. Figure 5 shows a sample feature vector of a record of the dataset.

id	recency	History Segment	history	mens	segment	Action
179	5	3)-200−350	269.99	True	Mens E-mail	True

Figure 5. A Sample Feature Vector of a Record of the Dataset.

- **Class:** This feature is used in the training stage of the AIRS classifier in the process of proliferating memory cells and ARBs. It is also used in detecting the correct class of the antigen and in calculating the predictive score for the antigen. Class attribute types can be nominal, binary, or numeric.
- **ActionState variable:** To assess the effect of the action on each object of the dataset, it's necessary to perform the classification and predictive score calculation process in two stages: "taking the action" and "taking no action". Therefore, the ActionState variable is embedded inside the antigen structure to store the state of action in the first stage of classification and predictive score calculation. This variable can have True or False values. The value of the ActionState variable in the second stage of classification and predictive score calculation can be obtained by reversing the value from True to False or vice versa.
- **Predictive Score:** The likelihood of the antigen belonging to the detected class is recognized as the predictive score for that antigen. According to equation 1, to calculate the uplift value, the classification and predictive score calculation should be performed in two stages. In one stage the predictive score of the antigen where it is subjected to the action will be estimated and stored in its relative field. In the other stage, the predictive score will be estimated and stored where the antigen is not subjected to the action. To store these estimations, "Predictive Score (First Stage)" and "Predictive Score (Second Stage)" are embedded in the antigen structure.

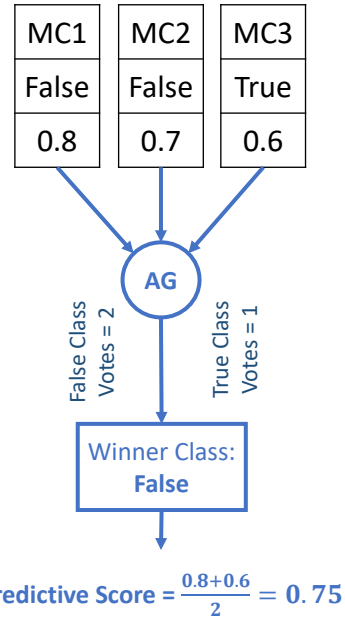

Figure 6. Classification and Predictive Score Calculation Process for a Given Antigen.

Figure 6 depicts the process of performing classification and calculating the predictive score for a given antigen. Assume that an AIRS classifier has been built on the training set and has completed the training phase. The classification and predictive score calculation can now be done using the memory cells list that was produced in the training phase. To do that, every memory cell existing in the list of memory cells is exposed to the antigen presence. The stimulation value is calculated for each memory cell using equation 2. Then the K most stimulated memory cells are selected for doing the classification task. The class of antigen is determined using a majority vote from among K's most stimulated memory cells. The probability of the antigen belonging to a class of winner group in voting is considered the average of the winner's stimulation values. This probability value is stored in the antigen as "Predictive Score (First Stage)" or "Predictive Score (First Stage)".

- **Uplift Score:** This value is calculated using equation 1 and is stored in its relative field.

The final step of preprocessing is to divide the anti-

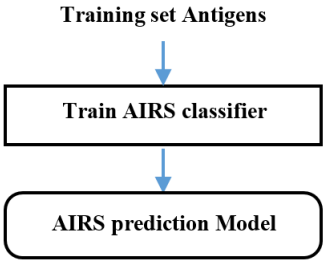

Figure 7. Steps to Build AIRS Prediction Model.

gen list into two separate lists of antigens for training and validation purposes. Antigens of the training set are used for training and building the AIRS classifier model and antigens of the validation set are to score the model and uplift calculation process.

4.2 Building a Predictive Model

To calculate the predictive score of each antigen, it's necessary to build a predictive model for estimating the conditional probability mentioned in equation (1). To build such a model, an AIRS classifier is developed. This is done in line 9 of Figure 3. Figure 7 shows the way to build the AIRS predictive Model.

