# A HYBRID APPROACH FOR ARTIFICIAL IMMUNE RECOGNITION SYSTEM

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# ABSTRACT

Various data mining techniques are being used by researchers of different domains to analyze data and extract valuable information from a data set for further use. Among all these techniques, classification is one of the most commonly used tasks in data mining, which is used by many researchers to classify instances into two or more pre-determined classes. The increasing size of data being stored have created the need for computer-based methods for automatic data analysis. Many researchers, who have developed methods and algorithms within the field of artificial intelligence, machine learning and data mining, have addressed extracting useful information from the data. There exist many intelligent tools, which try to learn from the patterns in the data in order to predict classes of new data. One of these tools is Artificial Immune Recognition System (AIRS), which has been used increasingly. Results of AIRS have shown its potential for classification purposes. AIRS is an intelligent classifier offering robust and powerful information processing capabilities and is becoming steadily an effective branch of computational intelligence. Although AIRS has shown excellent results, it still has potentials to perform even better and deserves to be investigated. AIRS uses a linear function to determine the amount of resources that needs to be allocated and this linearity increases the running time and thus reduces the performance of AIRS. Resource competition part of AIRS poses another problem, here, premature memory cells are generated and therefore classification accuracy decreases. Further AIRS uses k-Nearest Neighbor (KNN) as a classifier and that makes it severely vulnerable to the presence of noise, irrelevant features, and the number of attributes. KNN uses majority voting and a drawback of this is that the classes with the more frequent instances tend to dominate the prediction of the new instance. The consequence of using KNN is ultimately reduction of classification accuracy.

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This dissertation presents the following main contributions with the goal of improving the accuracy and performance of AIRS2. The components of the AIRS2 algorithm that pose problems will be modified. This thesis proposes three new hybrid algorithms: The FRA-AIRS2 algorithm uses fuzzy logic to improve data reduction capability of AIRS2 and to solve the linearity problem associated with resource allocation of AIRS. The RRC-AIRS2 uses the concept of real-world tournament selection mechanism for controlling the population size and improving the classification accuracy. The FSR-AIRS2 is a new hybrid algorithm that incorporates the FRA, RRC, and the SVM into AIRS2 in order to produce a stronger classifier. The proposed algorithms have been tested on a variety of datasets from the UCI machine learning repository. Experimental results on real-world machine learning benchmark data sets have demonstrated the effectiveness of the proposed algorithms.

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# ABSTRAK

Pelbagai teknik perlombongan data telah digunakan oleh para penyelidik daripada domain yang berbeza untuk menganalisis data dan mengekstrak maklumat yang berharga daripada set data untuk kegunaan selanjutnya. Di antara semua teknik ini, pengelasan adalah salah satu tugas yang paling biasa digunakan dalam perlombongan data, yang digunakan oleh kebanyakan pengkaji untuk mengklasifikasikan *instance* kepada dua atau lebih kelas yang telah ditetapkan. Peningkatan saiz data yang disimpan telah mewujudkan keperluan bagi kaedah berasaskan komputer untuk analisis data secara automatik. Kebanyakan penyelidik yang telah membangunkan kaedah dan algoritma dalam bidang kepintaran buatan, pembelajaran mesin dan perlombongan data, telah mengenalpasti maklumat yang sangat berguna daripada data. Terdapat banyak alat pintar yang wujud yang cuba untuk belajar daripada paten dalam data untuk meramalkan kelas bagi data yang baru. Salah satu alat pintar itu adalah *Artificial Immune Recognition System (AIRS)* yang telah meningkat penggunaannya. Keputusan AIRS telah menunjukkan potensinya untuk tujuan pengkelasan. AIRS adalah pengelas pintar yang menawarkan keupayaan pemprosesan maklumat yang mantap dan berkuasa yang menjadi semakin berkesan untuk kepintaran berkomputer. Walaupun AIRS telah menunjukkan hasil yang sangat baik, ia masih mempunyai potensi untuk prestasi yang lebih baik dan wajar dikaji. AIRS menggunakan fungsi linear untuk menentukan jumlah sumber yang perlu diperuntukkan dan kelinearan ini meningkatkan semasa latihan dan dengan itu mengurangkan prestasi AIRS. Sumber persaingan sebahagian daripada AIRS menimbulkan masalah lain iaitu sel-sel memori pra-matang dihasilkan dan oleh itu ketepatan klasifikasi berkurangan. Seterusnya AIRS menggunakan *k-Nearest Neighbor (KNN)* sebagai pengelas menjadikan ia teruk terdedah kepada kehadiran bunyi, ciri-ciri yang tidak relevan, dan bilangan atribut. KNN menggunakan undian majoriti dan kelemahannya adalah bahawa kelas-kelas dengan *instance* yang lebih kerap cenderung untuk menguasai ramalan *instance*

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yang baru. Penggunaan KNN ini akhirnya mengakibatkan pengurangan ketepatan pengelasan.

Disertasi ini membentangkan sumbangan utama yang bermatlamat untuk meningkatkan ketepatan dan prestasi AIRS2. Komponen algoritma AIRS2 yang menimbulkan masalah akan diubah suai. Tesis ini mencadangkan tiga algoritma hibrid yang baru: Algoritma FRA-AIRS2 menggunakan *fuzzy logic* untuk meningkatkan keupayaan pengurangan data AIRS2 dan untuk menyelesaikan masalah kelinearan yang berkaitan dengan peruntukan sumber AIRS. RRC-AIRS2 menggunakan konsep mekanisme pemilihan kejohanan dunia yang nyata untuk mengawal saiz penduduk dan meningkatkan ketepatan klasifikasi. FSR-AIRS2 adalah algoritma hibrid baru yang menggabungkan FRA, RRC, dan SVM kepada AIRS2 untuk menghasilkan pengelas yang lebih kukuh. Algoritma yang dicadangkan telah diuji pada pelbagai set data dari gedung *UCI machine learning*. Keputusan eksperimen ke atas penanda aras set data pembelajaran mesin yang sebenar telah menunjukkan keberkesanan algoritma yang dicadangkan.

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# LIST OF SYMBOLS AND ABBREVIATIONS

| | | |
|---|---|---|
| AIRS | : | Artificial Immune Recognition System |
| AIS | : | Artificial Immune Systems |
| AINE | : | Artificial Immune NEtwork |
| ANN | : | Artificial Neural Network |
| ARB | : | Artificial Recognition Ball |
| AUC | : | Area Under the ROC Curve |
| CI | : | Computational Intelligence |
| CSA | : | Clonal Selection Algorithm |
| DNA | : | Deoxyribo Nucleic Acid |
| FIS | : | Fuzzy Inference System |
| FRA | : | Fuzzy-based Resource Allocation |
| GA | : | Genetic Algorithm |
| INT | : | Immune Network Theory |
| IS | : | Immune System |
| KNN | : | k Nearest Neighbor |
| LVQ | : | Learning Vector Quantization |
| MLP | : | Multi-Layer Perceptron |
| NAT | : | Network Affinity Threshold |
| RLAIS | : | Resource Limited Artificial Immune System |
| ROC | : | Receiver Operating Characteristics |
| RRC | : | RWTS Resource Competition |
| RWTS | : | Real World Tournament Selection |
| SVM | : | Support Vector Machine |
| WEKA | : | Waikato Environment for Knowledge Analysis |

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# CHAPTER 1: INTRODUCTION

## 1.1 Background and Motivation

Modern computer technologies, sensors and networks have enabled companies, governments, organizations and all branches of science and engineering to store and organize massive quantities of data in their databases. The abundant amount of captured data and generating numerous sets of data in digital form needs to be transformed into useful knowledge. Increasing the amount of data in science and business has called for computer-based methods of automatic data analysis where analyst use more sophisticated and complex tools (Han, Kamber, & Pei, 2012; Kantardzic, 2011).

However, the gap between the storing of data and our understanding is growing and there is an inverse relationship between them; the greater the increase in volume of data, the smaller the proportion of it that human understands (Witten, Frank, & Hall, 2011). The idea that patterns in data can be searched automatically, identified, validated, and used for prediction has existed among statisticians, economists, communication engineers, and forecasters for a long time (Witten et al., 2011). However, the opportunities for discovering patterns in data are increasing at a staggering rate (Witten et al., 2011).

With the increase in size and complexity of data, it has been inevitable to move away from the manual data analysis toward automatic data analysis where the analysts use complex and sophisticated tools (Kantardzic, 2011). Data mining has become the only hope for finding patterns in a complex world that is overwhelmed by the data. Intelligently analyzed data is a valuable resource that can lead to new insights (Witten et al., 2011).

There are different definitions for knowledge discovery and data mining, a simple definition for data mining is: extracting knowledge from large amount of data (Han et al., 2012) and a more comprehensive definition is: a nontrivial procedure of detecting valid,

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previously unknown, potentially useful patterns in observed data, and ultimately communicating the discovered knowledge to people in an understandable way (Feyyad, 1996; Goebel & Gruenwald, 1999). The whole procedure of applying computer-based techniques for retrieving knowledge from data is basically called data mining (Kantardzic, 2011). Data mining has been heavily used by insurance companies, banks, credit card issuers, manufacturing firms, telephone companies, drug and food industries, in the medical field, police and security agencies, and many other applications. Data mining is among the most rapidly growing field in the computer science (Kantardzic, 2011). Thus, data mining is a technique for discovering previously unknown, hidden and useful information that would assist users in making proper decision.

There are several approaches to illustrate hidden patterns including classification, clustering, sequential pattern discovery, and association rule discovery (Soman, Diwakar, & Ajay, 2006).

One of the most commonly used tasks in data mining is classification (Džeroski, 2010). It is about classifying instances into two or more pre-determined classes. Classification rules are extracted from a set of pre-classified instances, this set is called training set and the actual procedure of extracting the classification rules is known as learning.

The tasks of classification and pattern recognition are common to many scientific, medical and engineering applications. Common subjects among researchers in the field of science, medicine and engineering are classification and pattern recognition. In recent years, the data mining area has attracted scientists in numerous fields including machine learning and many classifiers have been widely studied and have served as solutions for the classification and machine learning problems. Classification is one of the most important tasks that are widely researched by the machine learning and fuzzy communities (Cintra, Monard, & Camargo, 2013). Classification is also known as one of

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major tasks of data mining (Cadenas, Garrido, Martínez, & Bonissone, 2012; Shafigh, Hadi, & Sohrab, 2013). Maximizing the predictive accuracy of a classifier is one of the most important goals of classification algorithm (Pappa & Freitas, 2010). Improving classification performance is very important and many researchers across the globe work on finding ways to achieve this goal (Chou, Cheng, & Wu, 2013; Mastrogiannis, Boutsinas, & Giannikos, 2009; Pham & Triantaphyllou, 2011) to name a few. Still, many of the presently existing classifiers are computationally intensive, which makes them sometimes unsuitable to be applied on real-life issues that require immediate response. Furthermore, many of them are not intuitive in mimicking the learning behavior of human being (Witten et al., 2011).

Data mining employs machine learning methods, mathematical algorithms and statistical models to discover valid relationships and patterns in large data sets (Dua & Du, 2011).

Machine learning consists of computational methods that are applied to data in order to discover or learn new things about the data, or to be able to predict an outcome, based on some prior knowledge (Timmis & Knight, 2002). Machine Learning: is a subfield of AI, which is concerned with programs that learn from experience (Russell & Norvig, 2016). Programs use sample data or experience for optimizing a performance criterion. Being a part of AI, machine learning needs to be intelligent; because in a changing environment, the program should have the ability to learn. Program designer does not need to predict and offer solutions for all possible circumstances. Machine learning applies statistical theories to build mathematical models, since its major task is to infer from samples (Alpaydin, 2014).

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From the information-processing perspective it is remarkable that the immune system (IS) is a highly adaptive, distributed and parallel system, it is based on principles of the natural system, which is capable of solving complex classification tasks. It learns to recognize relevant patterns, remember previously identified patterns, and builds pattern detectors efficiently, it is also capable of feature extraction, self-regulation and fault tolerance, these tasks are very important in the field of natural computation (Dipankar Dasgupta, 1999; De Castro & Timmis, 2002b). The human immune system is capable of undertaking a myriad of tasks it can cope with highly dynamically changing situations, while it maintains a memory of past events, it is capable of continually learning about new events (Dipankar  Dasgupta, 1998; Timmis & Knight, 2002). The immune system has offered productive ideas for models of computation and from the computational point of view, the most important features are the capabilities to generalize, remember, and classify confronted substances (Watkins, 2001).

These abilities have inspired scientists and researchers to build systems that are able to mimic various computationally appealing features of the immune systems (Timmis, Knight, De Castro, & Hart, 2004), they are able to solve a variety of computationally based problems. One of these systems is called Artificial Immune Systems (AIS). The AIS is an immune system inspired computational system that is also categorized under computational intelligence (Brownlee, 2011; Elsayed, Rajasekaran, & Ammar, 2012). AIS is also known as one of the artificial intelligence techniques that offers robust and strong information processing capabilities for solving problems (Leung, Cheong, & Cheong, 2007a). AIS, is actually a class of adaptive algorithm (Brownlee, 2005) that abstracts the structure and function of the human immune system into computational systems (Wikipedia, 2012). The field of AIS has attracted many researchers, and has found a wide range of theoretical discussions and application domains. Applications of AIS are increasing rapidly and AISs are offering robust and powerful information

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processing capabilities for solving complex problems (Leung et al., 2007a). They are also building progressively an effective division of computational intelligence within data mining and knowledge discovery field.

Artificial Intelligence (AI): The term AI is applied when a machine imitates cognitive functions that humans associate with other human minds, such as learning and problem solving. The definition for AI is still incomplete; however, researchers have identified four possible goals to follow in AI: one of the goals is concerned about thought processes and reasoning, another one is about behavior, another one is about measuring success in terms of human performance, and the last one is about rationality, which measures against an ideal concept of intelligence. AI has been grouped in four categories: Systems that think like humans, systems that think rationally, systems that act like human, and systems that act rationally (Russell & Norvig, 2016).

Scientists, mathematicians, engineers, and other researchers have been interested in the capabilities of AIS, and AIS has found applications in a wide variety of areas, some of them are: *anomaly detection* (Dipankar Dasgupta & Forrest, 1998; Greensmith, Aickelin, & Tedesco, 2010; Yi, Wu, & Chen, 2011); *classification* (Carter, 2000; Leung, Cheong, & Cheong, 2007b; Watkins, Timmis, & Boggess, 2004; Zhang & Yi, 2010); *clustering* (Graaff & Engelbrecht, 2011; Knight & Timmis, 2003; Tang & Vemuri, 2005); *data analysis* (Drozda, Schaust, Schildt, & Szczerbicka, 2011; Timmis, 2000; Timmis, Neal, & Hunt, 2000); *machine learning* (Cheng, Lin, Hsiao, & Tseng, 2010; Das & Sengur, 2010; De Castro & Von Zuben, 2002; Glickman, Balthrop, & Forrest, 2005; Knight & Timmis, 2003); *pattern matching, recognition* (Dipankar Dasgupta, Yu, & Majumdar, 2003; Tarakanov & Skormin, 2002); *web data mining* (Mao, Lee, & Yeh, 2011; Nasaroui, Gonzalez, & Dasgupta, 2002; Rahmani & Helmi, 2008; Yang, Kiang, Chen, & Li, 2012; H. Zhao, Chen, Zeng, Shi, & Qin, 2011).

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AIS is a computational paradigm in artificial intelligence and its focus was mainly on the development of unsupervised learning algorithms rather than the supervised one (Watkins & Timmis, 2002). AIS was designed and developed for data clustering or feature extraction, therefore its performance for classification was not satisfactory. Watkins and Timmis (Watkins, 2001) introduced Artificial Immune Recognition System (AIRS) which was designed to fill the gap and focus on classification problems (Brownlee, 2005).

The interest for immune-system-inspired information processing algorithms such as AIRS have been growing (Chikh, Saidi, & Settouti, 2012; Tay, Poh, & Kitney, 2013). More recently there have been substantial efforts in exploiting and exploring the potential of AIRS for applications in computer science, medicine and engineering. AIRS was designed specifically and applied to classification problems. As discussed earlier, scientists were motivated by several characteristics of the immune systems of mammals, such as learning and recognition capabilities and they have been developing algorithms for a broad spectrum of applications. Some of these algorithms are concerned with classification issues; these are very common real-world data mining tasks. AIRS is a competitive classification system (Brownlee, 2005), and it is comparable to well-established classifiers in terms of accuracy (Golzari, 2011; Tay et al., 2013).

AIRS is a reasonably complex algorithm which has demonstrated substantial accomplishments on a broad range of classification problems (Brownlee, 2005), and it is well-known that classification problems play a significant role in data mining and computer science (Shafigh et al., 2013; Zhu & Guan, 2004). AIRS has enhanced considerably the classification performance (Polat, Şahan, Kodaz, & Güneş, 2007), and it has been identified as an effective classifier for a number of machine learning problems

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(Doraisamy & Golzari, 2010; Goodman, Boggess, & Watkins, 2003). A recent study argues that the methodology of AIRS is useful for data classification (Tay et al., 2013).

Even though AIRS has shown many good features, it has the potential to accomplish even better. Given the excellent results, AIRS has rooms for improvement and is deserved to be investigated  (Brownlee, 2005), and its full potential is still unleashed (Tay et al., 2013). A recent study carried out by (Jenhani & Elouedi, 2012) demonstrated that insufficient efforts have been made for improving the classification accuracy of AIRS, they argued that the bulk of circulated articles is about applications of AIRS for solving “real-world” problems; however few works were dedicated to improving the algorithm itself. In particular they argued that the use of k nearest neighbor may reduce the accuracy of AIRS (Jenhani & Elouedi, 2012). Polat et al. have demonstrated that classification performance of AIRS could be improved if the number of resources and running time were reduced (Polat, Şahan, Kodaz, et al., 2007). Golzari et al. have documented that one of the problems of the AIRS is its very high selection pressure during resource competition; they argued that this causes loss of diversity, and may produce premature memory cells. They argued that high selection pressure decreases the classification accuracy (Golzari, Doraisamy, Sulaiman, & Udzir, 2009a). On the other hand, AIRS’ classifier is the k-Nearest Neighbor (KNN), and it is known in the machine learning that KNN does not demand for an exact match with any cases or stored patterns, in order to identify patterns of data which means, arguably, low accuracy. In addition choosing k for KNN may affect the performance of KNN, if k is chosen to be too small, the outcome might be subtle to noise in data, and if k is chosen to be too large, then it is possible to have points from other classes in the neighborhood (Wu et al., 2008).

One of common practice for improving classification accuracy is using hybrid models through combining several models together; the goal of the hybrid models is using unique

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capability of each component in order to improve pattern recognition in the data (Khashei, Zeinal Hamadani, & Bijari, 2012). It is also known that AISs are hybrid systems (De Castro & Timmis, 2002b) and literature review reveals that concepts of AIS have been used in connection with classifiers such as KNN and SVM for different purposes and applications. For example a hybrid of AIS and KNN was used for pattern recognition by (W. Zhao & Davis, 2011) and Şahan et al. introduced a hybrid of fuzzy AIS and KNN algorithm to classify breast cancer data set (Şahan, Polat, Kodaz, & Güneş, 2007). Hybrid of AIS and SVM were also developed by researchers, a recent approach shows the use of AIS-SVM algorithm for anomaly detection by (Aydin, Karakose, & Akin, 2011) and in another research study, a hybrid of AIS-SVM ensemble has been successfully used for text classification (Antunes, Silva, Ribeiro, & Correia, 2011b). Researchers also developed AIS-SVM hybrid algorithm to identify voltage collapse prone areas and overloaded lines in the power system (Woolley & Milanović, 2009).

AIRS is considered as a hybrid of elements and methods developed for supervised and unsupervised artificial immune system's algorithms (Brownlee, 2005). Watkins applied KNN inside AIRS in order to carry out the classification tasks. KNN have been added to other components and procedures to create what is known as AIRS thus, it could also be interpreted as a hybrid algorithm of AIRS that includes KNN. Some researchers even argued that AIRS is a pre-processor for KNN (Seeker & Freitas, 2007) Although this remark is correct, however a review of the literature clearly reveals that AIRS has been accepted as a classifier by all other researchers on the topic of AIRS.

A hybrid algorithm is a composite of two or more algorithms that are created in order to perform tasks in a new and eventually more sophisticated fashion. As such, AIRS is a hybrid algorithm, which has borrowed concepts from various algorithms in the field of artificial intelligence such as: AIS (Brownlee, 2005), Artificial Recognition Ball (ARB)

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(Farmer, Packard, & Perelson, 1986), Artificial Immune NEtwork (AINE) (Thomas Knight & JonathanI Timmis, 2001; Watkins, 2005) and random mutation, clonal expansion, and clonal selection from other AIS-based algorithms (Brownlee, 2005).

Because of the need for new and efficient ways of classification, researchers have been developing hybrid algorithms with the aim of improving classification accuracy, performance of classifiers and obviously for solving specific problems. Literature review reveals that there exists no hybrid model of AIRS-SVM algorithm, both AIRS and SVM have strengths that when combined could lead to a new and more efficient immune based classifier.

Classifiers play an important role in solving real-world problems, and AIRS, as an immune inspired classifier needs further improvement. As a contribution to the field of computer science and artificial intelligence, this study introduces a modification of AIRS which enhances the classification accuracy and retains or improves performance and efficiency of the resulting classifier.

## 1.2 Research Problem

AIRS is an effective and well-known classifier (Igawa & Ohashi, 2009). AIRS' performance is higher than other classifiers (Deng, Tan, He, & Ye, 2014) or comparable to well-respected classifiers in terms of accuracy (Golzari, 2011; Tay et al., 2013) and it has the following desirable algorithmic characteristics: it is self-regulatory, efficient, stable under a wide range of user-set parameters, and has data reduction capability. There is no need for the user of the AIRS to select any architecture during training phase since its adaptive process discovers an appropriate architecture automatically. AIRS does not use the whole training dataset for classification, instead the algorithm uses a minimum number of exemplars to create new training instances and then produces the resulting classifier (Brownlee, 2005). One study evaluated AIRS as a stable classifier with near

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average results and concluded it can safely be added to the data mining toolbox (Meng, van der Putten, & Wang, 2005; Van der Putten, 2010). In fact, AIRS is listed (Machaka, Mabande, & Bagula, 2012) as one of the classifiers in the data mining tool, the WEKA, which has been developed at the university of Waikato in New Zealand (Soman et al., 2006) and maintained by (Mark Hall et al., 2009). The WEKA is considered as a popular workbench in the domain of machine learning (Bouckaert et al., 2010) and a comprehensive tool bench for both machine learning and data mining (Soman et al., 2006).