4.3 AIS-Based Uplift Model

The prediction model having been prepared, an uplift model can be designed and developed to estimate the amount of uplift produced by each individual in the dataset. To do that, a unit called Uplift Calculation Unit (UCU) is introduced. This unit takes the antigen list as input. By performing procedures of lines 10 to 23 of the pseudocode previously explained in detail in 4.3.1 of this article, UCU can calculate the uplift value for every antigen in the validation set.

4.3.1 Uplift Calculation Unit

According to Figure 8, the input to UCU is a list of validation set antigens. At the beginning, this list is scored by the AIRS predictive model. This operation is called the first stage of scoring. After the first stage of scoring is finished, the calculated score that the AIRS model predicts for each antigen is stored in the antigen as its first-stage predictive score.

The next step is to invert the value of the Action variable for the feature vector of every antigen in the list. This inversion process is done using equation 4. Figure 9 shows an example of inverting the value of the Action variable for three sample antigens and their feature vectors.

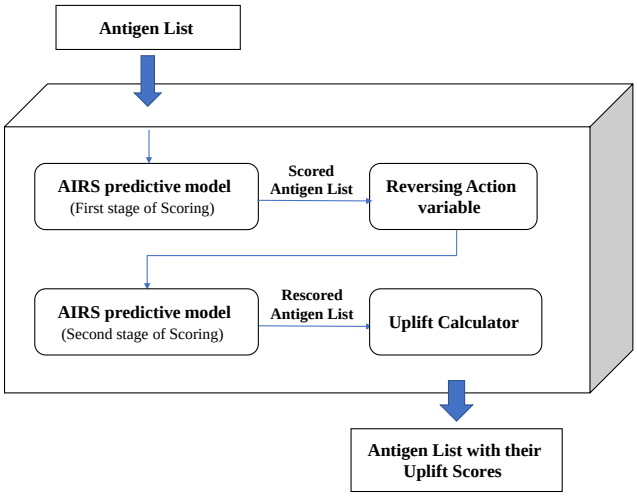

Figure 8. Uplift Calculation Unit Block Diagram.

id	recency	History segment	history	mens	segment	Action
1	10	$200 - $100 (2	142.44	1	Womens E-Mail	True
2	6	$350 - $200 (3	329.08	1	No E-Mail	False
3	7	$200 - $100 (2	180.65	0	Womens E-Mail	True

Inverting the value of Action variable

id	recency	History segment	history	mens	segment	Action
1	10	$200 - $100 (2	142.44	1	Womens E-Mail	False
2	6	$350 - $200 (3	329.08	1	No E-Mail	True
3	7	$200 - $100 (2	180.65	0	Womens E-Mail	false

Figure 9. Inversion Operation for Three Sample Antigen Feature Vector.

$$Action = \begin{cases} True & \text{if } Action = False \\ False & \text{if } Action = True \end{cases} \quad (4)$$

By performing this inversion process, the status of each antigen can be assessed in both "Taking Action" and "Taking No Action" states. After finishing the inversion process, the list of antigens with their new value for their Action variable is handed to the AIRS model as input. The AIRS model classifies each antigen and then calculates the predictive score for them. This operation is called the second stage of scoring.

The second stage of scoring is finished, and the predictive scores for both the first and second stages of the prediction are already stored in their relative fields inside the antigen structure. Now the last step of the uplift calculation process can be done by assessing the causal effect of the action for each antigen using equation 1. To analyze this issue more clearly, the antigen Ag1 in Figure 10 is analyzed through the process. This antigen has passed the second stage of scoring.

Null	0.8998	0.9998	True	0	FV1

Figure 10. Status of the Antigen After the Second Stage of Scoring.