Although AIRS has shown to have many good features, it still has the potentials to perform even better. The full potential of the AIRS is still unleashed (Tay et al., 2013). Researchers have identified some weaknesses that needed to be addressed. Jenhani & Eloudi showed that relatively few efforts have been made to improve the classification accuracy of AIRS, majority of published articles have applied AIRS to solve a particular classification problem (Jenhani & Elouedi, 2012). Intensive research on AIRS shows that following problems needed to be addressed:

- As mentioned earlier, AIRS is a hybrid algorithm that uses the concepts of AIS and KNN to perform classification tasks. AIRS uses k-NN as a classifier, and in machine learning, KNN was developed in such a way that it identifies patterns of data without demanding for an exact match to any cases or stored patterns, this means, relatively speaking, low accuracy. Also selecting k for KNN affects the performance of KNN, if k is chosen to be too small, the result might be sensitive to noise in data, and if too large a value of k is, then the neighborhood may include points from other classes (Wu et al., 2008) and KNN also tends to be computationally expensive (Goodman, Boggess, & Watkins, 2002). SVM and KNN are among the top 10 classifiers (Wu et al., 2008) however, without looking

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at the application of KNN in AIRS, outcome of other researches have revealed that SVM outperforms KNN (D. S. Huang, Gan, Bevilacqua, & Figueroa, 2011) this is particularly true when the number of features increases (Hmeidi, Hawashin, & El-Qawasmeh, 2008). A recent research has also indicated that using KNN reduces the classification accuracy of AIRS (Jenhani & Elouedi, 2012). Despite the superiority of SVM over the KNN, to the best knowledge of this research, there exist no hybrid algorithm that uses the concepts of the AIRS and the SVM. Therefore this research aims to verify whether or not a hybrid algorithm dubbed as FSR-AIRS2 (see section 4.4) which uses SVM as the classifier will perform better than AIRS2.

- AIRS has inherited many of the elements from the Artificial Immune Network (AINE), which is a form of clonal selection algorithm, such as the concept of the Antigen Recognition Ball (ARB) (see details in section 2.4), and an unusual way of resource limitation for controlling the population size; an ARB presents the idea of cell concentrations into clonal selection, and represent a data structure of multiple, identical antibodies, therefore, a population of ARBs represents a much bigger population of antibodies more efficiently (Garrett, 2005). Intensive comparison of the AIRS with the Learning Vector Quantization (LVQ) method, introduced by (Kohonen, 1990), have shown mixed results (Goodman et al., 2002; Watkins & Timmis, 2002) Garrett argued that AIRS outperforms LVQ, however it tends to do so by using high computing resources (Garrett, 2005; Golzari, 2011; Golzari, Doraisamy, Sulaiman, Udzir, & Norowi, 2008; Polat & Güneş, 2007), and the use of a linear method for allocating resources, causes high running time (Golzari, Doraisamy, Sulaiman, & Udzir, 2011).
- Generally a high selection pressure causes premature convergence (Ahn, 2006). Although high selection pressure can increase the speed of optimization, it

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increases the probability of getting stuck in local optima. It means we have a trade-off between accuracy and efficiency (Kramer, 2008). Golzari et al. have identified that AIRS' selection pressure is very high during resource competition, and this leads to loss of diversity, and may cause premature memory cells. If selection pressure becomes too weak, the population may drift aimlessly for a long time, and the quality of the solutions found is not likely to be good. On the other hand, rapid convergence is desirable, but an excessively fast convergence may cause the algorithm to converge prematurely to a suboptimal solution (Cantú-Paz, 2000). Thus the consequence of high selection pressure is decreased classification accuracy (Cantú-Paz, 2000; Golzari, 2011; Golzari, Doraisamy, Sulaiman, & Udzir, 2009b).

## 1.3 Research Objective

The main objective of this thesis is to address the shortfalls explained in the previous subsection and to demonstrate and explore the classification capabilities through a detailed presentation of the proposed algorithms and through an evaluation of the algorithm's performance on real world datasets that have been used throughout machine learning literature. The datasets are introduced in subsection 3.3.2. This objective is achievable by undergoing the following processes:

- Introducing a new resource allocation method based on fuzzy logic in order to reduce number of resources and increase the classification accuracy of AIRS2. This method is dubbed as Fuzzy-based Resource Allocation (FRA-AIRS2).
- Introducing a new resource competition method for AIRS2 based on the concept of real world tournament selection in order to reduce premature memory cells and thus increase the classification accuracy. This method is dubbed as Real-world-tournament-selection-based Resource Competition (RRC-AIRS2).

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Introducing and evaluating a new immune inspired hybrid system of instance handling components of AIRS2 and SVM with the goal of improving performance of AIRS2, in particular, its classification accuracy. The new hybrid model consisting of concepts used in FRA-AIRS2, RRC-AIRS2, SVM, and AIRS2. The new hybrid model is dubbed as FSR-AIRS2.

## 1.4 Research Scope

Given the fact that classification is one of the most important tasks of data mining, and that there is increasing number of applications of AIRS for real-world data mining tasks, this thesis focuses on the AIRS algorithm and develops a new algorithm with the goal of improving AIRS' performance. For reducing and controlling the number of resources this study uses fuzzy logic during resource allocation stage of the algorithm; in order to avoid premature memory cells and reducing loss of diversity, RWTS method is applied during resource competition stage of the algorithm; and in the classification stage, this study incorporates SVM as the classifier instead of KNN.

This study uses a wide range of publicly available real world datasets from UCI machine learning repository.

The following performance measures will be carried out: classification accuracy, n-fold cross validation, data reduction, overall runtime, area under ROC (AUC), and student's t-test. These measures are discussed in detail in section 3.4.

## 1.5 Thesis Outline

This section describes the structure and content of the thesis. The chapters of this thesis are organized as described below.

Chapter 2 provides the relevant background on classification tasks and presents an overview of the human immune system and evolutionary computing. Then it introduces

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the common framework used for designing bio-inspired computational algorithm. Next this chapter presents terminologies used in the immune system and their counterparts used in the algorithms, followed by a brief explanation of affinity measures. Then it presents an extensive literature review on immune algorithms, biologically-based classification algorithms, and artificial immune recognition system.

Chapter 3 explores the methodology used in this study. It gives an overview of the research and presents the experimental setup including system specification, datasets and parameter setup.  Further this chapter provides a brief overview of performance metrics used in this dissertation.

Chapter 4 presents details of the proposed algorithm, it evaluates the performance of the new algorithms on benchmark datasets and compares its performances with that of AIRS2 and some well-known algorithms and discusses the results of experiments.

Chapter 5 provides a summary of the dissertation, its contribution to the field of computer science and data mining, and outlines the conclusions that can be drawn and there are some comments on future extensions of this work.

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# CHAPTER 2: LITERATURE REVIEW

## 2.1 Introduction

An extensive literature review on classification algorithms that are used in this thesis are presented in this chapter. Section 2.2 describes one of major data mining tasks, the classification. In order to draw attention to the relevant features of human immunology, section 2.3 highlights important points of the human immune system. Since immune-based classifiers are related to evolutionary computation, section 2.3.1 provides a brief description of evolutionary computation which is an important research area in computer science. Section 2.3.2 discusses a common framework that is used in designing bio-inspired algorithms. Section 2.3.3 presents terminologies used in the immune system and their analogies used in the algorithms. Section 2.3.4 briefly explains the affinity measure which is closely related to the representation mechanism. Section 2.3.5 presents an extensive literature review on immune algorithms and section 2.4 presents literature review on biologically-based classification algorithms. Section 2.5 reviews some of hybrid algorithms that were introduced for classification tasks within the domain of artificial intelligence. Section 2.6 focuses on the literature related to the artificial immune recognition system. Section 2.7 presents other classifiers that are used in this study as benchmark.

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## 2.2 Classification

As mentioned earlier classification is one of the most important tasks that are widely researched by the machine learning and fuzzy communities (Cintra et al., 2013) it is also one of major data mining tasks (Cadenas et al., 2012; Shafigh et al., 2013). Many researchers work on finding ways to improve classification performance (Chou et al., 2013; Mastrogiannis et al., 2009; Pham & Triantaphyllou, 2011) to name a few.

Classification is a process of assigning an object into a predefined class or group based on observation of a number of attributes belonging to that object. It is also a process of finding a set of functions or models that differentiate and describe data concepts or data classes with the goal of being able to use the model for predicting the class of objects whose class label is unknown. Many problems in areas such as medicine, loan approval, business, and industry can be treated as classification applications. Some examples are: classifying financial marketing trends, bankruptcy prediction, credit scoring, image and pattern recognition, speech recognition, handwritten character recognition, medical diagnosis, and quality control (Han et al., 2012).

The major strength of classification is that it is possible to classify data into groups of known labels; it is quantifiable and may use statistical methods for classification. However, the weakness is that we need labled data, which are often difficult to obtain, the effect of labeling may be stigmatisation, and the question of correct labelling may arise. It is also desirable to have equal proportion of data for each class label.

Classification tasks have specific goals; they use instances with known class labels for constructing a predictive model in which class labels are assigned to the new instances. Most classification methods are built in two-stages, which are cleanly separated: the initial stage or the training phase, where the algorithm uses one part of a dataset to analyze and learn the underlying classes. A training dataset consists of a number of instances, and each instance consists of attributes, also known as features. Each training vector can be represented by T = {($x_i$,$y_i$) | $x_i \in \Re^m$ , $y_i \in \mathbb{Z}^n$ {0, 1, 2, …} , i= 1,2,...,n}, where $x_i$ is a real m-dimensional input vector and each $y_i$ represents the class label to which the point $x_i$ belongs. In a supervised learning the class label of each instance is known, while in an unsupervised learning the class label is not known (Han et al., 2012).

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The second stage of classification is called the training phase, in this stage the model which was built in the first stage is used for classification. Initially the predictive accuracy of the classifier has to be estimated, if the accuracy is acceptable, then the classifier can be used to predict class label of new, previously unknown instances (Han et al., 2012). Examples for models that use the training data are support vector machines, neural networks, rule-based methods, and decision trees (Aggarwal, 2014b). Use of test data set in estimating the accuracy also helps to avoid overfitting. Evaluation is essential for making real-progress in data mining (Witten et al., 2011) and machine learning, with a wide range of existing classifiers there is a need to measure their performance. The common approach to assessing the classifier's accuracy is to evaluate its error rate on an independent test set of instances, held back from the training data set (Witten et al., 2011). Not only there are different kinds of classifiers but also many classifiers come with different options and parameters that can be set by the users, different settings may lead to different results (Golzari, 2011). A classifier's accuracy is the percentage of correctly classified instances by the classifier, related class label of each test record is then compared with the class label of the learned classifier for the same instance. Misclassification happens when a classifier predicts a wrong class for an instance, and the error rate is the ratio of errors made over entire set of instances (Witten et al., 2011).

It is wishful to have a classifier that makes no error on all data sets mostly because of lack of adequate information about underlying data sets and possible noise.

The importance of evaluation of a new approach was emphasized by (Adya & Collopy, 1998) in their survey. They emphasized that a new approach must be compared with alternatives that are or could be used; otherwise, it is difficult to argue about the value of the model.

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Some criteria for evaluation of classification performance are: classification accuracy, n-fold cross validation, data reduction, overall runtime, area under the ROC curve. All these performance criteria are presented in detail in subsection 3.4.

Different techniques are used in various classification algorithms; some of them are: support vector machines, rule-based techniques, decision-tree learning algorithm, instance-based learning algorithms, statistical-based learning algorithm, and biologically-inspired techniques. The latter one includes techniques that are based on Artificial Neural Network, Genetic Algorithm, and AIS (Golzari, 2011). Figure 2.1 illustrates some common classification techniques. The focus of this thesis is mainly on AIS-based algorithms.

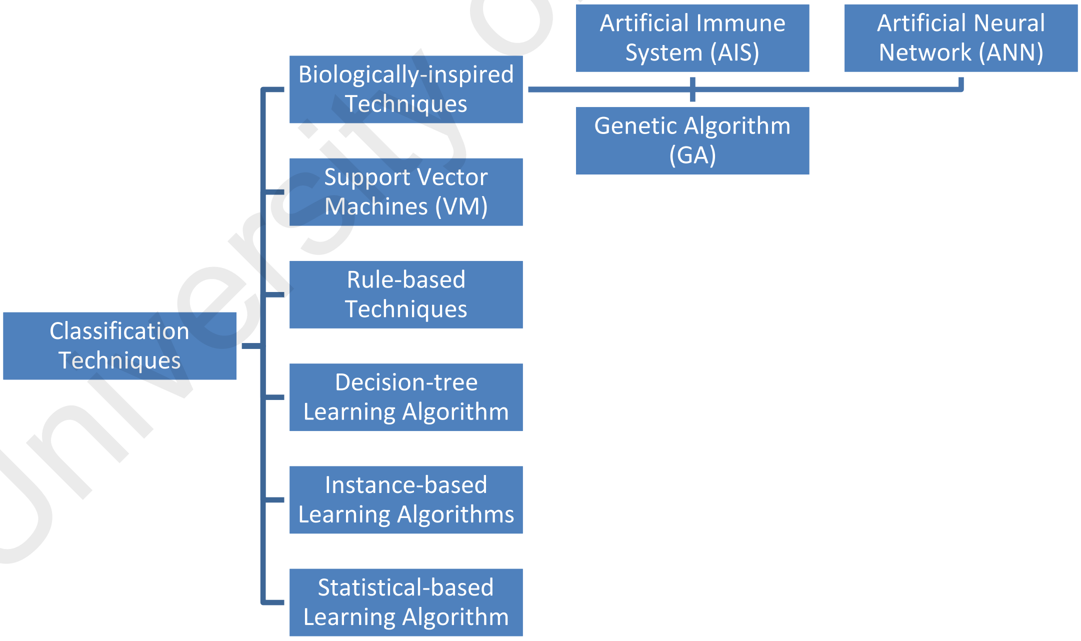
Classification Techniques
Biologically-inspired Techniques
Artificial Immune System (AIS)
Artificial Neural Network (ANN)
Genetic Algorithm (GA)
Support Vector Machines (VM)
Rule-based Techniques
Decision-tree Learning Algorithm
Instance-based Learning Algorithms
Statistical-based Learning Algorithm

**Figure 2.1: Common Classification Techniques**

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Improving the performance of AIRS2, and AIS-based algorithm is the focus of this study. AIRS2 has shown comparable performance with other classifiers and it is identified as one of the clever algorithms (Brownlee, 2011).

The rest of this section focuses on a brief introduction and description of some common supervised learning (classification) techniques.

There are two types of learning algorithms: lazy and eager. The difference between these two types is that while lazy learning algorithm postpones the work as long as possible, eager methods produce a generalization immediately after the data has been seen (Witten et al., 2011). In other words lazy method works little during the training and does more during the classification phase, whereas eager learning algorithm the model tries to build a generalization function during training of the model (Golzari, 2011; Hendrickx & Van den Bosch, 2005). Hardarean et al. provided a comparative analysis of the lazy and eager methods (Hadarean, Bansal, Jovanović, Barrett, & Tinelli, 2014), and showed that they are complementary in terms of the kind of problems they can solve. In their study of deciding bit-vector constrains, they argued that in contrast to the eager approach, the lazy methods provide a wide range of optimization techniques that are only available to the lazy approach. Their empirical evaluation also showed that lazy solver were able to solve such problems that the eager solvers failed to solve.

Instance-based classification algorithms belong to the family of the lazy learning algorithms. In instance-based classification, a distance metric is used to compare each new instance with the existing ones, and the class of the nearest (closest) existing instance is used to assign it to the new instance. This is known as the nearest-neighbor classification algorithm. It may happen that there is more than one nearest-neighbour; in this case majority vote method is used to determine the class of the new instance, meaning the majority class of closest k neighbours is assigned to the new instance. This is the well-

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known k-Nearest Neighbour (KNN) method  (Witten et al., 2011). The most popular distance metrics are the Euclidean and the Manhattan distance (Golzari, 2011; Shahid, Bertazzon, Knudtson, & Ghali, 2009). Examples for eager learning models are: artificial neural network, linear regression, and support vector regression (Wei, 2015).

One of popular classification methods is the decision tree; this is because its construction does not need any domain knowledge or parameter setting which makes it suitable for exploratory knowledge discovery. Decision tree looks like a flowchart tree, where each internal node represent a test on an attribute, each branch denotes an outcome of the test, and each leaf node holds a class label (Han et al., 2012). Quinlan (Quinlan, 1986) argued that because of the simplicity, decision trees are natural ways for decision makings however, it is more complex to learn decision trees from the data. Decision tree algorithms have found extensive applications in machine learning and classification tasks (Gokgoz & Subasi, 2015). Construction of decision trees involves two stages, the first stage the tree is growing here the algorithm uses attribute selection measures to select the best feature that discriminate between the distinct classes and then splits the data into two new nodes based on that feature. This is applied recursively to the resulting data subsets until a class assignment can be made for each leaf. After decision trees are constructed, many branches may represent outliers or noise in the training instances, therefore the second stage known as pruning jumps in, it attempts to identify and clip off branches of the tree that are least useful in order to improve the classification accuracy on the training data with the complexity of the model (Han et al., 2012; Nisbet, Elder, & Miner, 2009). Quinlan got the idea of developing the predecessor of the C4.5, the ID3 (Quinlan, 2014), from the Hunt’s Concept Learning Systems. C4.5 is one of widely used decision trees, it was developed by (Quinlan, 1993). C4.5 has been frequently used as a benchmark for comparing newer supervised learning algorithms (Han et al., 2012). C4.5 applies an entropy-based information gain measure to find most relevant feature to grow decision

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tree (T.-h. Kim et al., 2011). It starts with a general tree and continues to grow until maximum classification is achieved; it then clips off the tree as far as possible up to pre-set adequate misclassification rates (T.-h. Kim et al., 2011). C4.5 uses the pruning process to solve the over-fitting problem (Mantas & Abellán, 2014).

One of the oldest and well-known classifier is Bayes classifier (Duda & Hart, 1973) it is based on Bayesian theorem (Nisbet et al., 2009) with strong independent assumptions. Document classification is one of good applications of Naïve Bayes classifier (Aggarwal, 2014a). It computes the likelihood that a given instance belongs to a particular class. It has shown high speed and accuracy when applied to large databases (Han & Kamber, 2006). A simple Bayesian classifier known as Naïve Bayesian classifier is comparable to decision trees in terms of performance (Han & Kamber, 2006).

Bayes' classifier would need two parameters to do the classification namely the 'a priori probability' and the 'class conditional density'; however in practice it is possible that both parameters are unknown and that makes the classification task difficult. Therefore Bayes' classifier tries to estimate the class based on limited conditions (Bandyopadhyay & Pal, 2007). The probability of the class labels are easily estimated from the training data, however estimating the distribution of attribute values given the class is more complex. For this purpose, the Bayes rule is used to calculate the conditional likelihood of the class given the attributes. After the classifier has been trained, it is used for classification of new instances. Applying Bayes' theorem, it is possible to determine the posterior probability of each class, and then the new instance will get the class with maximum posterior probability (Bethlehem & Van Der Heijden, 2000). Some researchers have argued that prior probabilities of Naïve Bayes are unreliable, and have shown that prior probabilities might yield an incorrect classification (Gelgi, Vadrevu, & Davulcu, 2007).

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Artificial neural network is a mathematical model that simulates human neural system. An artificial neural network consists of multi-layers and nodes, where nodes represent the neurons on human neural system. Connections between the nodes are known as weights, their values depend on the learning procedure (Kecman, 2001). If a classification problem consists of m-classes and n-features, the neural network will have m input and n output nodes. Throughout the learning phase, artificial neural network try to adjust weights in order to get optimal outputs. Once the learning phase is over, artificial neural network assigns the class with the maximum output to the new unknown instance (Golzari, 2011). One drawback of the neural network is that the training process is inefficient and that the knowledge representation is unknown (Chien, Lin, & Yang, 2006; Golzari, 2011). In another study, Osyk et al. reported that producing false alarms was the primary weakness of the neural network (Osyk, Hung, & Madey, 1994).

## 2.3 From Human Immune System To Artificial Immune System

One of the tasks of the immune system is to attack and try to eradicate pathogens or other infectious organisms that invade human body (Timmis et al., 2004). The human immune system consists of a network of cells, tissues, and organs that work together to protect the body (Prasad, 2010). Leucocytes or white blood cells are engaged in finding and destroying disease-causing substances or organisms (Prasad, 2010). There exits two basic types of leukocytes: phagocytes and lymphocytes, in this thesis we focus only on lymphocytes. The lymphocytes empower the body to remember and recognize previously identified pathogens (invaders) and help the body to destroy them (Sompayrac, 2012). There are two types of leukocytes: B-lymphocytes and T-lymphocytes. Lymphocytes originate from bone marrow where they can mature into B cells or move to thymus gland and mature into T cells (Sompayrac, 2012). B cells and T cells have different functionalities, while B cells seeks their targets and use defense mechanism to lock onto them, T lymphocytes (cells) are responsible for eliminating the invading germs after being

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identified by the immune system (Sompayrac, 2012). The process of affinity maturation which is also known as immunological B-cell maturation is a process of variation and selection, undifferentiated B cell transform to one that secretes antibodies with particular specificity. These antibodies are specialized proteins that lock only onto specific antigens (Sompayrac, 2012). This transformation and activation of the B cell occurs when its affinity threshold is exceeded. While antibodies bind to pathogens and inactivate them, B-cell clones itself. However, produced clones are not faultless. The cloning process is vulnerable to very high mutation rates which means cloned B cells may have to some extent different receptors from their parents.  These new cloned cells will also have the opportunity to bind with the pathogens. To determine which B cell is the strongest, B cells compete for available pathogens. Some cells will have stronger affinity levels than others, and B cell with highest affinity for the pathogens is the "fittest" and therefore will be cloned or replicated the most. Hyper-mutation provides the variation aspect, and the selection aspect is provided by competition for pathogens (Hofmeyr & Forrest, 2000).