As the relative field of the ActionState variable in antigen bears the value of True, the calculated predictive score in the first scoring stage is related to the state where the antigen has taken action. It can be concluded that the estimated predictive score in the second scoring stage is related to the state where the antigen has not taken the action. Accordingly, the first stage predictive score is considered as the probability that an individual will return the desired response given that he takes the action. Therefore, the second stage predictive score is considered as the probability that an individual will return the desired response given that he takes no action. It's now possible to set Equation 1 with relative probability values of the first and second-stage predictive scores as follows.

$$P_{Ag1}(Success|Action = True) = 0.9998$$
$$P_{Ag1}(Success|Action = False) = 0.8998$$
$$U_{Ag1}(Success|Action = True) = P_{Ag1}(Success|Action = True) - P_{Ag1}(Success|Action = False) = 0.1$$

After estimating the uplift score for the given antigen, this value is stored in the uplift score field for the antigen. Figure 11 shows the antigen status after performing the uplift score calculation by UCU. The highlighted field shows the stored value of the uplift score in antigen structure.

0.1	0.8998	0.9998	True	0	FV1

Figure 11. Final State of the Antigen After Passing the Uplift Calculation Step.

The example depicted in Figure 12 shows how the UCU operates step by step. In this figure, three antigens are selected to form the validation set antigen list. This antigen list is used as input for UCU. Antigens of this list are passing the first and second stages of scoring respectively. In the end, they finish the process of uplift calculation by calculating the uplift value for each one using Equation 1 and storing this value in their relative fields.

4.3.2 Uplift Curve Producer Unit Calculation Unit

The objective of uplift modeling is to find individuals in a population who are affected the most by the action. Individuals having this feature are those who produce the highest uplift score. In the proposed algorithm each antigen represents an individual in the population. Hence, sorting antigens in descending order regarding their uplift score helps to generate the largest amount of uplift in the first decades of population. By doing so, targeting fewer percentages of the whole population

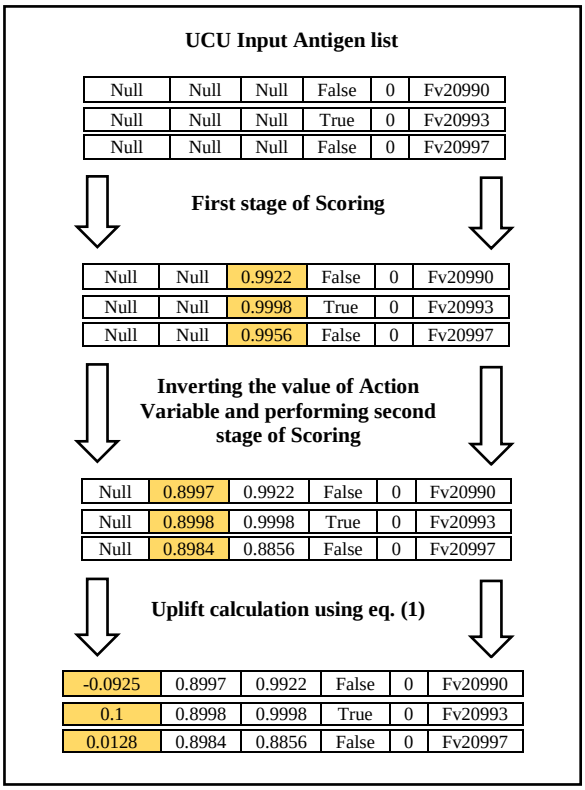

Figure 12. An Example of UCU Operation on an Input Antigen List.

leads to spending the least cost and achieving the highest productivity.

Based on these facts, the first thing the Uplift Curve Producer Unit (UCPU) does is to sort the antigens in the antigen list in descending order regarding their uplift score. Then, the uplift is summed up for each percentage of the population in the sorted list. These calculated uplifts for each percentage of the population are coupled with their respective percentage of the population and form an array of uplift scores for the whole percentage of the population. Each index of the array is regarded as a percentage of the population and the value stored in that index represents the amount of uplift that can be produced by that percentage of the population. Therefore, each index of the array with its relative value represents a point in the uplift diagram. With the array of uplift scores for the whole population, a curve named uplift curve can be drawn in a two-dimensional space.

The horizontal axis of the uplift diagram represents the percentage of the population and the vertical axis is the amount of uplift produced by that percentage of the population. The domain of the horizontal axis includes all the integers in the interval of [0,100]. The domain of the horizontal axis includes all the real numbers in the interval of $[-\infty, +\infty]$. The area under the uplift curve (AUUC) is a performance measure of

an uplift model. In order to obtain a more meaningful number, a subtraction of the area under the diagonal line from the value of AUUC is done [13]. The AUUC is calculated using equation 3. The produced uplift curve and the diagonal line are shown in Figure **??**. The discussed operation is mentioned in lines 24-28 of Figure 3 pseudocode.

5 Experimental Results

Experiments were done using a computer with specifications of Intel® Core™ i7-4700HQ CPU with a frequency of 2.40 GHz, 8GB DDR4 RAM, and Windows 10 64-bit operating system. All experiments were performed in a 5-fold cross-validation manner, splitting each dataset into training (80 % of the data) and test (the remaining 20 %) parts. Each experiment was repeated 128 times, and the resulting uplift curves were averaged.

The benchmark dataset selected to assess the performance of the proposed approach was the Hillstorm-visit dataset [34] containing 64000 records of different customers, split into three parts based on the type of email they got, Control Group got no-email, Women's Group, and Men's Group. In this paper, the hillstorm-visit-w dataset containing only the women's group was used. The women's group campaign was considered as the group that had taken the action. And the control group which didn't receive any email was considered to be the group that did not take action.

5.1 Measuring the Effect of the Stimulation Threshold Parameter

The first parameter that has a direct effect on the uplift score is the stimulation threshold parameter. The reason behind this is that only the ARBs with higher stimulation than the stimulation threshold can go through the clonal expansion and mutation process. Therefore, choosing a small value for the stimulation threshold leads to a larger amount of ARBs capable of doing the clonal expansion process. A disadvantage of selecting a small value for the stimulation threshold is that some of these ARBs have a lower stimulation with the antigen. The antibody of these ARBs will have the chance to form a memory cell. This memory cell will be used in classification and predictive score calculation. If the number of these memory cells increases, the classification accuracy and the uplift calculation process will be done with lower efficiency.

An advantage of selecting a small value for the stimulation threshold is that an antibody of an ARB with low stimulation with antigen does have the chance to form a good memory cell after passing the mutation

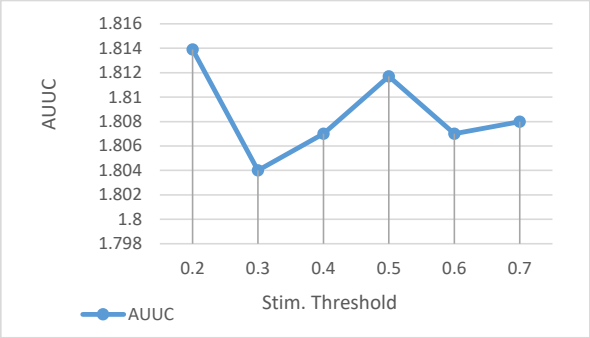

Figure 13. Effect of Stim. Threshold Parameter on AUUC.

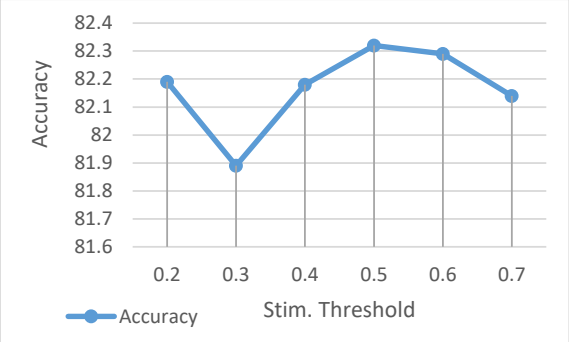

Figure 14. Effect of Stim. Threshold Parameter on Classification Accuracy.

stage. If a large value of stimulation threshold is selected, the ARB with lower stimulation to the antigen will not have the chance to undergo clonal expansion. Some of these ARBs may be capable of producing good memory cells if they can get the chance to pass the mutation process. So, varying stimulation threshold values may lead to a positive or negative impact on the performance of the presented approach.