Figure 2.2 shows B cell activation pathway, when a B cell comes across its specific antigen, with the help of T cells, B cell multiply and mature into plasma cells, which in turn produce antibodies that identify and neutralize invaders such as bacteria and viruses. Around ten percent of plasma cells become long-lived antigen specific memory B cells (Wikipedia, 2013).

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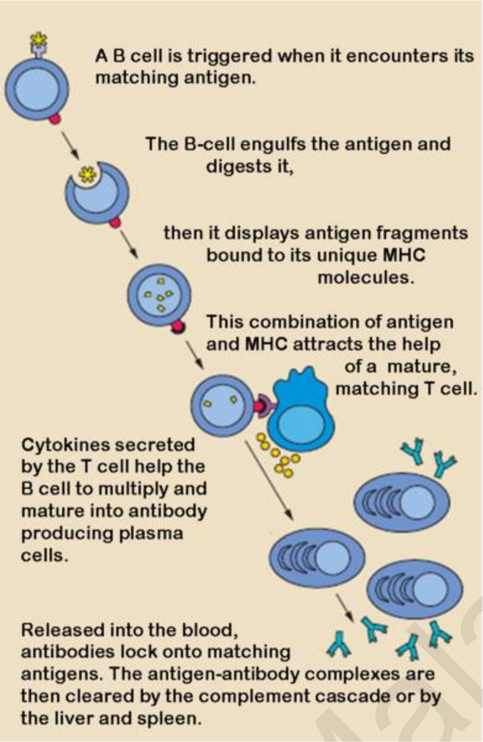
A B cell is triggered when it encounters its matching antigen.
The B-cell engulfs the antigen and digests it,
then it displays antigen fragments bound to its unique MHC molecules.
This combination of antigen and MHC attracts the help of a mature, matching T cell.
Cytokines secreted by the T cell help the B cell to multiply and mature into antibody producing plasma cells.
Released into the blood, antibodies lock onto matching antigens. The antigen-antibody complexes are then cleared by the complement cascade or by the liver and spleen.

**Figure 2.2: B cell activation, NIH Publication No. 035423, September 2003 (modifications: April 9, 2013), Wikipedia, May 1, 2013**

Antibodies are created and distributed throughout the body, so that if the same substance enters the body, the immune system's response is to bind the existing antibodies onto the antigens so that T cells can neutralize antibodies (Sompayrac, 2012). For additional information about the immune system refer to (Sompayrac, 2012; Travers, Walport, Janeway, & Murphy, 2008).

### 2.3.1 Evolutionary Computing

Computer scientists have been increasingly inspired by the efficiency found in natural systems to solve complex computational problems (Watkins, 2005). Evolutionary computing is the common term for a variety of problem-solving techniques that are based on principles of biological evolution. These techniques have been broadly applied to a variety of practical applications in industry and commerce as well as to leading-edge scientific research (Eiben & Smith, 2008).

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Biological metaphors have led to the development of evolutionary programming that was introduced by (Fogel, Owens, & Walsh, 1966), Holland introduced the concepts of genetic algorithms and classifier systems (Holland, 1975). (Bäck & Schwefel, 1993) and (Rechenberg, 1973) introduced evolution strategies.

(Eiben & Smith, 2008) explained that many different evolutionary algorithms exist, however the concept behind all of them is similar: there is a population of individuals who live in the same environment with limited resources, individuals compete for those resources and this leads to natural selection, which is also known as survival of the fittest. These competitions have the effect that fitness of the population rises. Components of evolutionary algorithms are (Eiben & Smith, 2008):

- *Representation (definition of individuals)*
- *Evaluation function (or fitness function)*
- *Population*
- *Parent selection mechanism*
- *Variation operators, recombination and mutation*
- *Survivor selection mechanism (replacement)*

In the nature, species evolve through mutation and natural selection, in which the strongest are more likely to survive and reproduce (Mitchell & Taylor, 1999). The questions around population size and the mechanism to control it are very important both in the nature and in the evolutionary computation.

In the context of the immune system, the number of B cells is finite and it cannot grow exponentially, therefore researchers argue that the available resources for creating and sustaining B cells within the immune system are limited (Timmis & Neal, 2001). This resource limitation leads to a survival competition between B cells: the strongest or the most stimulated ones will survive (Timmis & Neal, 2001). This is also known as a natural selection mechanism to control the population size (Golzari, 2011; Timmis & Neal, 2001).

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“How big should the population be? How many offspring should be produced per generation?” (De Jong, 2006) these are questions that concerns computer scientists when they develop their evolutionary algorithms. These algorithms are formal models of biological metaphors and are developed to solve computational problems.

Surviving individuals evolve through reproduction and mutation from generation to generation. Through mutation individuals may learn to improve themselves for the next generation. In every generation individuals undergo an evaluation; the best ones will survive and will be able to reproduce again. This process is repeated over the time in order to create optimized individuals that can sustain in their environment (Golzari, 2011).

Evolutionary algorithms represent a problem solving paradigm within a population of individuals, where each individual has the capacity of being both a search point within the region of potential answers to a given problem and a temporal carrier of current status about the “laws” of the environment. An algorithm-dependent algorithm is used to initialize the starting population, and through randomized processes of recombination, mutation, and selection the population evolves towards gradually better regions of the search space. Essentially the environment measures the performance or fitness of a new search point and creates quality information known as the fitness value for the new search points, whereby the selection process considers those individuals of higher fitness (quality) more often than less fit individuals. While the recombination strategy allows for mixing of parental information and passing it to their offspring, the mutation mechanism introduces innovation in to the population (Bäck, 1995).

One of the major drawbacks of the evolutionary algorithms is its tendency of premature convergence toward a not suitable solution; a strong selection pressure may cause this problem (Golzari, 2011). By definition selection pressure is “the degree to which better individuals are favored” (Sivanandam & Deepa, 2007). Selection pressure

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determines the convergence rate of genetic algorithm; the higher the selection pressure, the higher the convergence rate (Miller & Goldberg, 1995; Sivanandam & Deepa, 2007). While a strong selection may reduce the diversity of the population, a weak selection may slow down the convergence (Kress, 2010). In case of a weak selection pressure the algorithm will need unnecessarily more time to find a solution, and in case the selection pressure is very strong there is a tendency of premature convergence. It is important to note that selection mechanism can preserve population diversity and provide selection pressure (Golzari, 2011). One of the important issues in genetic algorithms is the preservation of the diversity, since it helps to avoid premature convergence (Sivanandam & Deepa, 2007). Therefore there is a need to balance the selection pressure (Kress, 2010).

While evolutionary computation (EC) has been used successfully for solving many real-world problems, still there is no single EC-algorithm that can solve all problems. EC-algorithms try to find optimal solution, however these solutions are not always perfect.

Solving large, multidimensional, and complex problems, by means of classical techniques are sometimes challenging and/or costly, and whenever traditional solvers fail to solve problems, because of sheer size of the problem or because of existing constrains, nonlinearities, uncertainty, multimodality, and discontinuities in the search space, EC-algorithms have shown good result (Eiben & Smith, 2008).

Three mainstreams of evolutionary algorithms are: evolutionary programming, evolution strategies, and genetic algorithms (Bäck, 1995). Figure 2.3 shows main divisions of evolutionary algorithms.

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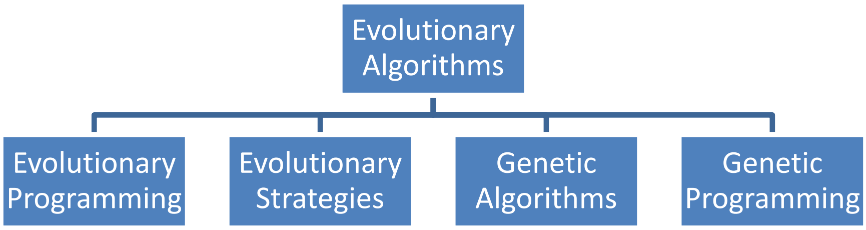

**Figure 2.3: Evolutioanry Algorithms**

The immune algorithms is the youngest family member that has enriched the evolutionary computation scientific community (De Castro & Von Zuben, 2002). Genetic algorithms are the most widely used form of evolutionary algorithms (Golzari, 2011; F. Li, Xu, Jin, & Wang, 2011; Sivanandam & Deepa, 2007). Genetic algorithms techniques have a strong theoretical foundation that were developed by (Holland, 1975). These techniques are considered as optimization methods. Using these algorithms for solving optimization problems has provided near-optimal solutions (Kowalik & Puźniakowski, 2012).

Genetic algorithms are stochastic optimisation searching techniques that look for a solution space for the optimal solution to a problem. It tries to simulate the process of natural evolution. This process is a multi-directional search. In order to do the classification, genetic algorithms start with a randomly initialised population of candidate solutions. A single solution from the population is known as an individual. A fitness (evaluation) function, which mimics the environment, is used to distinguish between different solutions, this function implements a probabilistic, parallel search in the solution space using domain-independent genetic operators (crossover, mutation, inversion and selection) to form a new population of candidate solutions. To facilitate the crossover operation, each candidate solution is represented by an array of bits, where the size of the array is fixed and each bit represents a gene. The new population consists of the fittest rules in the current population along with offspring of these rules. In crossover, substrings

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from pairs of rules (parents) are selected and swapped. Resulting strings are the children. In order to maintain genetic diversity the mutation technique is used. In mutation, one or more randomly selected bit(s) in a rule's string is (are) altered. The population undergoes a simulated evolution process until each rule in the population satisfies a pre-set fitness threshold. At each generation the relatively good solutions reproduce, while the relatively bad solutions die. The fitness of a rule is determined by the classification accuracy on a set of training (Ghosh & Jain, 2005; Golzari, 2011; Mera, Ingham, & Elliott, 2004; Sivanandam & Deepa, 2007).

### 2.3.2 Common Framework

AISs are bio-inspired computational systems (Timmis et al., 2004) and researchers have argued that the development of biologically-inspired algorithm should have a well-formed conceptual framework (Stepney, Smith, Timmis, & Tyrrell, 2004), one such framework was proposed by (De Castro & Timmis, 2002b, 2003), they argued that a framework to design a bio-inspired computational algorithm requires, at least, the following basic elements (De Castro & Timmis, 2002b, 2003):

- *A representation for the components of the system*;
- *A set of mechanisms to evaluate the interaction of individuals with the environment and each other*. *The environment is usually simulated by a set of input stimuli, one or more fitness function(s), or other mean(s);*
- *Procedures of adaptation that govern the dynamics of the system, i.e. how its behavior varies over time.*

Figure 2.4 illustrates the layered structure and the basic elements involved in the framework of designing an AIS. This design is based on an application domain that has

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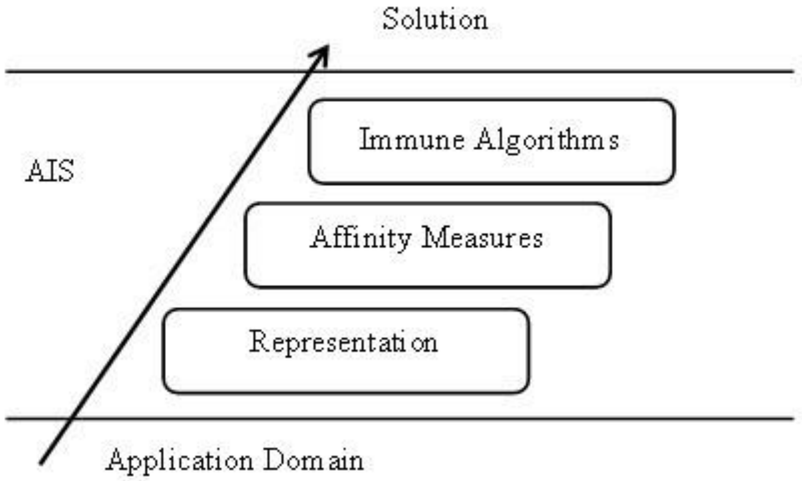

**Figure 2.4: Layered Framework for AIS (De Castro & Timmis, 2003)**

to be determined and when the domain is defined, a type of shape-space (representation) is used to create an abstract model for immune cell components: the antibodies and the antigens. The shape-space will determine the affinity measure to evaluate the interactions of cell receptors with the antigens and each other. The final layer corresponds to the application of algorithms that will govern the behaviour of AIS over time (De Castro & Timmis, 2003). These include (however not limited to) a negative selection, a clonal selection and discrete, and immune network (De Castro & Timmis, 2002a).

In an adaptation for the AIS, researchers proposed that in the context of multidisciplinary conceptual framework, best developed and analyzed bio-inspired algorithms should provide sophisticated biological models and sound analytical principles. Building these models is an interdisciplinary process and in order to construct the models, it is necessary to have collaboration between biologists, mathematicians, and computer scientists (Stepney et al., 2004).

Following subsections introduce briefly the above mentioned layers: the representation methods, the affinity measures, and the algorithms.

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### 2.3.3 Representation

An antibody (Ab) represents a candidate solution to the target problem (De Castro & Timmis, 2002b), in general Ab is represented by an L-dimensional vector $Ab = (Ab_1, \dots, Ab_L)$ where L is the length and the number of attributes of the vector (Freitas & Timmis, 2007).

Three different types are usually used to represent antibodies, namely binary, numeric and nominal. In case of the binary data type, antibodies and antigens are represented by sets of bits and bitwise operations are used to calculate the affinity between them. In case of numeric data types antibody and antigens are represented by either real or integer values. Many researchers use the Euclidean or the Manhattan distance measurement to calculate the affinity between antibodies and antigens. In case of nominal or categorical data type, all features of the vectors are represented by nominal values (Golzari, 2011).

### 2.3.4 Affinity Measures

Affinity function in AIS is concerned about which antibodies should be cloned and how many clones of them should be produced (Freitas & Timmis, 2007). This function has a close relationship with the representation mechanism (Golzari, 2011). The importance of selecting an appropriate affinity function has been emphasized by (Freitas & Timmis, 2007; Hart & Ross, 2004). In case of binary type representation, the Hamming distance or its complement is the most commonly used technique for measuring the distance between bit strings, another binary-distance affinity function that has found applications is the r-contiguous-bits matching rule. (Golzari, 2011; Harmer, Williams, Gunsch, & Lamont, 2002). Literature review revealed that the majority of the AIS researchers have used the Euclidean distance to measure numeric type of data. Another affinity function for the numeric data type is the Manhattan distance; it has been frequently used by the researchers (Golzari, 2011). In case of nominal representation,

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there are two options for the values of antibody and antigen, either they are similar or different. The affinity function indicate similarity if the values are the same otherwise it shows dissimilarity (Golzari, 2011). Freitas and Timmis have proposed that the selection of affinity function should be problem-oriented, they argued that there is no such thing as the “best” distance measure, and suggested to carefully study the dataset in detail and then choose the affinity function which is most suitable for that particular dataset  (Freitas & Timmis, 2007).

### 2.3.5 Immune Algorithms

The immune system with its remarkable self-learning and information processing capabilities has been a source of inspiration to build the AIS; a survey has shown that the field of AIS has gained a substantial degree of success as a division of computational intelligence since it was introduced in 1990s (Dipankar Dasgupta, Yu, & Nino, 2011). De Castro and Timmis proposed the following taxonomy for AIS algorithms: population-based and network-based. Population-based algorithms apply theories such as negative selection and clonal selection. Network-based algorithms are based on immune network theory. De Castro and Timmis classified clonal and negative-selection algorithms as population based, and continuous and discrete algorithms as network-based (De Castro & Timmis, 2003).  Dasgupta et al. have also revealed that in general four major categories of AIS-based algorithms exist: (1) negative selection; (2) artificial immune networks; (3) clonal selection algorithm; (4) danger theory and dendritic cell algorithms (Dipankar Dasgupta et al., 2011). Figure 2.5 shows categories of AIS, as described by Dasgupta (Dipankar Dasgupta et al., 2011). In this thesis, we mainly focus on clonal selection algorithms.

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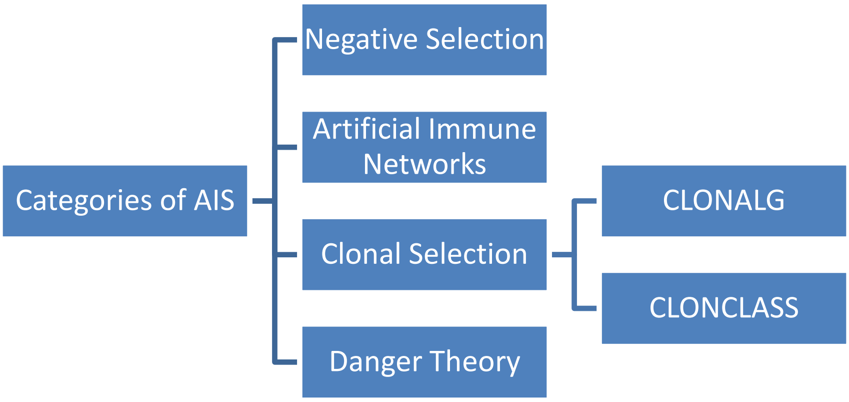

**Figure 2.5: Categories of Artificial  Immune System**

Dasgupta (Dipankar Dasgupta, 2006) divided AIS-based algorithms into two categories: population-based and network-based. Figure 2.6 presents the taxonomy of AIS introduced by Dasgupta. The focus of this research is on clonal selection mechanism. There are different views on clonal selection, while Hofmeyr et al. (Hofmeyr & Forrest, 2000) see clonal selection merely as genetic algorithms that use crossover operators, (De Castro & Von Zuben, 2000a) argue that genetic algorithms do not cover mutation, hypermutaion, and affinity proportional reproduction, which are also aspects of clonal selection (Zheng, Chen, & Zhang, 2010).

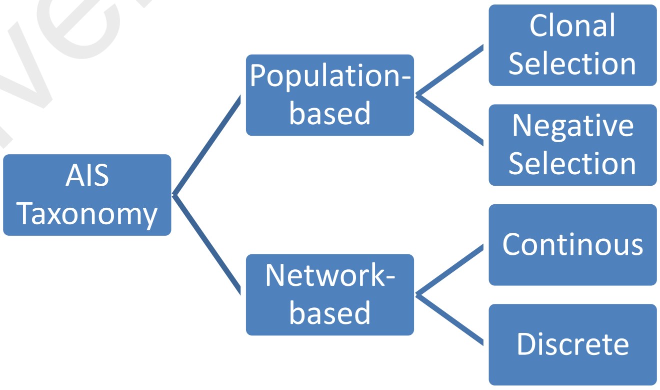

**Figure 2.6: Artificial Immune System Taxonomy**

A study carried out by (White & Garrett, 2003) showed that one of the most famous clonal selection algorithms, the CLONALG, has the strength of classifying unseen

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patterns, however its learning time is not suitable for time dependent problems and the authors presented an improved version of this algorithm, dubbed as CLONCLAS, which was able to reduce the number of generations. They argued that the reason for this poor performance of CLONALG is that it starts with a global search and then moves to a random local search and CLONALG uses only one of the mutated clones and discards the rest, although other high affinity candidates may still exist in the population. However, their method uses a direct walk in the search space for each example in order to optimize the population and in contrast to CLONALG, CLONCLAS tries to preserve a larger proportion of the matured population (White & Garrett, 2003).

Immune algorithms have also become popular for one of their capabilities, namely solving multi-objective optimization problems because they use population-based heuristics and these algorithms make possible to handle a set of potential solutions simultaneously, whereby solutions are the population. These algorithms can find several members of the Pareto set in a single run of the algorithms, and in contrast to common mathematical programming methods, they do not need to perform a series of separate runs and they are also less susceptible to the continuity and shape of the Pareto front (Villalobos-Arias, Coello, & Hernández-Lerma, 2004). Villalobos-Arias et al. (Villalobos-Arias et al., 2004) introduced a general mathematical framework to proof that an entire family of artificial immune algorithms are convergent and eliminated the need for proving the convergence of each algorithm separately (Timmis, Hone, Stibor, & Clark, 2008).

One of the most used algorithms for anomaly detection is the negative selection algorithm (Timmis et al., 2008). One of its strength is the ability of using only a single class for training the data; however, investigations have shown that a second class is

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required for tuning the system. Drawbacks of the negative selection algorithm are: high false positive rate, scaling- and complexity issues (Hart & Timmis, 2008).

A study conducted by Kim et. al (J. W. Kim et al., 2007) emphasized the need for further investigation into immune algorithms to verify whether or not the incorporation of up-to-date immunological findings in immune algorithms will ensure real advantages.

## 2.4 Biologically-based Classification

Although there have been relentless advances in computing technologies, scientist are still humbled by the sophistication, adaptability and variety of the natural world. (Turing, 1950) one of the pioneers in computational science asked whether computers could think. From the beginning of the computing technologies, many computational scientists have been arguing in favour of creating more efficient and faster algorithms, which exhibit centralized control, while others have been arguing in favor of creating robust, and adaptable algorithms and less emphasise on efficiency and speed. The latter approaches has led to biologically inspired computing (Bongard, 2009). One of the strength of bio-inspired algorithms, was shown by Giles (Giles, 2005); he has shown that Wikipedia, with low centralized editorial control, is almost as accurate as Encyclopedia Britannica (Giles, 2005). Although not strictly bio-inspired, Wikipedia uses swarm intelligence principles (Leitão, Barbosa, & Trentesaux, 2012) to improve the itself with little direction from above. However, bio-inspired computing does not guarantee performance in clearly defined domains. Bio-inspired algorithms' strengths lie in their flexibility; they perform well when the task is poorly defined; they are able to adapt to unanticipated amendments in the job environment (Bongard, 2009).

Jerne (Jerne, 1974) introduced the immune network theory (INT), according to his theory: immune system uses feedback mechanism to maintain a network of cells that are capable of learning and maintaining memory. In other words, something that has been

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learnt can be forgotten, unless other parts of the network reinforce it. Perelson (Perelson, 1989) who was motivated by the work of Jerne used the idea of shape space to introduce criteria for assessing the completeness and overlap in the antibody repertoire. He also suggested that the immune system is stable but not too stable.

Cooke et al. (Cooke & Hunt, 1995) were inspired by the INT (Perelson, 1989) and developed an human immune system based Artificial Immune System (AIS). Immunity-based techniques are a branch of artificial intelligence (Dipankar Dasgupta, Ji, & Gonzalez, 2003), and thus AIS is a branch of artificial intelligence (Polat, Şahan, & Güneş, 2006). De Castro et a. (De Castro & Timmis, 2002b) have shown that AIS is another computational intelligence (CI) paradigms which are systems that can adapt their behavior so that they can reach their goals which is to solve a particular problem, in a range of environments (De Castro & Timmis, 2002b). CI describes techniques that focus on strategy and outcome. CI covers not only AIS, but also Evolutionary Computation, Particle Swarm Optimization, Ant Colony Optimization, Artificial Neural Networks, and Fuzzy Systems (Brownlee, 2011). Cooke et al. (Cooke & Hunt, 1995) described how to use AIS to evolve antibodies that are capable of classifying DNA sequences. Figure 2.7 shows main divisions within computational intelligence.

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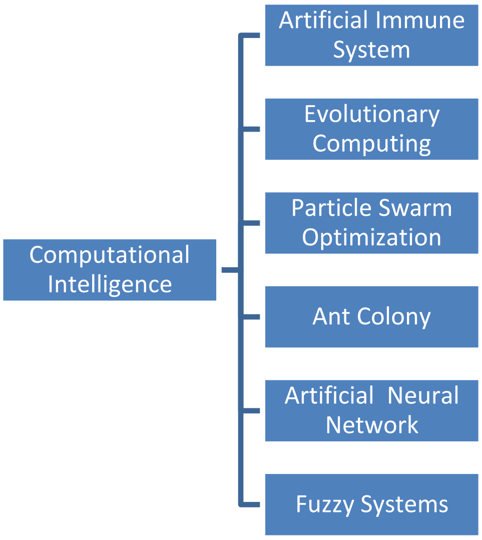
Computational Intelligence
Artificial Immune System
Evolutionary Computing
Particle Swarm Optimization
Ant Colony
Artificial Neural Network
Fuzzy Systems

**Figure 2.7: Major Groups of Computational Intelligence**

(Timmis et al., 2000) used the concept of INT to present the AIS, a primarily unsupervised machine learning method with the goal of providing the basis for a data analysis tool. They proposed a network of B cells (the population) where the primary stimulus was the similarity between the B cell and the pathogen, and the secondary stimulus for a B was the similarity of the particular B cell to its connected neighbors. The affinity (the Euclidean distance) is normalized in the range of [0, 1] and the stimulation is equal to 1 minus the affinity. This means when the distance decreases, the stimulation effect of the pathogen on the B cell will increase (Timmis et al., 2000). The proposed AIS uses a fixed mutation rate to clone and mutate B cells in order to construct a memory of B cells that are able to recognise similar patterns to the one that caused the cloning (Timmis et al., 2000). AIS consists of nodes and the links between them, which represent the similarity between the B cells. Timmis et al. defined network affinity threshold (NAT) as the average affinity associated with all the links in the network. Links between two cells are created if their affinity exceeds the NAT. Timmis et al. concluded that their networks were effective for clustering and visualization of the data (Timmis et al., 2000).

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The main problem with the immune network theory based artificial immune system was that it suffered from a population explosion (Brownlee, 2005). After extensive testing of the AIS, Timmis et al. (Timmis & Neal, 2001) identified this problem and proposed a new mechanism to control the population. Figure 2.8 shows algorithms that were developed based on the AIS.

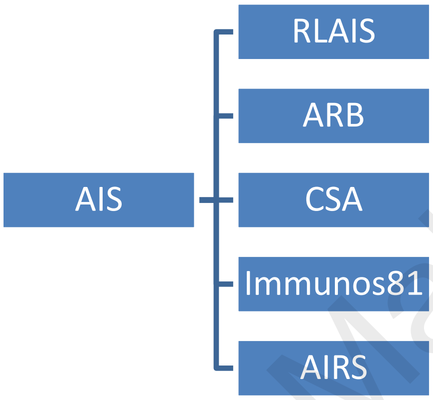

**Figure 2.8: Major Derivatives of Artificial Immune System**

The new system, which extended the AIS, was dubbed as a Resource Limited Artificial Immune System (RLAIS). RLAIS is able to limit the size of networks, and allows for termination conditions to be set, once RLAIS identifies a strong pattern, the network does not lose or deteriorate the pattern  (Timmis & Neal, 2001). For this new system Timmis et al. introduced the concept of an Artificial Recognition Ball (ARB) which represents a number of identical B cells; here, only a pre-defined number of B cells are allowed to exist, which the ARBs' must compete for. The higher the stimulation level of the ARB, the more B cell resources an ARB can allocate, and vice versa. Should an ARB loses all of its B cell resources it becomes unsuitable for learning and will be removed from the network. In the case that the amount of consumed resources exceeds the amount of available resources in the system, resources have to be removed from the B cells.  In order to remove these, the least stimulated (the weakest) resource is removed first, the process of removal of resources continues until there is no difference between the amount of

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allocated resources to all B cells and the maximum amount allowed. Further modification to the AIS is that the NAT is kept constant by calculating it once at the start of the training (Timmis & Neal, 2001).

De Castro and his colleague (De Castro & Von Zuben, 2000a) used two biological principles namely the clonal selection concept and the affinity maturation process to develop a new technique called the Clonal Selection Algorithm (CSA), it was an extension to the work of (Jerne, 1974) that was then applied to data clustering. Authors showed that CSA was able to learn and solve complex problems, it was also highly parallel and computational cost were manageable (De Castro & Von Zuben, 2000a). Researchers (De Castro & Von Zuben, 2002) renamed CSA to CLONALG. This evolutionary algorithm uses clonal selection and affinity maturation principles of the immune system to do machine-learning and pattern-recognition tasks. since the algorithm is capable of doing parallel search, after its adaptation, it can be used to solve optimization problems, authors also showed that CLONALG is capable of doing multimodal search, their empirical results also showed that it was able to outperform a fitness sharing technique by locating a higher number of local optima, including the global maximum (De Castro & Von Zuben, 2002). In a subsequent work De Castro et al. (De Castro & Von Zuben, 2000b) used genetic variation and selection strategy within a population of individuals to control the network dynamics and plasticity and named the proposed method aiNet. In this network clonal selection is used to control the amount and locations of the cells within the network, and the structure of the final network is defined through a minimal spanning tree (De Castro & Von Zuben, 2000b). The main goal for developing aiNet was to solve data analysis problems and authors have successfully applied it to several data compression and clustering applications (De Castro & Von Zuben, 2001). In order to perform multimodal optimization tasks, aiNet was further developed by (De Castro & Timmis, 2002a); empirical results showed that if there is a relative separation

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between the clusters, aiNet could be used to solve non-linearly separable problems using a minimal spanning tree of a trained network. Authors also identified many similarities between their model and the artificial neural networks (De Castro & Timmis, 2002a).

The history of supervised learning system (classification) using immune system principles starts with the work of Carter (Carter, 2000) when he introduced the Immunos-81. Carter used abstractions of T cells, B cells, antibodies as well as their interactions to develop his classifier. This classifier uses artificial T cells to control the formation of B cell populations, which compete for recognition of “unknowns” (Carter, 2000). Carter used two standard medical data sets to test the recognition capabilities of the classifier and achieved good classification results. Carter reported that Immunos-81 were a powerful, and an easy to build and train classifier. Carter concluded that Immunos-81 offers a viable paradigm for the design of pattern recognition (Carter, 2000).

Watkins’ investigations revealed that there was a lack of research in the arena of adding a supervised learning component to AIS (Watkins, 2001). The only known algorithm at that time was the Immunos-81 that was briefly described above. These investigations lead to the development of Artificial Immune Recognition System (AIRS).

## 2.5 Research Progress of Hybrid SVM-based Classifiers Within the AIS Domain

Literature is full with literature related to applications of SVM. In this section, we briefly introduce research progress of AIS-SVM-based classifiers. For this section we searched for related articles published either in ISI journals or in important conferences in the last decade (from 2006 to 2016).

Support vector machine (SVM) is originated from advanced statistical learning theory (SVMS.org, 2010) it is recognised as a robust and state-of-the-art classification technique.

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SVM is able to maximize the predictive accuracy of a model without overfitting the training instances. SVM is mainly suitable for analyzing data with very large numbers of predictor fields. SVM has found many applications in various disciplines, including bio sequence analysis, bioinformatics, classification, concept extraction, customer relationship management, character recognition, text mining, and speech and voice recognition.

Vapnik et al. introduced SVM in 1995, and later the “soft margin” SVM was presented by Cortes and Vapnik (Cortes & Vapnik, 1995).

An AIS-SVM hybrid algorithm was developed by (Woolley & Milanović, 2009) for identifying voltage collapse prone areas and overloaded lines in the power system. In their study, they used an AIS algorithm to optimize SVM’s parameters. They compared classification performance of two models, one without optimization- and another one with optimization of SVM parameters. Their test results showed that the model, which used AIS to optimize SVM’s parameters, could classify benchmark data sets significantly better than the standalone SVM model. They have carried out a good study and obtained good results; however, they did not compare running time of both models, nor did they report any comparison of their models with other well-known classifiers. It would have been better to use additional criterion besides the 10-fold cross validation for evaluation of the models.

Aydin et. al (Aydin et al., 2011) have proposed a model, a hybrid of AIS and SVM. Here, AIS was used to solve a multi-objective problem for optimizing SVM’s parameters. They have tested their model against two data sets, one for fault diagnosis, and another one for anomaly detection. They have achieved good results with their model; however, they only used cross-validation method to measure the performance of their model. More evaluation measurements could support their results.

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Antunes et. al (Antunes, Silva, Ribeiro, & Correia, 2011a; Antunes et al., 2011b) developed an ensemble of SVM and AIS for classifying text. Their model was applied on Reuters-21578 data set, and they have achieved good results; however, they did not report the running time of their models, nor did they compare their model with other available classifiers.

A hybrid of AIS and particle swarm optimization was introduced by Kuo et. al (Kuo, Chen, Liao, & Tien, 2013). Their aim was to use this hybrid model in order to optimize parameters of SVM. They proposed three models: HIP-SVM, AIS-SVM, and PSO-SVM. These models were applied on six different data sets. The first two models performed better than PSO-SVM, and both achieved same results with 5 data sets, and only in one case HIP-SVM performed slightly better than AIS-SVM. Their methodology and results are very good; however, they did not compare their model with other classifiers. It would have been better to use additional criterion besides the 10-fold cross validation for evaluation of the models.

## 2.6 Artificial Immune Recognition System

AIRS belongs to the field of Artificial Immune Systems, and thus, to the field of computational intelligence (Brownlee, 2011), and more broadly to the field of artificial intelligence, this relationship was discussed earlier. AIRS is a clonal selection  type of immune inspired supervised learning algorithm that was introduced by Watkins (Watkins, 2001) who was inspired by the work of (Timmis & Neal, 2001) and was also motivated by the work of (De Castro & Von Zuben, 2000b). Initially, it was known as AIRS however, later it was referred to as AIRS1. Based on the experience gained from the AIRS1, Watkins and Timmis decided to refine the process of the AIRS1 by reducing the complexity of AIRS1's approach while maintaining the accuracy of results, and introduced AIRS2 (Brownlee, 2011). Watkins et al. showed that the AIRS2 is simpler

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and computationally more efficient than AIRS1 (Watkins & Timmis, 2002, 2004). The clonal selection theory was introduced by (Burnet, 1959).

Subsection 2.3 briefly introduced relevant aspects of human immune system that have been utilized as motivation for developing AIS and AIRS. Some key terms that were discussed before are highlighted next.

B- and T-cells have an exclusive type of molecular receptors which represent locations in a shape space. The Shape space is defined as the attributes' features of the antigens. These receptors enable binding of antigens and antibodies, the higher the affinity between them the stronger the binding. The affinity is defined as the degree of similarity between antigens and B-cells. The Euclidean distance is one of the methods that can be used to measure the affinity which represent the interaction between elements. Antigenic presentation is another name for antigen/antibody binding; in AIRS it refers to matching between antigens (training data) and B-cells (potential solutions) (Watkins, 2005). As mentioned in subsection 2.4, the ARB represent a number of identical B cells (Timmis et al., 2000) and it reduces duplication as well as dictates survival within the population (Watkins, 2005). Affinity maturation is a learning process of the immune system; this process involves determining the affinity between an antigen and a B-cell and transforming the involved B-cell into a plasma cell (Watkins, 2005). During an immune response the recognition B-cell will undergo rapid clonal expansion in proportion to how well it matches the antigen; the goal is to generate as many clones of itself so that the next time it sees an antigen, it matches the antigen better. This response is antigen specific. The generated clones then undergo a process called somatic hypermutation proportional to the affinity between the B-cell and the antigen (Brownlee, 2005; Watkins, 2005). The generated clones have different features (receptors) than their parent; therefore it is possible that some of them are a better match to the antigen observed and since only those

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cells with highest affinity with the antigen are maintained there will be a competition between the clones (Brownlee, 2005). This selection process is called clonal selection, where a given cell may become a memory cell (Watkins, 2005). It is often said that the immune system has a kind of memory, it refers to the adaptive capability of the immune system to recognize an antigen, when it encounters the same antigen in the future (Brownlee, 2005). Therefore the memory cells are retained in order to react faster to the same or similar antigen, should the body get re-infected (Watkins, 2005). Continuous change of the B-cell population (proliferation and death) is known as the metadynamics of the immune system (Watkins, 2005).

Table 2.1 illustrates the mapping of terminologies between the immune system and the AIRS.

**Table 2.1: Mapping between the Immune System and AIRS (Watkins & Timmis, 2002)**

| ***Immune System*** | ***AIRS*** |
|---|---|
| *Antibody* | *Feature vector* |
| *Recognition Ball (RB)* | *Combination of feature vector and vector class* |
| *Shape Space* | *The possible values of the data vector* |
| *Clonal Expansion* | *Reproduction of ARBs that are well matched with antigens* |
| *Antigen* | *Training data* |
| *Affinity Maturation* | *Random mutation of ARB and removal of the lowest stimulated ARBs* |
| *Immune Memory* | *Memory set of mutated ARBs* |
| *Metadynamics* | *Continual removal and creation of ARBs and Memory cells* |

AIRS uses the affinity mutation and the clonal expansion to generate potential memory cells and these cells are then used for the classification (Watkins, 2005).

AIRS is a collection of procedures that were developed for supervised or unsupervised AIS algorithms (Brownlee, 2005). Watkins et al. (Watkins, 2005) borrowed the idea of a stimulation level for an ARB from (Farmer et al., 1986), the stimulation is the inverted affinity, and the affinity is normalized in the range of [0, 1] (Brownlee, 2005; Watkins, 2005). Furthermore AIRS has adopted the use of an affinity threshold, the concept of

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ARB and population control mechanism from AINE (Thomas Knight & JonathanI Timmis, 2001; Watkins, 2005) and borrowed random mutation, clonal expansion, and clonal selection from other AIS-based algorithms (Brownlee, 2005), these topics were introduced and discussed above.

This thesis uses the following definitions of the key terms and concepts that were introduced by (Watkins, 2001):

- ***Artificial Recognition Ball (ARB)*** *represents a number of identical B-Cells and is also a mechanism to reduce duplication and dictate survival within the population (Watkins, 2001).*
- ***Affinity threshold scalar (ATS)****: It is a value between 0 and 1 that when it gets multiplied by affinity threshold, it provides a cut-off value for memory cell replacement during training phase (Watkins, 2001).*
- ***Clonal rate****: It is an integer value that is used to determine the number of mutated clones a given ARB is allowed to attempt to produce (Watkins, 2001).*
- ***Hyper-mutation*** *rate: It is an integer value that is used to determine the number of mutated clones that a given memory cell is allowed to inject into the cell population (Watkins, 2001).*
- ***Seed cell****: It represents an antibody that is drawn from the training set and is used to initialize Memory Cell and ARB populations at the beginning of training (Watkins, 2001).*
- ***Stimulation value****: It is the value returned by the stimulation function, this function is used to measure the response of an ARB to an antigen or to another ARB. The function returns a value between 0 and 1 (Watkins, 2001).*
- ***Total resources****: It is a parameter which sets limitations on the number of ARBs allowed in the system. Each ARB is allocated a number of resources based on its stimulation value and the clonal rate* (Watkins, 2001).

In general, the goal of developing AIRS algorithm was setting memory cells that can be used for data classification. These artificial memory cells represent a number of features of the immune systems. They represent memory B cells that have gone through a maturation procedure in the human body.

Each ARB is represented by an n dimensional vector and a class to which the data belongs. Furthermore each ARB is assigned a stimulation value that is calculated through Equation 2.2, where x is feature vector of the ARB, and y is the training antigen; AIRS uses the Euclidean distance to measure the affinity (Watkins, 2005):

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$$affinity\ (x, y) = 1 - Euclidean\ Distance\ (x, y) \quad = 1 - \sqrt{\sum_{i=1}^{n} (x_i - y_i)^2} \tag{2.1}$$

$$S_x = \begin{cases} 1 - affinity\ (x, y) \colon if\ x\ and\ y\ have\ the\ same\ class \\ affinity\ (x, y) \colon if\ class\ of\ x\ and\ y\ are\ different \end{cases} \tag{2.2}$$

The smaller the Euclidean distance, the higher the affinity and higher affinity means generating larger number of clones. The affinity threshold is the average Euclidean distance between each instance in the training data set; cells with the highest affinity are selected for cloning and are ultimately used for creating an established memory set; how many clones are created depends on their antigenic affinity in other words, how well they match; in order to create diversity, ARBs also experience a random mutation  (Watkins, 2005).

Figure 2.9 illustrates the outline of AIRS2's algorithm. Algorithm AIRS2 consists of four stages to learning: 1) initialization, 2) memory cell identification, 3) resource competition, and 4) refinement of established memory cells (Watkins, 2005). In the first stage data is normalized and initialized so that the affinity of every two training records is in the range of [0, 1]. In this stage, there is an option for seeding the memory cell pool. This pool represents a collection of recognition elements that form the classifier which is produced at the end of training phase. Initialization stage also calculates affinity threshold which is used during training phase to determine whether prepared candidate memory cells can replace already existing memory cells in the classifier (Watkins et al., 2004).

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1. *Compare a training instance with all memory cells of the same class and find the memory cell with the best affinity for the training instance. Refer to this memory cell as $mc_{match}$*
2. *Clone and mutate $mc_{match}$ in proportion to its affinity to create a pool of abstract B-Cells*
3. *Calculate the affinity of each B-Cell with the training instance*
4. *Allocate resources to each B-Cell based on its affinity.*
5. *Remove the weakest B-Cells until the number of resources returns to a preset limit.*
6. *If the average affinity of the surviving B-Cells is above a certain level, continue to step 7, Else clone and mutate these surviving B-Cells based on their affinity and return to step 3.*
7. *Choose the best B-Cells as a candidate memory cell ($mc_{cand}$)*
8. *If the affinity of $mc_{cand}$ for the training instances is better than the affinity of $mc_{match}$ , then add $mc_{cand}$ to the memory cell pool. If, in addition to this, the affinity between $mc_{cand}$ and $mc_{match}$ is within a certain threshold, then remove $mc_{match}$ from the memory cell pool.*
9. *Repeat from step 3 until all training instances have been presented.*

*When the training routine is completed, AIRS uses kNN to classify instances with the developed set of memory cells (Watkins, 2005).*

**Figure 2.9: Outline of AIRS2 (Watkins, 2005)**

Figures 2.10 through 2.17 illustrate the process of AIRS algorithm. As mentioned earlier the goal is to generate recognition elements (records or feature vectors) that can be used to classify new instances at the end of training scheme. These recognition elements are collected in the memory cell pool. Initially the memory cell pool is empty and optionally can be seeded with few randomly selected records from the training data. The letter “A” in the circle represents an instance from the training data, for which the algorithm is going to generate recognition vectors.

The incoming training data items (records) represent antigens and the items that will be generated in the memory cell pool represent the antibodies also known as B cells which are obviously also vectors. The AIRS algorithm determines the affinity threshold (AT) which is the mean affinity between antigens (records) in the training dataset. This value is used later during the training phase to verify whether existing memory cells can be

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replaced with candidate memory cells which are prepared. Affinity represents the similarity between records (vectors), the higher the affinity the more similar are the vectors (Brownlee, 2005; Watkins, 2001).

The AIRS algorithm is a single-shot algorithm, meaning it only needs to pass once over the training data to prepare the classifier. One at a time, each record is exposed to the memory cell pool (Brownlee, 2005; Watkins, 2001).

Figure 2.10 shows the initial phase of the algorithm when an instance “A” is presented to the memory cell pool from where a matching record is sought. The vectors (cells) in the memory cell pool are stimulated by the record “A” and each vector in the memory cell pool is assigned a stimulation value. The stimulation value is given through the Equation 2.2.

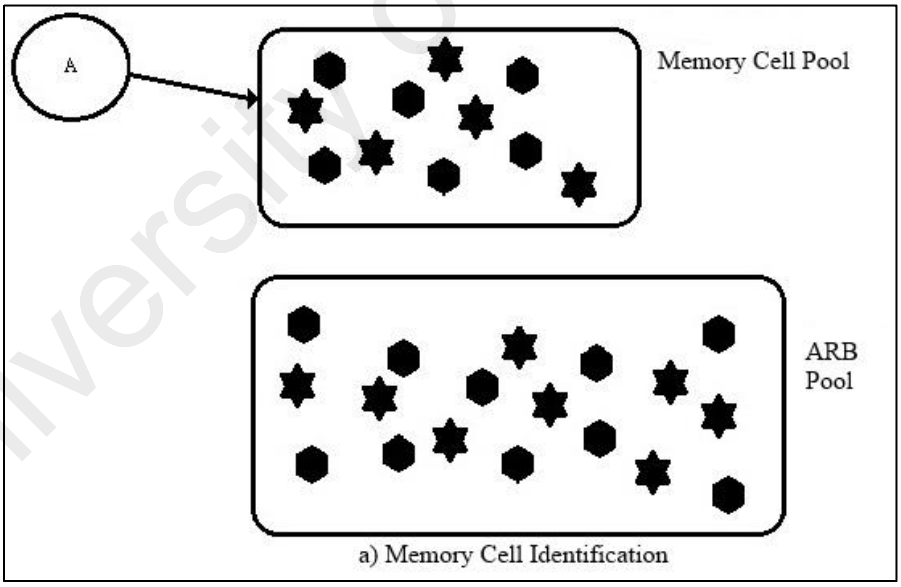

**Figure 2.10: Memory Cell Identification**

The AIRS2 algorithm uses the Euclidean distance as the primary metric for both affinity and stimulation, however other functions could also be used (Watkins, 2001). The vector with the greatest stimulation is selected as best match memory cell and is used in the affinity maturation process (Brownlee, 2005; Watkins, 2001).