Therefore, in order to choose an optimal value for the stimulation threshold parameter, it's necessary to design an experiment to analyze the effect of this parameter on model performance. The diagram shown in Figure 13 shows the effect of the stimulation threshold parameter on the AUUC produced by the model. The diagram of Figure 14 shows the effect of the stimulation threshold parameter on the classification accuracy of the model. To observe the effect of the stimulation threshold parameter, all other parameters of the AIRS are considered to be constant.

As indicated in Figure 13, by increasing the stimulation threshold from 0.2 to 0.7, the area under the curve experiences several fluctuations. Meanwhile, when the value of the stimulation threshold is 0.2 or 0.5, the model shows better performance in terms of the area under the uplift curve.

In Figure 14, by varying from 0.2 to 0.3, the model accuracy is decreased. The reason for the decrease

in accuracy is that the ARBs with low stimulation threshold values can undergo the clonal expansion and mutation process. The antibody of these ARBs may be selected as the candidate to produce a memory cell. This memory cell has lower quality in classification operation with respect to other memory cells with higher values for stimulation threshold. This low-quality memory cell can take part in the classification operation and voting process. This leads to misclassification and decreases the model accuracy.

As the diagram of Figure 14 shows, the best interval for stimulation threshold value is $[0.4, 0.6]$ because the highest value for accuracy exists in this interval. Also, the accuracy in the interval of $[0.5, 0.6]$ is descending with a much lower slope. It can be observed that the best value for stimulation threshold can be obtained in 0.5 because at this point the best value for AUUC and model accuracy can be achieved by the model.

5.2 Measuring the Effect of the K Parameter

One of the other parameters that can affect the amount of the area under the uplift curve is the K parameter of the AIRS model. Because by varying the value of K the number of memory cells taking part in the classification stage can be decreased or increased. Also, the first and second stages of predictive scores are computed using the average of the estimated probabilities of winner memory cells in the voting process. Hence, it's necessary to design experiments in order to choose the best value for the K parameter. The diagram of Figure 15 shows the behavior of AUUC in reaction to various values of the K parameter. Figure 16 shows model accuracies for different values of the K parameter.

As is clear from Figure 15 by increasing the value of the K parameter and keeping a constant value for other AIRS parameters, the AUUC experiences a decrease in value. Unlike the behavior of AUUC, as is shown in Figure 16, the accuracy of the model has increased by increasing the value of the K parameter. The reason behind such a decrease in AUUC is that by increasing the value of the K parameter, the number of memory cells participating in the classification and predictive score calculation stages will increase. Therefore, as the number of memory cells increases, the accuracy of the model increases, but low-quality memory cells produce lower prediction probabilities. This leads to a decrease in the AUUC. Hence, it's necessary to choose an optimal value for K so that a balance between AUUC and model accuracy can be established.

As the two experiments of Figure 15 and Figure 16 show, the K=7 has produced good results in terms of accuracy and AUUC. Despite the fact that in K=7 compared to K=15 the difference in model accuracy

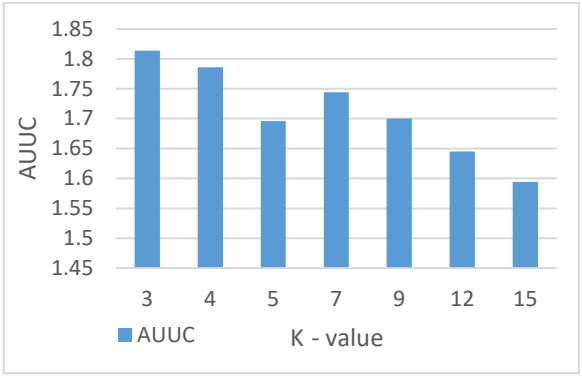

Figure 15. Amount of AUUC Produced by Different Values of the K Parameter.