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Figure 2.11 illustrates the situation when a matching record is found and is marked as the MCmatch.

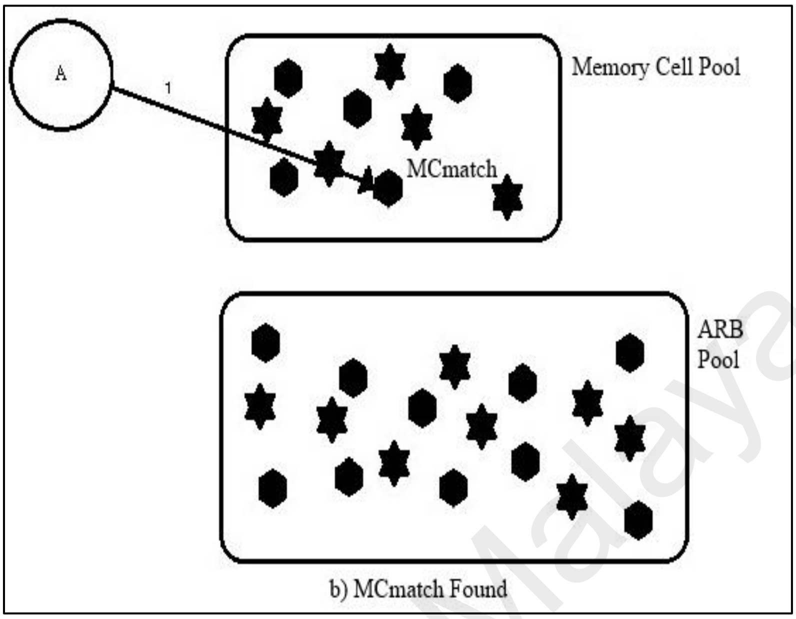

**Figure 2.11: Identifing  MCmatch**

Figure 2.12 shows the process of generating new ARBs (vectors) which are a number of mutated clones of the MCmatch that are added into the population (ARB pool).

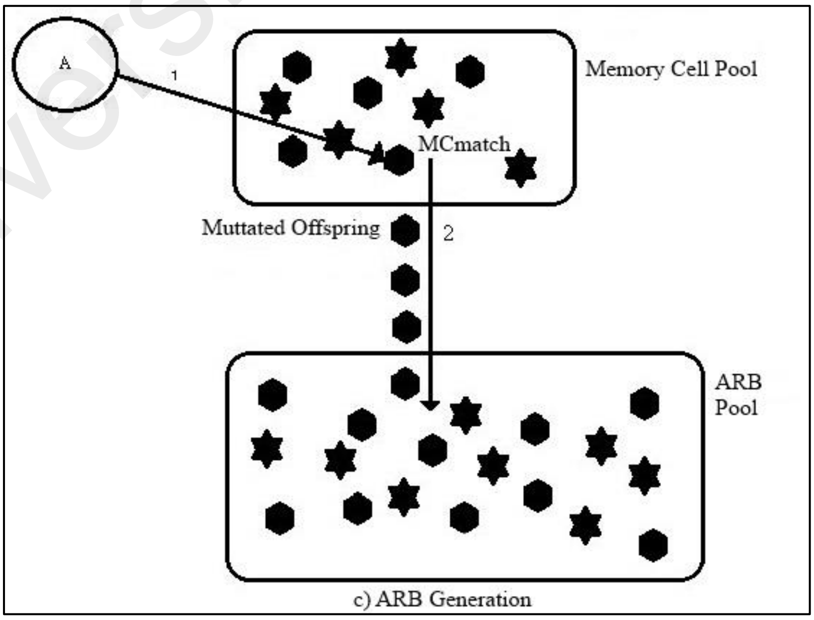

**Figure 2.12: Process of Generating ARBs**

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Clonal selection is referred to selection of those cells (vectors) that exhibit the greatest affinity (similarity) to an incoming training data item which are most stimulated and used to produce new vectors (offspring). In the terms of AIRS, producing offspring means to only produce mutated offspring and this occurs in the form of random feature mutation. This means when a particular feature of an ARB is selected for mutation, it will randomly mutate to any value within a given range (Watkins, 2001).

Figure 2.13 illustrates the procedure of cloning and mutation used by the AIRS algorithm.

```
Determine the number of clones to produce
numClones = stim * clonalRate * hyperMutationRate
For i=0 To numClones DO   // Generate Clones
    mutationRange = 1- stim // Calculate Mutation Range
    Instance_cloned =  copy of MCmatch  //Clone MCmatch
    FOR each Feature of Instance_cloned DO //Start Mutation
        IF Attribute is the class value THEN never change its value
        IF AttributeType = Nominal THEN
            FeatureValue =  new random Nominal value
        IF AttributeType = Numeric THEN
            MinRange = max(AttributeValue – (mutationRange/2.0), 0.0)
            MaxRange = min(AttributeValue + (mutationRange/2.0), 1.0)
            FeatureValue = min + RandomNumber * (MaxRange – MinRange)
        END IF
    DONE
DONE
Add Mutated Clones to ARB pool
```

**Figure 2.13: Clone and Mutate of the Best Match Cell: The MCmatch**

An ARB represents a similar or identical recognition cell (vector). The ARB pool represents the work place where the AIRS algorithm refines mutated clones of the best match memory cell for a specific antigen (instance) (Brownlee, 2005).

The number of mutated clones generated from the best match is determined through the Equation 2.3:

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$$\text{numClones} = \text{stim} * \text{clonalRate} * \text{hypermutationRate} \quad (2.3)$$

where the stim is the stimulation value between the best match memory cell (Vector) and the antigen (the instance “A”). The values for other two parameters, the clonalRate and the hypermutationRate are defined by the user (Brownlee, 2005; Watkins, 2001).

Figure 2.14 represents the process of competition for system wide resources and the use of mutation for diversification and shape-space exploration as well as the use of average stimulation threshold as a criterion for determining when to stop training on a given antigen (instance) (Brownlee, 2005; Watkins, 2001).

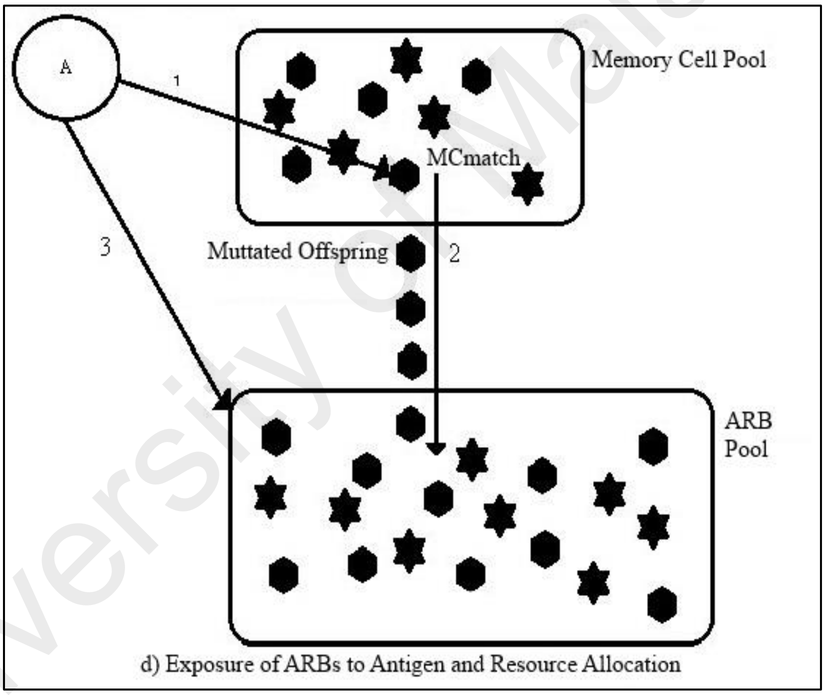

**Figure 2.14: Process of Resource Allocation and Competition**

Training for an antigenic pattern has to stop at some time, therefore the algorithm verifies whether or not ARBs have been stimulated enough for the training, the algorithm uses the average stimulation values for the ARBs of each class as termination condition, if each of these averages becomes greater than a pre-defined threshold the training ends for that particular pattern (Watkins, 2005; Watkins et al., 2004).

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In the third stage the algorithm handles competition for resources during development procedure of a candidate memory cell. The goal of this stage is to develop a memory cell that is most successful in accurately classifying a given antigen. To achieve this goal the algorithm uses three mechanisms. The first mechanism is about system wide resource competition. A number of mutated clones of the best matching memory cell MCmatch are added to the ARB pool and the process of generation of recognition vectors and competition starts. The process of competition is necessary for controlling the size of the ARB pool as well as promoting those ARBs that have greater affinity (stimulation) to the antigen (instance) being trained on (Brownlee, 2005). This process considers only ARBs of the same class as the antigen (the instance). The flow chart of this process is illustrated in Figure 2.15 (Brownlee, 2005):

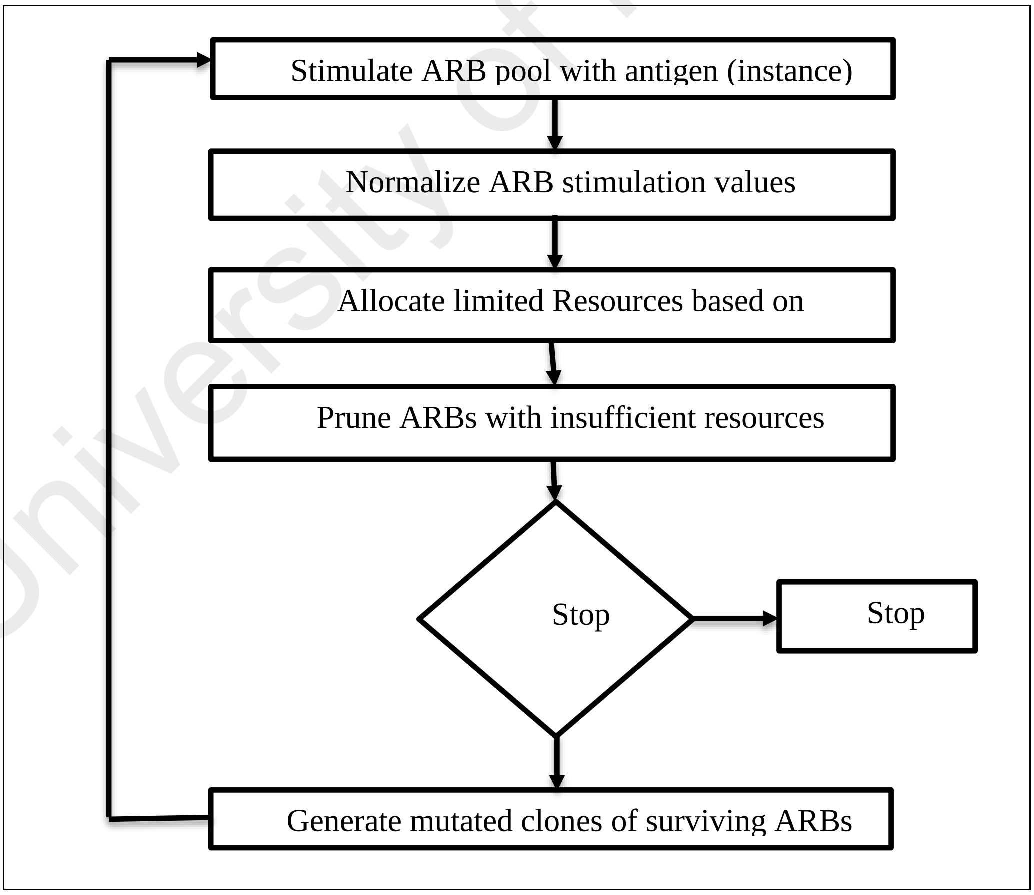
Stimulate ARB pool with antigen (instance)
Normalize ARB stimulation values
Allocate limited Resources based on
Prune ARBs with insufficient resources
Stop
Stop
Generate mutated clones of surviving ARBs

**Figure 2.15: Flow Chart for Resource Allocation and Competition of AIRS**

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Then the algorithm uses the same clonal expansion and hypermutation as it has used to generate mutated clones of the best match memory cell MCmatch, to mutate each ARB in the pool. Equation 2.4 used to determine the number of clones for each ARB in the pool (Brownlee, 2005).

$$\text{numClones} = \text{stim} * \text{clonalRate} \tag{2.4}$$

In order to allocated resources, Watkins (Watkins, 2001) followed the methods that were outlined by (Timmis et al., 2000) and enhanced by (Thomas Knight & Jonathan Timmis, 2001). Resource allocation is based on the stimulation value which indicates the fitness of the recognizer (Watkins, 2001). Normalized stimulation value of the ARB indicates the fitness of ARB that will become a recognizer of an antigen. This value is used to determine the amount of resource allocation. A user defines the maximum amount of resources to be allocated, and the number of resources allocated to each ARB is determined through the Equation 2.5:

$$\text{resource} = \text{normStim} * \text{clonalRate} \tag{2.5}$$

where normStim is normalized stimulation value and clonalRate is the clonal Rate. The second mechanism uses mutation for shape-space search and divergence.

Marwah and Boggess (Marwah and Boggess 2002) allocated resources differently; they assigned more resources to the antigen classes that occurred more frequently. AIRS2 as well as Marwah’s proposed algorithm use linear resource allocation, and because of this linearity the algorithms need longer time for classification and require higher number of memory cells (Golzari, Doraisamy, Sulaiman, & Udzir, 2008; Polat, Şahan, Kodaz, et al., 2007).

The third mechanism defines the stopping condition whereby this condition depends on the average of stimulation threshold (Watkins et al., 2004). Production of ARBs

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continues until the stopping criteria are met, and then the candidate memory cell is selected based on its stimulation value and class.  The candidate memory cell is the one with the maximum stimulated ARB of the same class as the antigen (Watkins, 2005; Watkins et al., 2004).

In the process of resource allocation the total resources allocated by all ARBs is determined and compared to the allowed maximum total resources.

Then the ARB pool is sorted by allocated resources in descending order, if the total resources allocated is greater than the maximum allowed resources, then resources are removed from ARBs starting at the end of the list (from the weakest thus least stimulated ARBs) until the total allocated resources fall below the maximum allowed resources.

If an ARB's resource becomes zero, it will be removed from the ARB pool. The process of refinement of ARB has a stopping condition which occurs when the mean stimulation becomes greater than the stimulation threshold that is given by the user (Brownlee, 2005; Watkins, 2001).

Figure 2.16 illustrates the process of comparing response of MCmatch and MCcandidate to the antigen and comparison of the affinity value of MCmatch and MCcandidate to each other.

When the refinement process of the ARB is completed, the ARB with the greatest stimulation value is selected as a memory cell candidate MCcandidate (Brownlee, 2005).

In the fourth stage of the algorithm the potential candidate memory cell is introduced into the set of already established memory cells for training.

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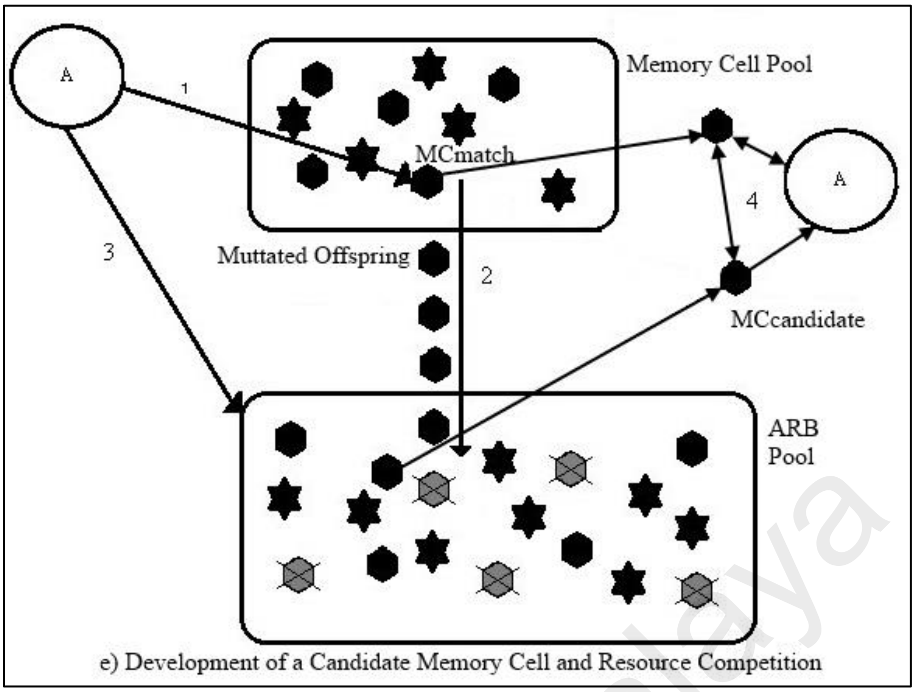
A
1
Memory Cell Pool
MCmatch
A
4
3
Muttated Offspring
2
MCcandidate
ARB
Pool
e) Development of a Candidate Memory Cell and Resource Competition

**Figure 2.16: Development of MCcandidate and Resource Competition**

Figure 2.17 illustrates the process of introducing the just-developed candidate memory cell (vector), the MCcandidate, into the set of existing memory cells MC.

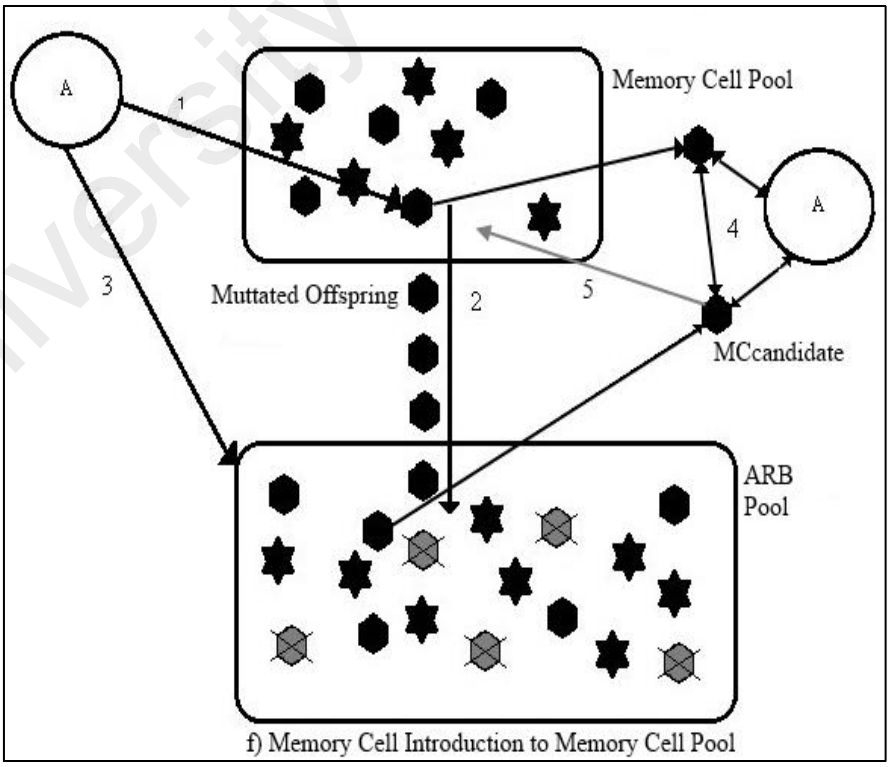

**Figure 2.17: Introduction of Memory Cell to Memory Cell Pool**

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If MCcandidate's stimulation value is higher than that of the original best matching memory cell, MCcandidate will be added into the memory cell pool (Brownlee, 2005). Then the algorithm verifies if MCmatch can be replaced by MCcandidate; this happens when the affinity between the MCcandidate and the best matching cell is less than a cut-off. The cut-off is given by the following Equation 2.6:

$$\text{cutOff} = \text{affinityThreshold} * \text{affinityThresholdScalar} \tag{2.6}$$

where the affinityThreshold is the variable that was prepared during the initialisation phase of the algorithm, and the affinityThresholdScalar is a user defined parameter (Brownlee, 2005).

The above process repeats until all antigens (that is: all instances of training data set) have been introduced to the system (Watkins et al., 2004). After the training process is completed the evolved memory cells in the memory cell pool are available for use for classification. AIRS uses a k-Nearest Neighbor classifier to perform the classification task, here the k-best matches to data instances are identified and via majority vote the class is determined (Brownlee, 2005).

### 2.6.1 Differences between AIRS1 and AIRS2

As mentioned above AIRS1 was the first version of AIRS, detailed explanation of this algorithm was given by (Watkins, 2001). Differences between the AIRS1 and the AIRS2 are explained next.

Somatic hypermutation (affinity proportional mutation) is used by the majority of AIS techniques; however AIRS1 did not use this metaphor, instead it used a naïve random generation of mutations (Watkins, 2005). AIRS1 maintained two independent pools of cells, namely the ARB pool and the memory cell pool. The ARB pool was used to evolve a candidate memory cell belonging to the same class as the training antigen, and at the

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same time AIRS1 maintained ARBs of other classes which were taken care of previously (Watkins, 2005). All these ARBs participated in the competition for the limited resources and as a result the algorithm would need more time for rewarding and refining those ARBs that have the same class as the concerned antigen (Brownlee, 2005). Through animated analysis of the ARB pool Watkins et al. figured out that the effort to evolve ARBs of a different class than the training antigen was useless, and they concluded that a good potential memory cell must have the same class label as the training antigen (Watkins, 2005). This led to the elimination of maintaining multiple classes in the memory of system ("resource management of AIRS2") and thus improving the overall runtime and a simplification of AIRS2 algorithm (Watkins, 2005).

AIRS1 used to generate clones of multiple classes however only clones of the same class as the antigen are used in the ARB pool (Brownlee, 2005), AIRS2 maintains only the ARBs of the same class and does not allow mutation of the class value (switching classes are not permitted) this is in contrast to how AIRS1 dealt with ARBs (Watkins, 2005).

While in AIRS1 a user has the ability to set the "mutate rate" parameter to control the degree to mutate a created clone, AIRS2 uses the notion of somatic hypermutation where the quantity of mutation of a produced clone is proportional to its affinity to the concerning antigen (Brownlee, 2005).

Evaluation results showed that classification accuracy of both AIRS1 and AIRS2 was similar, however AIRS2 is simpler and has better computation performance and provides improved data reduction of the training instances (Brownlee, 2005).

Details about the differences between the AIRS1 and the AIRS2 can be found in (Watkins & Timmis, 2002).

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### 2.6.2 AIRS in the Literature

Applications of AIRS1 on various benchmark classification problems revealed that its performance was as good as other well-respected supervised learning techniques for equal benchmarks (Watkins & Boggess, 2002).

Goodman et al. studied the behaving manner of AIRS on many publicly existing classification problems. While keeping the number of features constant, they incremented the number of classes, and they compared the obtained results with a well-known classifier, the Kohonen's Learning Vector Quantization (LVQ). They showed that average performance of AIRS on one of the problems was even the best for that particular problem (Goodman et al., 2002). Under the condition of similar number of elements, AIRS outperformed both LVQ and an optimized version of the LVQ in almost all cases for the real-world classification problems (Brownlee, 2005). Goodman et al. did a valuable evaluation of AIRS; however, a comparison with only one classifier, the LVQ, is not adequate for determining the performance's quality of AIRS. It would have been better to use additional criterion besides the 10-fold cross validation for evaluation of the models.

In another research, Goodman et al. also investigated AIRS empirically. They exchanged one of the two potential sources of its classification strength with another modifications. They concluded that outcomes were marginally less effective, however it was statistically insignificant. The modifications delivered quick test version of AIRS. They compared AIRS's performance with other best classifiers on the same multiple-class problems and demonstrated that AIRS was competitive with top classifiers. They showed that the mechanism for replacement and maintenance of AIRS' memory cell population is the source of AIRS' classification power. (Goodman, Boggess, & Watkins, 2003). Their evaluation method could be more powerful, if they ran other classifiers by themselves under equal computational circumstances that existed for AIRS. Instead they

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used the online result of (Duch, 2000). Their evaluation could have included broader classification tasks (that is: more data sets).

In another study, Marwah et al. (2002) inspected many different algorithms for situations when two or more classes had equal number of memory cells among the k strongest stimulated memory cells. Their study revealed that in average, AIRS’ accuracy was higher for one of the development environment than any reported at the UCI repository for that environment (Marwah & Boggess, 2002). They have done a great evaluation of AIRS’ handling of ties, by modifying competition process for resource allocation of AIRS; however, their methods did not really improve the performance of AIRS algorithm.

Boggess et al. (Boggess & Hamaker, 2003) studied the effect of adding irrelevant features to datasets and compared classification accuracies obtained from AIRS and LVQ, their result showed that LVQ outperformed AIRS when prepared with the equal number of codebook vectors discovered by AIRS; however, LVQ was not able to outperform AIRS when it was configured independently (Brownlee, 2005).

Meng et al. did a comprehensive benchmark experiment on AIRS, and have concluded that results of AIRS were reasonable and it could be used for real-world classification tasks (Meng et al., 2005). They used two versions of AIRS: AIRS-1 and AIRS-7; however, they did not mention what their differences are. They also did not provide the values for the parameters of either AIRS algorithms, and it would have been better to use additional criterion besides the 10-fold cross validation for the evaluation of proposed algorithms.

Hamaker et al. studied how using non-Euclidean distance measures affects the classical AIRS algorithm; they used four well-known classification problems with numerous amounts of real, nominal, and discrete features. Their study showed the need

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for further research into non-Euclidean distance measure that performs best for a particular data set (Hamaker & Boggess, 2004). Their results revealed that AIRS can obtain better classification accuracy, if more natural and useful measure of comparison is used (Brownlee, 2005). Hamaker & Bogges (2004) have carried out an extensive investigation into the rule of various distance measures in AIRS; however, they did not discuss whether their results were statistically significant different from the traditional AIRS.

Polat et al. incorporated fuzzy logic into resource allocation procedure of AIRS in order to improve classifer's performance. They reasoned that long running time, excessive resource allocation, and high number of memory cells of classical AIRS are due to the linearity of resource allocation procedure. Their method accomplished higher classification accuracy than various well-known classifiers on the same data sets (Polat & Güneş, 2008). Although they have achieved a very good result with their hybrid algorithms, however their report did not show how much "fuzzy resource allocation" contributed to the success of the algorithm.

Golzari et al. introduced real-world tournament selection procedure inside resource competition part of AIRS1 and achieved higher classification accuracy than other benchmark classifiers including the AIRS1. They argued that during competition stage of AIRS1, high selection pressure is the reason for loss of diversity and this may produce premature memory cells. They reported that their method achieved significantly higher classification accuracy than AIRS1 in all cases on the benchmark datasets from the UCI machine learning repository (Golzari et al., 2009a, 2009b). They have achieved very good results with AIRS1; however, they did not report whether the use of RWTS would also improve the performance of AIRS2.

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Polat et al. developed a hybrid method involving AIRS and fuzzy weighted pre-processing; with this method, they classified the thyroid disease dataset. They compared their result with that obtained from AIRS, and reported their method performed better than ARIS (Polat, Şahan, & Güneş, 2007). Their result for the thyroid data set is very good, however they did not discuss why did they use fuzzy weighting pre-processing of the data set, nor did they report the running time of their algorithm. They did not describe how they have determined the parameter values for their fuzzy AIRS.

Saidi et al. as well as Chikh et al. argued that k-NN's classification time depends on the number of data points that are used. Therefore, in order to reduce memory cell pool of AIRS2, they introduced fuzzy k-nearest neighbor to assign a class membership to each instance; they found that reducing number of memory cell pool improves algorithms' performance. Authors compared their results with the result obtained with AIRS2, and concluded that their model achieved higher classification accuracy (Chikh et al., 2012; Saidi, Chikh, & Settouti, 2011). Their proposed method was able to reduce the size of memory cell pool and at the same time achieve higher classification accuracy than AIRS2. However, they did not discuss one important issue, namely the running time of their algorithm and its comparison with that of AIRS2.

Forouzideh et al. presented an application of AIRS for in text-document classification. In their study, different versions of AIRS were compared with RBF and multi-layer perceptron (MLP); their results showed that different versions of AIRS classified better than both RBF and MLP. They expected more successful and diverse applications of AIRS to emerge in the future, because of its high performance (Forouzideh, Mahmoudi, & Badie, 2011). They did a good comparison of various versions of AIRS for text mining. They wrote that they have proposed fuzzy AIRS model, however they didn't provide the pseudocode for this model. They have used the fuzzy KNN, which was developed by

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Keller et. al.  (Keller, Gray, & Givens, 1985) in AIRS1, but they did not discuss why they did not use it in AIRS2.

Another area where  researchers have found promising capability for AIRS is analyzing microarray data (Chen, Xu, Bie, & Gao, 2008). They only used AIRS2 to classify microarray data sets, and did not introduce any new model.

Le et al. combined E-algorithm with AIRS and created a novel Fuzzy AIRS dubbed as FAIRS; this new algorithm was used to identify the reason of power outage. Results obtained with FAIRS, AIRS, and E-algorithms were comparable, however FAIRS was considerably faster in computing time than E-algorithm (Le & Mo-Yuen, 2008). They have introduced an interesting algorithm, but converting the antibodies into different format for representing fuzzy classification rules, seems to be rather complicated. Their algorithm appears to have been customized for their data set, and their report does not show how this algorithm would behave on other data sets. Although the results are good, further investigation into their model and its application with other data sets are still needed to make a better conclusion.

There are many applications with substantial results in diagnosing several diseases. Latifoğlu et. al. developed an AIRS-based application to diagnose atherosclerosis. With a classification accuracy of 99.29%, they concluded that their model could help medical specialists in diagnosing atherosclerosis patients (Latifoğlu, Kodaz, Kara, & Güneş, 2007).  They have achieved a very good result, and reported classification accuracy, specificity, and sensitivity, however they did not compare their results with other available classifiers, and did not report about the running time of their model.

In another study, Kodaz et al. developed an AIRS-based algorithm in order to diagnose thyroid disease. Their model reached a classification accuracy of 94.82% (Kodaz,

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Babaoğlu, & İşcan, 2009). They have achieved very good result, however they did not compare their results with other available classifiers, instead they have presented what other researchers have reported, and this makes the comparison almost impossible, because the classifiers were ran under different circumstances.

A hybrid algorithm of fuzzy-weighted pre-processing and AIRS was developed by Polat et al. for diagnosing heart disease, they classified the disease with an accuracy of 96.3% (Polat, Güneş, & Tosun, 2006). Their result for diagnosing heart disease is very good, however they did not discuss why did they used fuzzy weighting pre-processing of the data set, nor did they report the running time of their algorithm. It seems they have used AIRS1, and they do not report why they did not use AIRS2.

Şahan et al. introduced a hybrid fuzzy-artificial immune system with KNN in order to classify Wisconsin Breast Cancer Dataset; this hybrid model classified the disease with an accuracy of 99.14% (Şahan et al., 2007). Their result for diagnosing breast cancer is very good, however they did not discuss why did they used fuzzy weighting pre-processing of the data set, nor did they report the running time of their algorithm. It seems they have used AIRS1, and they do not report why they did not use AIRS2. They did not compare their model with other available classifiers; instead, they have presented what other researchers have reported on the same data set. This comparison is not accurate, since the experiments were ran under different circumstances.

Kara et al. introduced another medical application of AIRS, for classifying microorganism species, they developed an information gain based AIRS (IG-AIRS) and reported they classified the species with an accuracy of 92.35% (Kara et al., 2009). The result of their model was compared with that of other benchmark classifiers; however, their model was not verified with other datasets, and they only used fivefold cross validation for evaluation of their model.

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Shamshirband et al. combined AIRS with fuzzy labeling for diagnosing tuberculosis disease. Their model classified the disease with an accuracy 99.14% (Shamshirband et al., 2014). They have achieved a very good result, however they did not compare their model with other classifiers by themselves. Instead, they have presented what other researchers have reported on the same data set. This comparison is not accurate, since the experiments were ran under different circumstances.

In another related study, Lin et al. used AIRS, logistic regression, and SVM to predict type 2 diabetes among pregnant women. Researchers compared results obtained with AIRS, SVM, and logistic regression and reported that AIRS achieved highest classification accuracy among these three classifiers, and that their obtained accuracy was 62.8% on the diabetes data set (Lin, Su, & Wang, 2011). They achieved a good result with AIRS; however, they did not modify AIRS, and thus did not provide a new model. Their report does not show any running time of the applied models either.

Sunny et al. showed the robustness of AIRS to identify gases/odors. They compared the classification performance of AIRS1, AIRS2 and Parallel AIRS to that of Radial Basis Function Neural Network, Naïve Bayes, and Learning Vector Quantization whereby they used principal component analysis to reduce the dimensions of the raw data. They concluded that AIRS-based algorithms performed better than other three classifiers (Mishra, Dwivedi, & Das, 2013). They achieved good results with different versions of AIRS; however, they did not modify AIRS, and thus did not provide a new model. Their report does not show any running time of the applied models either.

Tay et al. were motivated by the capability of AIRS to perform classification and developed an evolutionary data-conscious AIRS, which was dubbed as EDC-AIRS. Their model mimics the response of antibodies to the antigens, which depends on the density, location and type of invaders (antigens). The performance of their model was evaluated

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on four benchmark data sets and was compared with other classifiers; their model ranked in the top 3 positions, and outperformed AIRS2 in all cases. Classification accuracies obtained with EDC-AIRS for Ionosphere, Iris, Sonar, and Pima Indians were 98.0%, 99.6%, 90.9%, and 77.3% respectively (Tay et al., 2013). They have introduced a very interesting model with very good results; however, they did not report one important issue, the running time, of their models.

In our study of the literature, we found that the term AIRS has been used by many researchers, but majority of them did not clearly distinguish whether they refer to AIRS1 or AIRS2. In this thesis however, the focus is to make changes to AIRS2 algorithm. In this section we have introduced and analyzed AIRS-based models that have been developed by other researchers. Some of models were built to solve a particular classification problem and therefor their authors did not verified their model with other data sets. In order to verify whether these models perform well with other data sets, additional tests with other data sets are required. In many cases, the authors did not compare their models with other well-known classifiers. Instead, they presented results from the literature, these kind of comparisons are not valid, because all of the models ran under different computing circumstances and not under equal computing conditions. One important issue was missing in all articles, the running time of the models. It is important to know, how long a classifier does needs to do the classification.

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## 2.7 Classifiers Used In This Research As Benchmark Classifiers

In this subsection, we introduce classifiers that are used in this research. Some benchmark classifiers were introduced in previous subsections of this chapter. Names of all well-known classifiers that are used as benchmark classifiers, in this study, are presented in subsection 3.4.8.

LibSVM stands for library for support vector machines (SVM) that has been actively developed by Chang et  al. (Chang & Lin, 2011). It is popular in machine learning and other areas. LibSVM has found applications in  computer vision (Grauman & Darrell, 2005; Hu et al., 2012), natural language processing (Nivre et al., 2007), neuroimaging (Hanke et al., 2009), bioinformatics (Dorff, Chambwe, Srdanovic, & Campagne, 2010), to name few domains. Support vector machines are discussed in detail in subsection 4.3.1. LibSVM supports: one-class SVM, support vector regression (SVR), and support vector classification (SVC) for two-class and multiclass cases.

Platt (Platt, 1999) developed an algorithm for training of SVM dubbed as Sequential Minimal Optimization (SMO). In contrast to SVM that solves large quadratic programming (QP) optimization problem, SMO first divides these large QP problem into a series of smallest possible QP problems. By solving these small QP problems analytically and iteratively, the algorithm bypasses a time-consuming QP optimization. Since SMO does not use large matrix computation, its training set size for various test problems scales somewhere between linear and quadratic values (Platt, 1999). Applications of SMO can be found in (Bach, Lanckriet, & Jordan, 2004; Q. Li, Salman, Test, Strack, & Kecman, 2013; Zięba, Tomczak, Lubicz, & Świątek, 2014).

The statistician David Cox (Cox, 1958) developed logistic regression, it uses a logistic function to estimate the probability of the relationship between one or more independent variables and the categorical dependent variables. The logistic function provides values between 0 and 1 and that makes the logistic function so popular, because the model describes a probability that is always somewhere between 0 and 1 (Kleinbaum & Klein, 2010). Logistic regression analysis is a suitable tool for classification problems, however it is possible to get high misclassification rate (D. Liu, Li, & Liang, 2014). Logistic regression has found many applications: in linear model and survival analysis (Harrell,

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2013), in decision making of financial company (Swiderski, Kurek, & Osowski, 2012), in hyperspectral image classification (Felicísimo, Cuartero, Remondo, & Quirós, 2013), in classification of breast cancer (M.-L. Huang, Hung, Lee, Li, & Wang, 2012), and many more.

A multi-layer perceptron (MLP) is known as a feed-forward neural network. It is one of most widely used version of neural network. MLPs are popular among engineers, scientists and other professionals. They are used to tackle a wide variety of information processing tasks. Like all neural networks, multi-layer perceptron are trained to do the chosen task. One of popular research areas within the field of neural computing is the development of fast and reliable training algorithms for MLPs (Shepherd, 2012). Multilayer feedforward neural networks are ideal for handling difficult tasks in pattern recognition, because its structure is highly adaptable (Strzelecki, Szczypinski, Materka, & Klepaczko, 2013). MLPs have been successfully used in a wide variety of tasks such as speech recognition (Siniscalchi, Yu, Deng, & Lee, 2013), image compression (Kalita & Sarma, 2015), pattern recognition (Chauhan, Goel, & Dhingra, 2012; Dervilis et al., 2014), features reduction (Phinyomark et al., 2013; Strzelecki et al., 2013), and many more.

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Since the introduction of artificial neural networks in 1990, multilayer neural networks and radial basis function (RBF) networks have found many applications in various domains (J. Liu, 2013), because its network structure is simple, has a good generalization ability, and avoids unnecessary lengthy calculations (Sundararajan, Saratchandran, & Li, 2013). RBF neural network consists of three layers: the input layer, the hidden layer, and the output layer. A radial basis function activates the neurons at the hidden layer, which consists of computing arrays known as hidden nodes. Each hidden node has a center vector that has the same dimension as the input vector. A nonlinear activation function produces the output of the hidden layer. The final network output layer is the summation of weighted hidden output layers (J. Liu, 2013).

## 2.8 Summary

An extensive literature review on classification algorithms that are used in this thesis were presented in this chapter. This chapter started with one of the major data mining tasks, the classification, and the attention to the relevant features of human immunology were drown. It was followed by highlighting important points of the human immune system. Since immune-based classifiers are related to the evolutionary computation, this chapter provided a brief description of evolutionary computation which is an important research area in the computer science. Further, the common framework that is used in designing bio-inspired algorithms were discussed. Then analogies between the terminologies used in the immune system and the terms that are used in the proposed algorithms were presented. Next, a brief explanation of the affinity measure which is closely related to the representation mechanism were presented. Then, an extensive literature reviews on the immune algorithms, biologically-based classification algorithms, as well as the artificial immune recognition systems were presented.

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# CHAPTER 3: METHODOLOGY

## 3.1 Introduction

This chapter introduces theoretical background of the methodology used in this thesis. Section 3.2 presents an overview of the current research. Section 3.3 explains the experimental setup including system specification, benchmark data sets, and parameter setup. Section 3.4 introduces the performance metrics used in this thesis to evaluate the performance of classifiers. The metrics are classification accuracy, n-fold cross validation, data reduction, running time, the area under ROC curve, student’s t-test. Classification modelling is introduced in section 3.4. Section 3.4.8 introduces some well-known classifiers that are used as benchmark to compare the performance obtained with the proposed algorithm to the ones obtained with the well-known classifiers.

## 3.2 Research Overview

Figure 3.1 illustrates an overview of research framework used in this study. The goal of this study is to improve the performance of AIRS2. One attractive area of research in the field of machine learning and data mining is constructing effective and efficient classifiers, and improving classification accuracy is one of top priorities for the researchers, as it is highly demanded. These issues have motivated us to do an extensive research in the field of classification and artificial immune system. For this study, we reviewed and analyzed the algorithm of AIRS2 and proposed an algorithm that would improve its performance. In order to improve the efficiency of the algorithm, the resource allocation method was replaced with fuzzy-based resource allocation method, and in order to increase the classification accuracy, real world tournament selection mechanism was incorporated into resource competition of the algorithm, and instead of using KNN as a classifier, Support Vector Machine was used as a classifier which has shown to be more accurate. Details of the proposed algorithms are presented in chapter 4.

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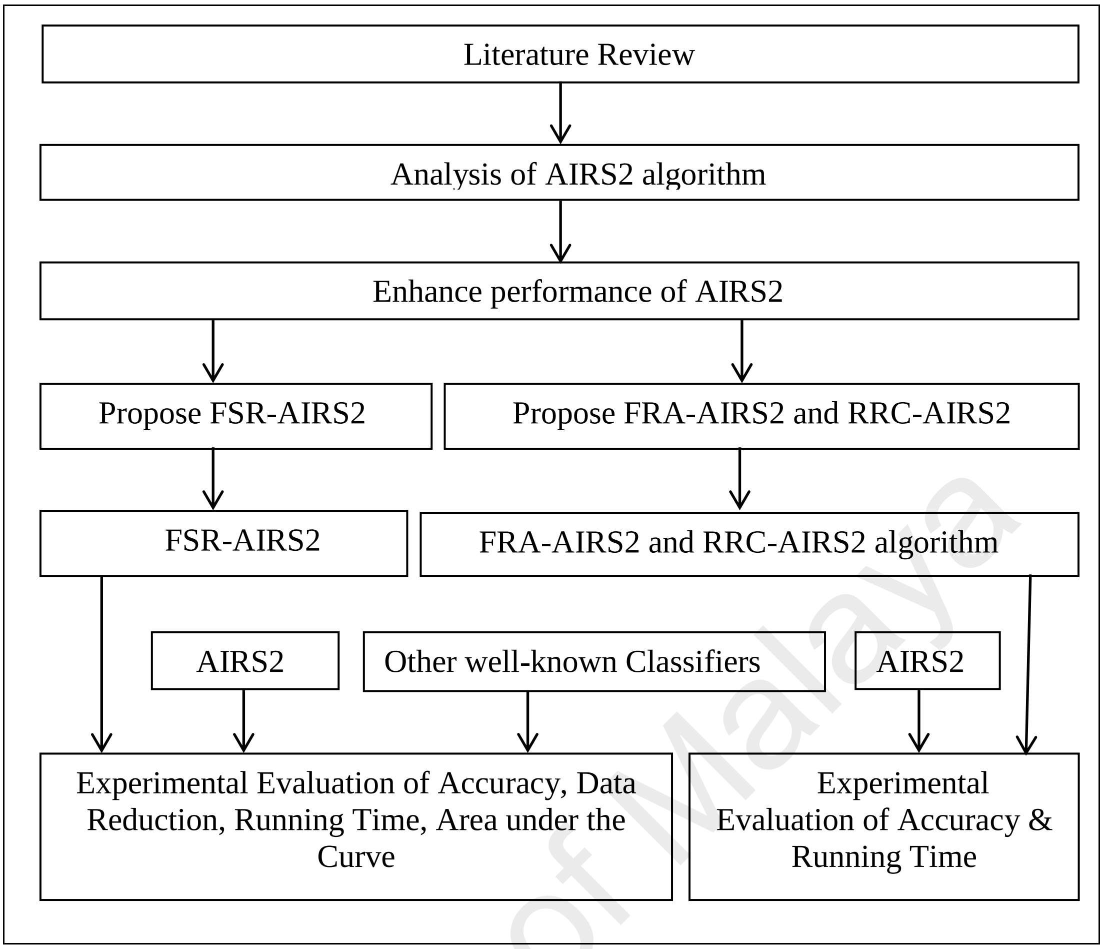
Literature Review
Analysis of AIRS2 algorithm
Enhance performance of AIRS2
Propose FSR-AIRS2
Propose FRA-AIRS2 and RRC-AIRS2
FSR-AIRS2
FRA-AIRS2 and RRC-AIRS2 algorithm
AIRS2
Other well-known Classifiers
AIRS2
Experimental Evaluation of Accuracy, Data Reduction, Running Time, Area under the Curve
Experimental Evaluation of Accuracy & Running Time

**Figure 3.1: Overview of Research Framework**

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This study evaluated the performance of the proposed algorithms through quantitative experiments. The results of the experiments were analyzed through statistical techniques in order to verify the competence of the proposed algorithms, and these results were compared with the results obtained with some well-known classifiers.