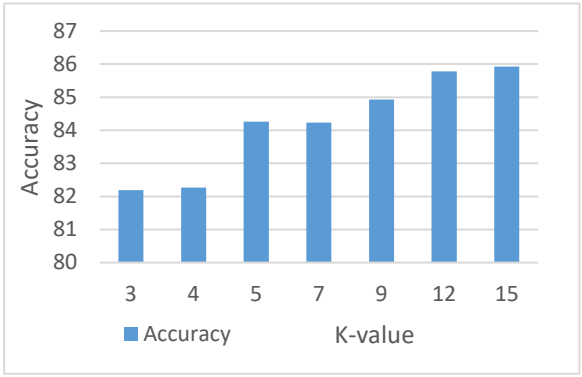

Figure 16. Model Accuracy Produced by Different Values of K Parameter.

is about 2 percent, the AUUC of K=7 is nearly twice as much as the AUUC of K=15. Also, the difference between the AUUC of K=7 and K=3 which is the maximum value for AUUC, is about 0.1. So, it can be concluded that the best value to set the K parameter is 7.

5.3 Measuring the Effect of Varying Stimulation Threshold Parameter for Different Values of the K Parameter

As previous experiments showed, changing K and stimulation threshold values in AIRS settings had influenced the model performance largely. Accordingly, an experiment is designed to analyze the effect of changing the stimulation threshold parameter on AUUC and model accuracy by considering three different constant values for the K parameter. Figures 17 and 18 show the results of the experiment for AUUC and model accuracy. As can be seen in Figure 17, by increasing the stimulation threshold and considering the values of 7 and 3 for the K parameter, the values of AUUC are more stable than the values established for K=15. In Figure 18, by increasing the stimulation threshold and considering the values of 7 and 3 for the K parameter, the model accuracies show less fluctuation. However,

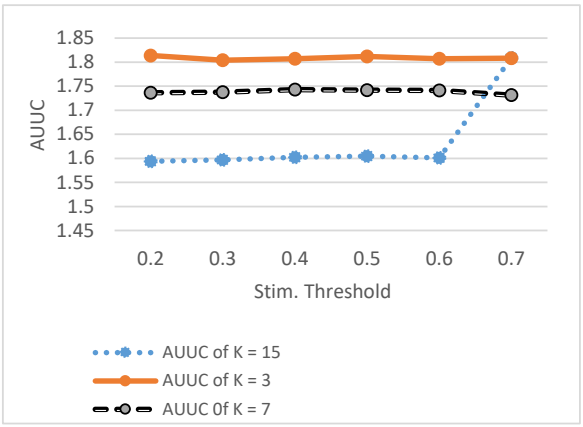

Figure 17. AUUC for Different Values of K and Stim.

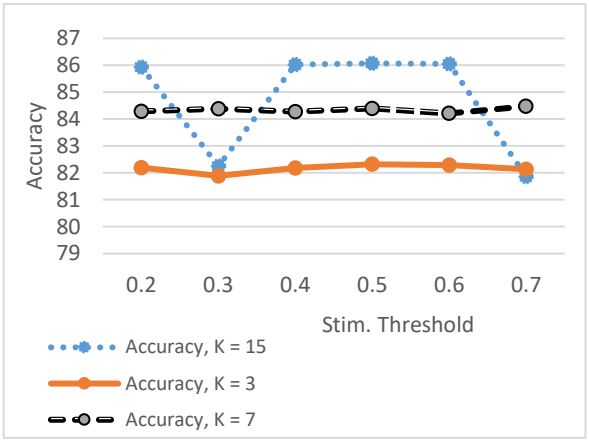

Figure 18. Model Accuracy for Different Values of K and Stim. Threshold.

in almost all values of the stimulation threshold, the values established for K=15 have performed better than K=3 and K=7 in terms of model accuracy.

K=15 shows significant instability in both the model accuracy and AUUC. Also, K=15 achieved less AUUC proportionate to K=3 and K=7. Therefore, it can be concluded that the value 15 should not be used in order to set the value of the K parameter.

K=7 has achieved good results in terms of model accuracy and AUUC. K=7 has achieved 2 percent accuracy more than K=3 and the AUUC of K=7 is nearly twice as much as the AUUC of K=15. Also, the difference between the AUUC of K=7 and K=3, the maximum value for AUUC, is about 0.1. So, the best value to set the K parameter is 7.