## 3.3 Experimental Setup

### 3.3.1 System Specification

Experiments were carried out on Intel® Core™ i5 CPU M430 @2.27GHz with 8GB of RAM on 64 bit Windows 7 operating system. The proposed algorithms were developed and incorporated inside WEKA (Mark Hall et al., 2009), a well-known data mining tool.

### 3.3.2 Datasets

Following benchmark data sets were used for evaluating proposed algorithms and other well-known classifiers. They were retrieved from the well-known UCI machine learning repository (Frank & Asuncion, 2010). These benchmark data sets cover varying number of instances, attributes and classes. These data sets cover from as easy as Iris to as difficult as Sonar data set. Attribute characteristics include categorical (C), real (R), and integer (I). Table 3.1 presents features such as number of instances, number of attributes, number of classes, and attribute characteristics of each data set.

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**Table 3.1: Data Sets Used in Experiments**

| Data Sets | Number of Instances | Number of Attributes | Number of Classes | Attribute Characteristics |
|---|---|---|---|---|
| Balance Scale | 625 | 5 | 3 | C |
| Breast Cancer Wisconsin (Diagnostic) | 569 | 31 | 2 | R |
| Contact Lenses | 24 | 5 | 3 | C |
| Ionosphere | 351 | 35 | 2 | I, R |
| Iris | 150 | 5 | 3 | R |
| Liver Disorders | 345 | 7 | 2 | C, I, R |
| Lung Cancer | 32 | 56 | 3 | I |
| Pima Indians | 768 | 9 | 2 | I, R |
| Statlog (Heart) | 270 | 14 | 2 | C, R |
| Statlog (Image Segmentation) | 2310 | 20 | 7 | R |
| Statlog (Vehicle Silhouettes) | 846 | 19 | 4 | I |
| Sonar, Mines vs. Rocks | 208 | 61 | 2 | R |
| Vertebral Column_2C | 310 | 7 | 2 | R |
| Vertebral Column_3C | 310 | 7 | 3 | R |
| Wisconsin Breast Cancer Data Set (WBCD) (Original) | 699 | 11 | 2 | R |

**Balance Scale:** "*This data set was generated to model psychological experimental results. Each example is classified as having the balance scale tip to the right, tip to the left, or be balanced. The attributes are the left weight, the left distance, the right weight, and the right distance.*" (Frank & Asuncion, 2010). *This data set consists of 625 categorical instances with 5 attributes and 3 classes. Attribute information: Class Name:*

*3 (L, B, R); Left-Weight: 5 (1, 2, 3, 4, 5), Left-Distance: 5 (1, 2, 3, 4, 5), Right-Weight: 5 (1, 2, 3, 4, 5), and Right-Distance: 5 (1, 2, 3, 4, 5)* (Lichman, 2013; Siegler, 1976).

**Breast Cancer Wisconsin (Diagnostic):** "*Features are computed from a digitized image of a fine needle aspirate (FNA) of a breast mass. They describe characteristics of the cell nuclei present in the image*" (Frank & Asuncion, 2010). *This data set consists of 569 real instances with 31 attributes and 2 classes. Attribute Information: 1) ID number 2) Diagnosis (M = malignant, B = benign) 3-32) Ten real-valued features are computed for each cell nucleus:a) radius (mean of distances from center to points on the perimeter) b) texture (standard deviation of gray-scale values) c) perimeter d) area e) smoothness (local variation in radius lengths) f) compactness (perimeter^2 / area - 1.0) g) concavity (severity of concave portions of the contour) h) concave points (number of concave portions of the contour) i) symmetry j) fractal dimension ("coastline approximation" - 1)* (Street, Wolberg, & Mangasarian, 1993). *This breast cancer databases was obtained from the University of Wisconsin Hospitals, Madison from Dr. William H. Wolberg*

**Contact Lenses**: *This data set is a collection of conditions under which an optician may prescribe soft contact lenses, hard contact lenses, or no contact lenses at all* (Witten et al., 2011). *This data set consists of 24 categorical instances with 5 attributes and 3 classes. The examples are complete and noise free. Each instance is complete and correct. 9 rules cover the training set. The classes are: 1) the patient should be fitted with hard contact lenses, 2) the patient should be fitted with soft contact lenses, and 3) the patient should not be fitted with contact lenses. Age of patient: (1) young, (2) pre-presbyopic, (3) presvyopic. Spectacle prescription: (1) myope, (2) hypermetrope. Astigmatic: (1) no, (2) yes. Tear production rate: (1) reduced, (2) normal* (Cendrowska, 1987; Lichman, 2013).

**Ionosphere:** "*This radar data was collected by a system in Goose Bay, Labrador. This system consists of a phased array of 16 high-frequency antennas with a total transmitted*

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*power on the order of 6.4 kilowatts. The targets were free electrons in the ionosphere. "Good" radar returns are those showing evidence of some type of structure in the ionosphere. "Bad" returns are those that do not; their signals pass through the ionosphere*" (Frank & Asuncion, 2010). *This data set consists of 351 integer and real instances with 35 attributes and 3 classes. Received signals were processed using an autocorrelation function whose arguments are the time of a pulse and the pulse number. There were 17 pulse numbers for the Goose Bay system. Instances in this databse are described by 2 attributes per pulse number, corresponding to the complex values returned by the function resulting from the complex electromagnetic signal. Attribute Information: All 34 are continuous. The 35th attribute is either "good" or "bad" according to the definition summarized above. This is a binary classification task* (Lichman, 2013; Sigillito, Wing, Hutton, & Baker, 1989).

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**Iris:** "*This is perhaps the best known database to be found in the pattern recognition literature. The data set consists of 150 real instances with 5 attributes and 3 classes of 50 instances each, where each class refers to a type of iris plant. One class is linearly separable from the other 2; the latter are NOT linearly separable from each other*" (Frank & Asuncion, 2010). *Attribute Information: 1. sepal length in cm, 2. sepal width in cm, 3. petal length in cm, 4. petal width in cm, 5. class:Iris Setosa, Iris Versicolour, and Iris Virginica* (Fisher, 1936; Lichman, 2013).

**Liver Disorders:** "*The first 5 variables are all blood tests which are thought to be sensitive to liver disorders that might arise from excessive alcohol consumption*" (Frank & Asuncion, 2010). *This data set contains 345 categorical, integer, and real instances with 7 attributes and 2(Forsyth, 1990) classes. Each line in the bupa.data file constitutes the record of a single male individual. It appears that drinks>5 is some sort of a selector on this database. Attribute Information: 1. mcv mean corpuscular volume, 2.*

*Alkphos alkaline phosphotase, 3. sgpt alamine aminotransferase, 4. sgot aspartate aminotransferase, 5. Gammagt gamma-glutamyl transpeptidase, 6. drinks number of half-pint equivalents of alcoholic beverages drunk per day, and 7. selector field used to split data into two sets* (Forsyth, 1990; Lichman, 2013).

**Lung Cancer:** "*The data described 3 types of pathological lung cancers. The Authors give no information on the individual variables nor on where the data was originally used*" (Frank & Asuncion, 2010). This data set contains 32 integer instances with 56 attributes and 3 classes. *In the original data 4 values for the fifth attribute were -1. These values have been changed to ? (unknown). In the original data 1 value for the 39 attribute was 4. This value has been changed to ? (unknown). Attribute Information: Attribute 1 is the class label. All predictive attributes are nominal, taking on integer values 0-3* (Hong & Yang, 1991; Lichman, 2013).

**Pima Indians:** *"The dataset was collected by Dr. Vincent Sigilito at the John Hopkins University. It was obtained from female population near Phoenix, Arizona. They were at least 21 years old of Pima Indian heritage"* (Frank & Asuncion, 2010). *This data set contains 768 instances of types integer and real with 9 attributes and 2 classes. Attribute Information: 1. Number of times pregnant, 2. Plasma glucose concentration a 2 hours in an oral glucose tolerance test, 3. Diastolic blood pressure (mm Hg), 4. Triceps skin fold thickness (mm), 5. 2-Hour serum insulin (mu U/ml), 6. Body mass index (weight in kg/(height in m)^2)7. Diabetes pedigree function, 8. Age (years), 9. Class variable (0 or 1)* (Lichman, 2013; Smith, Everhart, Dickson, Knowler, & Johannes, 1988).

**Statlog (Heart):** "*The Cleveland database is a heart disease database*" (Frank & Asuncion, 2010). *This data set contains 270 instances of types categorical and real with 14 attributes and 2 classes. Attribute Information:1. age, 2. sex, 3. chest pain type (4 values), 4. resting blood pressure, 5. serum cholestoral in mg/dl, 6. fasting blood sugar*

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*> 120 mg/dl, 7. resting electrocardiographic results (values 0,1,2), 8. maximum heart rate achieved, 9. exercise induced angina, 10. oldpeak = ST depression induced by exercise relative to rest, 11. the slope of the peak exercise ST segment, 12. number of major vessels (0-3) colored by flourosopy, 13. thal: 3 = normal; 6 = fixed defect; 7 = reversable defect. Attributes types: Real: 1,4,5,8,10,12, Ordered:11, Binary: 2,6,9 Nominal:7,3,13. Variable to be predicted: Absence (1) or presence (2) of heart disease* (Lichman, 2013)

**Statlog (Image Segmentation):** "*The instances were drawn randomly from a database of 7 outdoor images. The images were hand-segmented to create a classification for every pixel. Each instance is a 3x3 region*" (Frank & Asuncion, 2010). This data set contains 2310 integer instances with 20 attributes and 7 classes. *The instances were drawn randomly from a database of 7 outdoor images. The images were handsegmented to create a classification for every pixel.Each instance is a 3x3 region. Attribute Information:1. region-centroid-col: the column of the center pixel of the region. 2. region-centroid-row: the row of the center pixel of the region. 3. region-pixel-count: the number of pixels in a region = 9. 4. short-line-density-5: the results of a line extractoin algorithm that counts how many lines of length 5 (any orientation) with low contrast, less than or equal to 5, go through the region. 5. short-line-density-2: same as short-line-density-5 but counts lines of high contrast, greater than 5. 6. vedge-mean: measure the contrast of horizontally adjacent pixels in the region. There are 6, the mean and standard deviation are given. This attribute is used as a vertical edge detector. 7. vegde-sd: (see 6) 8. hedge-mean: measures the contrast of vertically adjacent pixels. Used for horizontal line detection. 9. hedge-sd: (see 8). 10. intensity-mean: the average over the region of (R + G + B)/3 11. rawred-mean: the average over the region of the R value. 12. rawblue-mean: the average over the region of the B value. 13. rawgreen-mean: the average over the region of the G value. 14. exred-mean: measure the excess red: (2R - (G + B)) 15. exblue-*

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*mean: measure the excess blue: (2B - (G + R)) 16. exgreen-mean: measure the excess green: (2G - (R + B)) 17. value-mean: 3-d nonlinear transformation of RGB. (Algorithm can be found in Foley and VanDam, Fundamentals of Interactive Computer Graphics) 18. saturatoin-mean: (see 17) 19. hue-mean: (see 17)* (Lichman, 2013).

**Statlog (Vehicle Silhouettes):** "*The purpose is to classify a given silhouette as one of four types of vehicle, using a set of features extracted from the silhouette. The vehicle may be viewed from one of many different angles"* (Frank & Asuncion, 2010). This data set contains 846 integer instances with 19 attributes and 4 classes. *The features were extracted from the silhouettes by the HIPS (Hierarchical Image Processing System) extension BINATTS, which extracts a combination of scale independent features utilising both classical moments based measures such as scaled variance, skewness and kurtosis about the major/minor axes and heuristic measures such as hollows, circularity, rectangularity and compactness. Attribute Information: COMPACTNESS (average perim)**2/area; CIRCULARITY (average radius)**2/area; DISTANCE CIRCULARITY area/(av.distance from border)**2; RADIUS RATIO (max.rad-min.rad)/av.radius; PR.AXIS ASPECT RATIO (minor axis)/(major axis); MAX.LENGTH ASPECT RATIO (length perp. max length)/(max length); SCATTER RATIO (inertia about minor axis) / (inertia about major axis); ELONGATEDNESS area/(shrink width)**2; PR.AXIS RECTANGULARITY area/(pr.axis length*pr.axis width);MAX.LENGTH RECTANGULARITY area/(max.length*length perp. to this); SCALED VARIANCE (2nd order moment about minor axis)/area ALONG MAJOR AXIS SCALED; VARIANCE (2nd order moment about major axis)/area ALONG MINOR AXIS; SCALED RADIUS OF GYRATION (mavar+mivar)/area; SKEWNESS ABOUT (3rd order moment about major axis)/sigma_min**3 MAJOR AXIS; SKEWNESS ABOUT (3rd order moment about minor axis)/sigma_maj**3 MINOR AXIS; KURTOSIS ABOUT (4th order moment about major axis)/sigma_min**4 MINOR AXIS; KURTOSIS ABOUT (4th order moment about*

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*minor axis) / sigma_maj**4 MAJOR AXIS; HOLLOWS RATIO (area of hollows)/(area of bounding polygon). Where sigma_maj**2 is the variance along the major axis and sigma_min**2 is the variance along the minor axis, and area of hollows= area of bounding poly-area of object. The area of the bounding polygon is found as a side result of the computation to find the maximum length. Each individual length computation yields a pair of calipers to the object orientated at every 5 degrees. The object is propagated into an image containing the union of these calipers to obtain an image of the bounding polygon. Number of classes 4: OPEL, SAAB, BUS, VAN* (Siebert, 1987). This dataset comes from the Turing Institute, Glasgow, Scotland.

**Sonar, Mines vs. Rocks:** "*The file sonar contains 111 patterns obtained by bouncing sonar signals off a metal cylinder at various angles and under various conditions and 97 patterns obtained from rocks under similar conditions. The transmitted sonar signal is a frequency-modulated chirp, rising in frequency*" (Frank & Asuncion, 2010). The classification goal it to verify whether a sonar signal bounced back from a rock or a metal object. This is in order to see if the system can recognizes the differences between a mine or a rock (Watkins, 2005). This data set contains 208 instances of type real with 61 attributes and 2 classes. *The data set contains signals obtained from a variety of different aspect angles, spanning 90 degrees for the cylinder and 180 degrees for the rock. Each pattern is a set of 60 numbers in the range 0.0 to 1.0. Each number represents the energy within a particular frequency band, integrated over a certain period of time. The integration aperture for higher frequencies occur later in time, since these frequencies are transmitted later during the chirp. The label associated with each record contains the letter "R" if the object is a rock and "M" if it is a mine (metal cylinder). The numbers in the labels are in increasing order of aspect angle, but they do not encode the angle directly* (Gorman & Sejnowski, 1988; Lichman, 2013).

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**Vertebral Column_2C Data Set :** "*Biomedical data set built by Dr. Henrique da Mota during a medical residence period in the Group of Applied Research in Orthopaedics (GARO) of the Centre MÃ©dico-Chirurgical de RÃ©adaptation des Massues, Lyon, France. The data have been organized in two categories: Normal (100 patients) or Abnormal (210 patients)*" (Bache & Moshe, 2013). This data set contains 310 instances of type real with 7 attributes and 2 classes. *Attribute Information: Each patient is represented in the data set by six biomechanical attributes derived from the shape and orientation of the pelvis and lumbar spine (in this order): pelvic incidence, pelvic tilt, lumbar lordosis angle, sacral slope, pelvic radius and grade of spondylolisthesis. The following convention is used for the class labels: Normal (NO) and Abnormal (AB)* (Lichman, 2013).

**Vertebral Column_3C Data Set :** "*Biomedical data set built by Dr. Henrique da Mota during a medical residence period in the Group of Applied Research in Orthopaedics (GARO) of the Centre MÃ©dico-Chirurgical de RÃ©adaptation des Massues, Lyon, France. The data have been organized in three categories: Normal (100 patients), Disk Hernia (60 patients) or Spondylolisthesis (150 patients).*" (Bache & Moshe, 2013). This data set contains 310 instances of type real with 7 attributes and 3 classes. *Attribute Information: Each patient is represented in the data set by six biomechanical attributes derived from the shape and orientation of the pelvis and lumbar spine (in this order): pelvic incidence, pelvic tilt, lumbar lordosis angle, sacral slope, pelvic radius and grade of spondylolisthesis. The following convention is used for the class labels: DH (Disk Hernia), Spondylolisthesis (SL), Normal (NO) and Abnormal (AB)* (Lichman, 2013).

**Wisconsin Breast Cancer Dataset (WBCD) (Original)** "This data set was *collected by Dr. W.H. Wolberg at the University of Wisconsin—Madison Hospitals taken from*

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*needle aspirates from human breast cancer tissue*". (Frank & Asuncion, 2010). *The dataset contains 699 real instances with 11 attributes and 2 classes. Attribute Information: 1. Sample code number: id number, 2. Clump Thickness: 1 - 10 , 3. Uniformity of Cell Size: 1 - 10, 4. Uniformity of Cell Shape: 1 - 10, 5. Marginal Adhesion: 1 - 10, 6. Single Epithelial Cell Size: 1 - 10, 7. Bare Nuclei: 1 - 10, 8. Bland Chromatin: 1 - 10, 9. Normal Nucleoli: 1 - 10, 10. Mitoses: 1 - 10, 11. Class: (2 for benign, 4 for malignant)* (Wolberg & Mangasarian, 1990).

## 3.4 Performance and evaluation measurements

Evaluation plays an important role in the progress of data mining, and there are many ways to inferred structure from data (Witten et al., 2011). In the following we describe the methods that are used to evaluate proposed models. In this chapter, we will describe classification accuracy, n-fold cross validation, data reduction, running time, the area under ROC curve, and the Student's t test.

### 3.4.1 Performance Metrics

There are many ways to infer structure from data (Witten et al., 2011). The following subsections will describe performance metrics that are used in this thesis to evaluate the models.

### 3.4.2 Classification accuracy

Classifier's accuracy is defined as the ability of a given classifier to correctly predict the class label of new or previously unseen data. The accuracy is calculated by dividing the number of truly classified instances by the number of instances in the test phase. The classification accuracy for the dataset was measured according to Equation 3.1 (Watkins, 2001):

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$$accuracy\ (T) = \frac{\sum_{i=1}^{|T|} assess\ (t_i)}{|T|}, \qquad t_i\ \in T \tag{3.1}$$

$$assess(t) = \begin{cases} 1, iff\ classify\ (t) = t.c \\ 0, otherwise \end{cases} \tag{3.2}$$

where *T* is the set of data items to be classified (the test set), $t \in T$, *t.c* is the class of the item *t*, and classify (*t*) returns the classification of *t* by AIRS.

### 3.4.3 N-fold cross validation

Classification accuracy is a critical design goal of any classifier (Brownlee, 2005). To validate the test results, this study used n-fold cross-validation. This validation minimize the bias associated with the random sampling that was present during training phase (Delen et al., 2005). One of robust methods for estimating the predictive accuracy of a classification algorithms is N-fold cross validation. In this method, the records are randomly separated into N equivalent stratified divisions. Each record is put in one division. In each repetition, N-1 divisions are combined to form the training set and the classification accuracy of the algorithm is measured on the remaining division. This procedure is reiterated N times, selecting a different division as the test set each time. Thus, all data records have been used N-1 times for training and once for testing. The final predictive accuracy is calculated over all folds in the common way with dividing the number of true classifications taken over all folds by the number of data records in all folds. This study used 10-fold cross-validation for evaluation purposes.

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### 3.4.4 Data reduction

Many real world data sets are large in volume, therefore any technique that is able to reduce the size of data while maintaining the significant feature of the data set is useful (Watkins, 2005; Watkins et al., 2004). One important feature of AIRS2 is its capability to perform the classification task with the reduced number of data instances. Pairing the number of data reduction in the resulting classifier with the classification accuracy could be used to measure usefulness of an algorithm; Equation 3.3 is used to calculate the data reduction percentage (Brownlee, 2005).

$$Data\ Reduction = \left(1 - \frac{TotalNumberMemory\ Cells}{TotalNumberTrainingInstances}\right) * 100 \qquad (3.3)$$

### 3.4.5 Overall Runtime

The overall runtime is defined as the sum of CPU training time and the CPU testing time, where CPU training time is the time a classifier needs to construct the model during the training phase of the model, and CPU testing time is the time the classifier needs to evaluate the model.

### 3.4.6 Area under the ROC Curve the AUC

Receiver Operating Characteristic (ROC) is originated from the Signal Detection Theory (SDT) that was developed during the Second World War for the analysis of radar images. Radar operators needed to know whether the blip on the screen represented a friendly ship, an enemy, or just noise. SDT measures the ability of radar receiver operators to distinct these three important signs. This ability of the operators was called the Receiver Operating Characteristics (Tape, 2013). ROC is a useful visualizing technique that is used for assessing data mining schemes; it is used to illustrate the trade-off between true hit rate and false alarm over a noisy channel (Swets, Dawes, & Monahan, 2000; Witten et al., 2011). ROC graphs are able to provide a richer measure of classification performance than error cost, accuracy or error rate (Fawcett, 2006). ROC curves illustrate the performance of a classifier regardless of the error costs or class distribution; vertical axis is used to plot the true positive rate and horizontal axis represents the true negative rate (Witten et al., 2011). Equations (3.4) and (3.5) show the formula for True Positive Rate (TP Rate) and False Positive Rate (FP Rate) (Witten et al., 2011):

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$$TP\ Rate = 100 * (\frac{TP}{TP + FN}) \tag{3.4}$$

$$FP\ Rate = 100 * (\frac{FP}{FP + TN}) \tag{3.5}$$

where TP is the number of true positives, FN is the number of false negatives, FP is the number of false positives and TN is the number of true negatives. TP and TN are correct classifications; FP is the number of outcomes when the prediction is positive when it is actually negative, and FN is the number of outcomes when the prediction is negative when it is actually positive (Witten et al., 2011).