5.4 Performance Comparison with other Existing Uplift Modeling Methods

An experiment was done on the hillstorm-visitw dataset, to assess the performance of the proposed approach against other existing uplift modeling approaches. In this experiment, the number of seed ARB

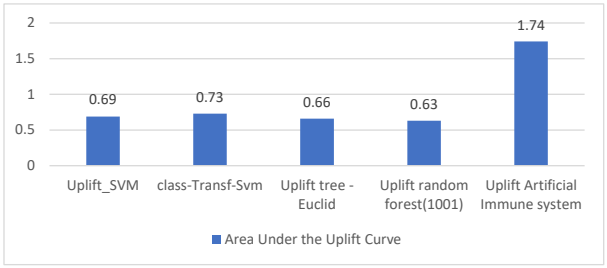

Figure 19. Comparison of Presented Approach Against other Uplift Modeling Approaches.

cells is set to 20 percent of the training set antigens. Also, the number of seed memory cells is set to 10 percent of the training set antigens. The number of allowed resources in the system was set to 100. The mutation rate, stimulation threshold scalar, clonal rate, and K parameter are respectively set to 0.5, 0.5, 5, and 7.

As Figure 19 shows, the presented approach achieved a relatively good performance in terms of the area under the uplift curve with respect to other compared approaches. For the purpose of comparison, we directly extracted the area under the uplift curve of the other approaches shown in Fig. 19 from their reported results. No simulations were conducted using their proposed algorithms.

As experimental results show, the utilization of the AIS-based model architecture has significantly improved the efficiency of uplift modeling. By harnessing the power of population-based methods, the AIS algorithm enhanced the exploration and exploitation of the solution space, enabling uplift models to capture intricate patterns and interactions that traditional approaches overlooked.

The AIS algorithm introduced diversity in the solution space through mechanisms inspired by the immune system, preventing premature convergence to suboptimal solutions and facilitating the discovery of novel and effective uplift models. Additionally, the adaptive nature of the AIS algorithm allowed it to dynamically adjust its parameters and strategies based on the specific problem at hand, ensuring that the uplift model remained robust and adaptable to changing data patterns. Furthermore, the AIS algorithm's ability to handle large-scale datasets and incorporate domain knowledge contributed to its improved the efficiency in uplift modeling. By leveraging parallel processing, distributed computing, and the integration of expert insights, the AIS algorithm streamlined the model training and evaluation process, leading to more efficient and interpretable uplift models. In summary, the AIS-based uplift model solved the uplift modeling problem with improved efficiency and effectiveness in capturing the true value of targeted

interventions.

6 Conclusions

Uplift Modeling is a branch of machine learning that aims at detecting subgroups in a population with a specific response or reaction to an action taken on the targeted group. By using the Control set, the causal effect of the action can be analyzed. The objects of the population can be extracted in the form of subgroups in proportion to the amount of effect they receive from the action. In this paper, an Artificial Immune System-based Uplift Model is introduced to solve uplift modeling problems with improved efficiency. To achieve this goal, an artificial immune system-based algorithm was designed using an AIRS classifier that can solve uplift modeling problems.

To assess the performance of the suggested method, a series of experiments were done on the Hillstorm-visit-w dataset. The value achieved by the presented approach for the area under the uplift curve is equal to 1.74 which shows a 138% improvement in the area under the uplift curve compared to other existing uplift modeling approaches.

It was demonstrated that the AIS-based model architecture not only solved the uplift modeling problems but also outperformed other compared methods. This could potentially open a new fruitful avenue for researchers to design and employ this type of model architecture for a similar set of problems.

To extend this research in the future, an attempt to build an unsupervised model using artificial immune system theory can be made. Memory cells can find clusters that produce more uplift than other clusters. It's also possible to use this model for multi-treatment objectives. In that case, memory cells should find the best clusters for each treatment producing the most uplift values.

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