The area under the curve (AUC) is a single quantity that summarizes ROC curves. This area denotes the probability that a randomly selected positive instance is correctly ranked with greater suspicion than a randomly chosen negative sample (Bradley, 1997). AUC is the area under the ROC curve, the greater the area, the better the model (Witten et al., 2011). A rough guide for classifying the accuracy of a test is the common academic grading scale (Tape, 2013):

*Excellent (A) = .90 to 1*

*Good (B) = .80 to .90*

*Fair (C) = .70 to .80*

*Poor (D) = .60 to .70*

*Fail (F) = .50 to .60*

This means for example, if the area under ROC falls within [0.9, 1] the classifier performs excellent and if it falls within [0.5, 0.6] it fails.

### 3.4.7 Student's t test

It is common that the statistical significance between the mean of two results is tested through student's t-test (Jackson, 2012; Witten et al., 2011). When decisions are made,

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making speculations or expectations about the populations involved are common. Such expectations are called statistical hypotheses, which might or might not be true. There are usually two types of hypotheses: a null hypothesis (Ho) which is tested against an alternative hypothesis denoted by ($H_1$). And two types of errors exist when we decide. Type I error happens when we decide to reject a hypothesis although it should be accepted, but when we accept a hypothesis although it should be rejected, then a Type II error has occured. Both decision are wrong. The level of significance of the test is the maximum probability with which we accept to make a Type I error. This probability is usually represented by α. Although different values can be used for α, it is common to use either .05 or .01. If for instance a .01 or 1% level of confidence is selected, then there is 1 percent the chance that we would reject the hypothesis when in fact it should be accepted, in other words we are 99% confident that we have made the correct decision. In such case we would be wrong with probability 1 which means that the hypothesis has been rejected at 0.01 level of significance. α represents the level of significance, and the level of confidence of the test is (1-α). Equations (3.6) and (3.7) present the null hypothesis and its alternative hypothesis:

$$H_o: AIRS2_{Performance\ mean} = Proposed\ Algorithm_{performace\ mean} \tag{3.6}$$

$$H_1: AIRS2_{Performance\ mean} \neq Proposed\ Algorithm_{performace\ mean} \tag{3.7}$$

This thesis examines the hypothesis (Ho) that the mean values of two results are the same. Throughout this thesis, we use the two-tailed t-test to decide if we can accept or reject the null hypothesis. The p value will be determined and it is the likelihood that the two means are equal. If $p < \alpha$ (this thesis uses $\alpha = .05$), then we assume that this likelihood is not sufficient for the difference between the means to be based just on chance, and consequently we infer that there is a statistically significant difference in the means.

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### 3.4.8 Classification Modelling

There are many classification models in the literature – from simple techniques such as nearest neighbor and rule-based classifiers to more advanced techniques such as ensemble methods and support vector machine (Pang-Ning Tan, 2006). This study uses the support vector machine for classification modelling. The support vector machine is introduced later in section 4.4.

## 3.5 Well-known classifiers

In order to evaluate the performance of the proposed algorithm, this thesis used various well-known classifiers, these classifiers are used very often in business data mining and they correspond to a variety of classifier types  (Meng et al., 2005; Van der Putten, 2010) as benchmark.  These classifiers include AIRS2, 1-nearest neighbor (1-KNN), 7-nearest neighbor 7-KNN , C4.5/J48 decision tree, CLONALG, Immunos99, LibSVM, Logistic, multi-layer perceptron (MLP), Naïve Bayes, radial basis function network (RBF Network), sequential minimal optimization with poly kernel (SMO), and sequential minimal optimization with RBF kernel (SMO2). SMO is an implementation of John Platt's algorithm for training a support vector classifier.

In order to be consistent, all these classifiers were used under the same condition, and all of them were available through the same environment, the WEKA where the proposed algorithm was also implemented.

## 3.6 Summary

This chapter introduced theoretical background of the methodology that is used in this thesis. We presented an overview of the current research and explained the experimental setup including system specification, benchmark data sets, and parameter setup. Then we introduced the performance metrics used in this thesis that is used to evaluate the performance of classifiers. We concluded the chapter with introducing some well-known

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classifiers that are used as benchmark to compare the performance obtained with the proposed algorithm to the ones obtained with the well-known classifiers.

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# CHAPTER 4: IMPROVEMENT OF ARTIFICIAL IMMUNE RECOGNITION SYSTEM 2

## 4.1 Introduction

This chapter introduces the methodology used to improve the performance of AIRS2. Classification accuracy, running time, data reduction, and the area under ROC curve are metrics that are discussed in this section.

Section 4.2 presents changes that were made to the resource allocation of the algorithm and discusses fuzzy logic and its application for resource allocation. This section explains the stages involved in building one of the proposed algorithm (the FRA-AIRS2).

Section 4.3 introduces real-world tournament selection mechanism and presents its application in resource competition of the algorithm. This section explains the stages involved in building one of the proposed algorithm (the RRC-AIRS2).

Section 4.4 introduces support vector machine, which will be used as the classifier of the main proposed algorithm. This section explains the stages involved in building the main proposed algorithm (the FSR-AIRS2). It explains how the previously developed and discussed methods: FRA, RRC, and SVM are put together to build the FSR-AIRS2.

Section 4.5 introduces the experimental setup used to evaluate the performance of the proposed classifier (the FSR-AIRS2).

Section 4.6 evaluates the behavior of proposed models: FRA-AIRS2, RRC-AIRS2, and FSR-AIRS2 on benchmark data sets.

Section 4.6.1 evaluates and discusses performance of FRA-AIRS2. Section 4.6.1.1 compares classification accuracy obtained with FRA-AIRS2 and that of AIRS2 on

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benchmark data sets. Section 4.6.1.2 compares running time obtained with FRA-AIRS2 and that of AIRS2 on benchmark data sets.

Section 4.6.2 evaluates and discusses performance of RRC-AIRS2. Section 4.6.2.1 compares classification accuracy obtained with RRC-AIRS2 and that of AIRS2 on benchmark data sets. Section 4.6.2.2 compares running time obtained with RRC-AIRS2 and that of AIRS2 on benchmark data sets.

Section 4.6.3 evaluates and discusses performance of FSR-AIRS2. Section 4.6.3.1 evaluates and compares the classification accuracies obtained with AIRS2 and FSR-AIRS2 on benchmark data sets. Section 4.6.3.2 compares the classification accuracies obtained with the FSR-AIRS2 and other common classifiers. Section 4.6.3.3 discusses the data reduction capabilities of AIRS2, FRA-AIRS2, and FSR-AIRS2. Section 4.6.3.3(a) compares evolved memory cells through AIRS2 and FRA-AIRS2. Section 4.6.3.3(b) compares data reduction capability of FSR-AIRS2 with that of AIRS2.

Section 4.6.3.4 discusses and compares the average running time obtained with FSR-AIRS2 and other common classifiers

Section 4.6.3.5 discusses and compares the average area under the curve (AUC) obtained with FSR-AIRS2 and other common classifiers.

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## 4.2 Development of FRA-AIRS2

Following definitions (see Table 4.1) are taken from a document introduced by the International Electrotechnical Commission (International-Electrothechnical-Commission, 1997).

Fuzzy logic uses linguistic expressions to describe real numbers. Terms such as “Low” or “Very High” are designated as linguistic terms and input variables that are described by linguistic terms are known as linguistic values. Membership function is used to describe the membership degree of each element in the universe of discourse.

**Table 4.1: Definitions of Language Elements for Fuzzy Logic**

| Term | Definition |
|---|---|
| *Accumulation (or result aggregation)* | *Combinations of results of linguistic rules in a final result.* |
| *Aggregation* | *Calculation of the degree of accomplishment of the condition of a rule.* |
| *Activation* | *The process by which the degree of fulfilment of a condition acts on an output fuzzy set.* |
| *Crisp set* | *A crisp set is a special case of a Fuzzy set, in which the membership function only takes two values, commonly defined as 0 and 1.* |
| *Defuzzification* | *Conversion of a Fuzzy set into a numerical value.* |
| *Degree of membership* | *Membership function value.* |
| *Fuzzification* | *Conversion of an input value into degrees of membership for the membership functions defined on the variable taking this value.* |
| *Fuzzy Control* | *A type of control in which the control algorithm is based on Fuzzy Logic.* |
| *Inference* | *Application of linguistic rules on input values in order to generate output values* |
| *Linguistic rule* | *IF-THEN rule with condition and conclusion, one or both at least linguistic.* |
| *Linguistic term* | *In the context of Fuzzy Control linguistic terms are defined by Fuzzy sets.* |
| *Membership function* | *A function which expresses in which degree an element of a set belongs to a given Fuzzy subset.* |
| *Singleton* | *A singleton is a Fuzzy set whose membership function is equal to one at one point and equal to zero at all other points.* |
| *Rule base* | *Collection of linguistic rules to attain certain objectives.* |

Figure 4.1 shows the structure and functional elements of Fuzzy Control.

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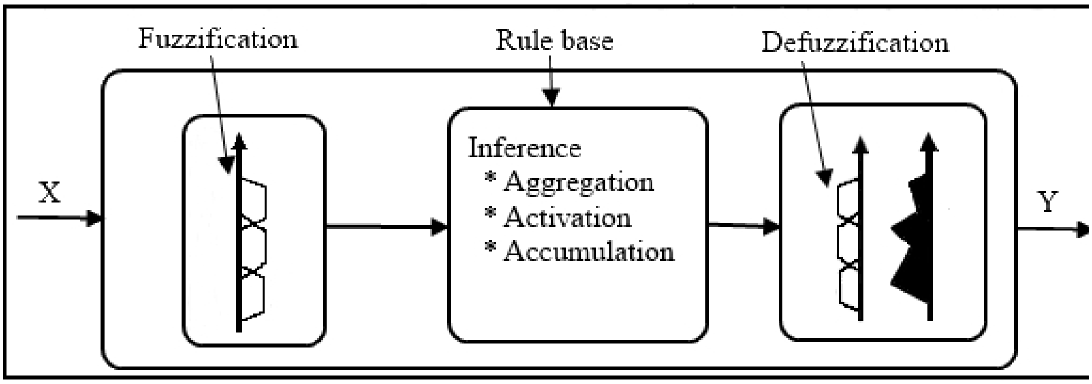

**Figure 4.1: Structure and Functional Elements of Fuzzy Control**

Fuzzy control consists of processing measured values based on a collection of linguistic rules which are also known as fuzzy rules. A Fuzzy Inference System (FIS) maps input variables to output values, and fuzzy rules define how FIS should make a decision about classifying an input or directing an output. The input variables are measureable variables and the output variables are correcting real values. The process of transferring input variables into degrees of membership values is called fuzzification; it matches the input variables with the linguistic terms using a set of input membership functions. A crisp output from a FIS represents the output and the process of transferring output variables from fuzzy sets into real numbers is called defuzzification. Briefly, a FIS calculates the output value as follows: first, it determines a set of fuzzy rules, then it fuzzifies the inputs using the input membership functions, next it combines the just fuzzified inputs based on the fuzzy rules in order to establish a rule strength, then it combines the membership function and the rule strength in order to determine the consequence of the rule. Further, FIS gets the output distribution by combining the consequences, and finally it defuzzifies the output (International-Electrothechnical-Commission, 1997).

There are many ways of defuzzification. The Center of Gravity (COG) method is used in this thesis, because it is general and easy to compute. This method calculates the crisp

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output by the sums of the center of gravities of the conclusions. Thus, a fuzzy inference system can compute output y of an input vector x. The main purpose is to make the best solution possible for each input vector. In the resource competition stage of AIRS, the algorithms aim to improve the selection probability of high-affinity ARBs, for next steps.

Resource competition is subject to each ARB’s number of allocated resources, the allocation depends on the similarity between the ARB and the antigen as well as its class. Resource allocation for each ARB in AIRS2 is equal to the product of clonal rate and stimulation value as it is presented in Equation (4.1):

$$\text{ARB.res} = \text{clonalRate} \ \text{x ARB.stim} \qquad (4.1)$$

where ARB.res, clonalRate, ARB.stim are the number of allocated resources, a user defined value, and stimulation value respectively. It means there is a linear relation between the amount of allocated resource and the stimulation. As mentioned earlier, researchers worked on solving similar linear issue in AIRS1, however this problem has not been addressed in AIRS2 yet. AIRS2 also uses a linear resource allocation method, and this linearity results in producing more memory cells which also causes longer running time. This is because the difference between the number of high-affinity ARBs and the number of low-affinity ARBs is low and this leads to allowing low-affinity ARBs into the process of cloning and mutation which increases the number of memory cells and prolongs the running time, one way to overcome the linearity issue and reduce the size of data sets is to use fuzzy logic in order to prioritize the memory cells with higher affinity over those with lower affinity therefore in this thesis the Equation (4.1) is replaced with the Equation (4.2).

$$\text{ARB.res} = \text{clonalRate} \times \text{FuzzyStimulation (ARB.stim)} \qquad (4.2)$$

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where FuzzyStimulation function is a non-linear approach (see Figure 4.4) for regulating the stimulation value. Figure 4.2 shows the process of fuzzy resource allocation of the cloned MCmatch instances. Initially an instance "A" is presented to the memory cell pool, "A" stimulates all memory cells in the pool and each cell in the pool is assigned a stimulation value according to the Equation 2.2. This thesis uses the Euclidean distance as the main metric for both affinity and stimulation; however, other distance metrics could also be used. A vector with the greatest stimulation value is then selected as the best match memory cell, and then the stimulation value of best match memory cell undergoes fuzzification, before it is used in the process of affinity maturation.

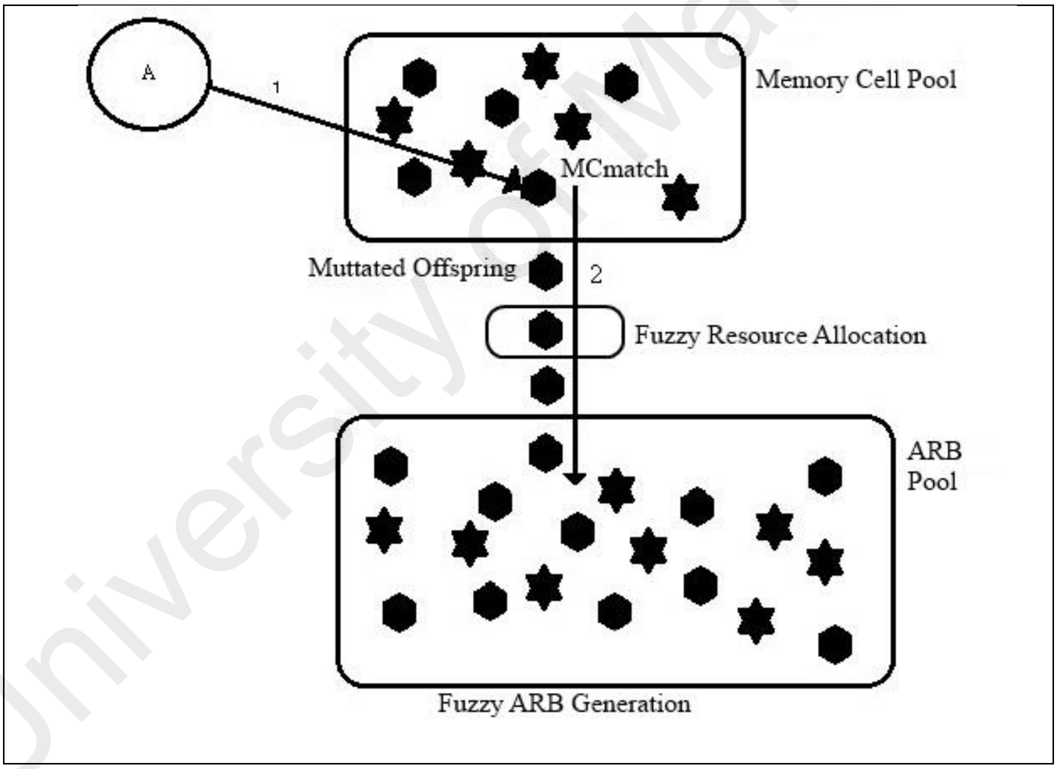

**Figure 4.2: Fuzzy Resource Allocation**

Figure 4.3 illustrates the pseudocode for resource allocation method of FSR-AIRS2. It is dubbed as Fuzzy Resource Allocation (FRA). This algorithm loops through all Cells in the Cell Pool and allocates resources to the cells based on their fuzzy stimulation value. In line 2 the algorithm calls FuzzyStimulation function (explained next) to get a fuzzy value for the control parameter "stimulation" and multiplies this value in line 3 by the

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ClonalRate to calculate the amount of resources. In line 4 the just calculated resource is added to the total number of resources allocated for the Cell Pool. In line 6 the algorithm orders the list of resources, so that the Cell with the highest stimulation is on the top of the list. Line 7 returns the total amount of allocated resource.

```
Input: CellPool; Output Resources
FuzzyResourceAllocation (CellPool) {
1   FOREACH Cell in CellPool DO {
2       fStim ← FuzzyStimulation (StimulatedResource) // get fuzzy stim
         value
3       res ← fStim * ClonalRate   // calculate resource allocation
4       resources ← resources + res
5   } ENDFOR
6   CellPool.orderByResources   //order by allocated resources
7    return resource       //output Resource
}
```

**Figure 4.3: Resource Allocation for RRC-AIRS2 and FSR-AIRS2**

Figure 4.4 shows the steps for determining fuzzy value of the stimulation. The algorithm uses Fuzzy Inference System (FIS), which is presented in line 1. In line 2 the algorithm reads instructions for building the fuzzy model and employs fuzzy control language for converting the variable ‘stimulation’ into degrees of membership for the membership functions defined on this variable; the term ‘Fstimulation’ refers to the output variable. The structure for fuzzy control language and its explanations follows (see below for explanations about Figure 4.5). In line 3 the input variable “stimulation” is defined, and line 4 uses the fuzzy instruction and input variable to evaluate the fuzzy value. Line 5 returns the fuzzy value for the stimulation dubbed as Fstimulation. The linguistic variable for ‘Fstimulation’ has to be defuzzified, i.e. converted into a value.

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```
Input: Stimulation Value
Output: Fstimulation // Fuzzy Stimulation Value
FuzzyStimulation (Stimulation) {
    FIS fis ← null
    fis ← FIS.load (control file)
    input ← Stimulation
    Fstimulation = fis.evaluate()
    return Fstimulation
}
```

**Figure 4.4: Determine Fuzzy Value for Stimulation**

Figure 4.5 illustrates elements of fuzzy control language that are used in resource allocation procedure of FRA-AIRS2 and FSR-AIRS2. As can be seen the fuzzy control language consists of a function block where the input and output variables are defined (lines 1-8). The value of the input variable is converted into degrees of membership for the membership function defined on this variable (lines 10-16). This thesis uses a trapezoidal membership function, and it is defined by a set of points. Each point is represented by a pair of values of the variable and the membership degree of that value. Pairs are separated by commas. The linguistic variable “stimulation” is described by the linguistic terms in order to fuzzify the variable (lines 11-15). The linguistic variable for the output variable “Fstimulation” is converted into a value; this conversion is called defuzzification (lines 18-29) In order to make the defuzzification easier, the singeltons, (special membership functions) are used. The defuzzification method used in this study is known as Center of Gravity for Singletons (COGS) (line 26), which is defined as:

$$Result\ of\ defuzzication = \frac{\sum_{i=1}^{n} r_i \mu_i}{\sum_{i=1}^{n} \mu_i} \tag{4.3}$$

where $r$ is output variable, $\mu$ is membership function, and $n$ is the number of singletons. The Center of Gravity is a very common defuzzification method and is easy to use.

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Linguistic values are so selected that higher allocated number of resources are assigned to ARBs, which have stimulation values in the range of [0.5, 1], and ARBs with stimulation values less than 0.5 would get lower resource-sizes.

The output variable is set to 0, if no rule activates the defuzzifier (line 28). Figure 4.5 illustrates the rules that were applied in this study for infer ting the fuzzy algorithm (lines 37-42). In this study, MIN fuzzy operator was used for activation process (line 34), it determines the degree of fulfillment of rules that act on the output. MIN operator is given by: $Min(\mu_1(x), \mu_2(x))$. For the accumulation of final results, MAX fuzzy operator was used (line 36). MAX operator is given by: $Max(\mu_1(x), \mu_2(x))$.

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```
FUNCTION_BLOCK Fuzzy_Command_File
        // Input variable is defined here
         VAR_INPUT
         stimulation: REAL;
         END_VAR
         // Output variable is defined here
         VAR_OUTPUT
         Fstimulation: REAL;
         END_VAR
         // Fuzzify 'stimulation'
         FUZZIFY stimulation
         TERM VeryLow := (0, 1) (0.2, 0) ;
         TERM Low := (0.1, 0) (0.2,1) (0.3,1) (0.4,0);
         TERM Medium := (0.3, 0) (0.4,1) (0.5,1) (0.6,0);
         TERM High := (0.5, 0) (0.6,1) (0.7,1) (0.8,0);
         TERM VeryHigh := (0.7, 0) (0.8,1) (1,1);
         END_FUZZIFY
         // Defuzzify 'Fstimulation'
         DEFUZZIFY Fstimulation
         TERM VeryLow := 0.1;
         TERM Low := 0.35;
         TERM Medium := 0.5;
         TERM High := 0.75;
         TERM VeryHigh := 1;
          // Defuzzification method: 'Center Of Gravity Singleton'
         METHOD : COGS;
          // Default value: 0 (in case no rule activates defuzzifier)
          DEFAULT := 0;
         END_DEFUZZIFY
         RULEBLOCK RB
          // For 'and' use 'min'
         AND: MIN;
          // For activation method use 'min'
         ACT: MIN;
          // For accumulation method use 'max'
         ACCU: MAX;
         RULE 1: IF stimulation IS VeryLow THEN Fstimulation IS
         VeryLow;
         RULE 2: IF stimulation IS Low THEN Fstimulation IS Low;
         RULE 3: IF stimulation IS Medium THEN Fstimulation IS Medium;
         RULE 4: IF stimulation IS High THEN Fstimulation IS High;
         RULE 5: IF stimulation IS VeryHigh
                             THEN Fstimulation IS VeryHigh;
         END_RULEBLOCK

END_FUNCTION_BLOCK
```

**Figure 4.5: Fuzzy Control Language for Resource Allocation of FRA-AIRS2 and FSRAIRS2**

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Figure 4.6 shows the membership function for the input variable 'stimulation' and Figure 4.7 shows the membership function for the output variable 'resources'.

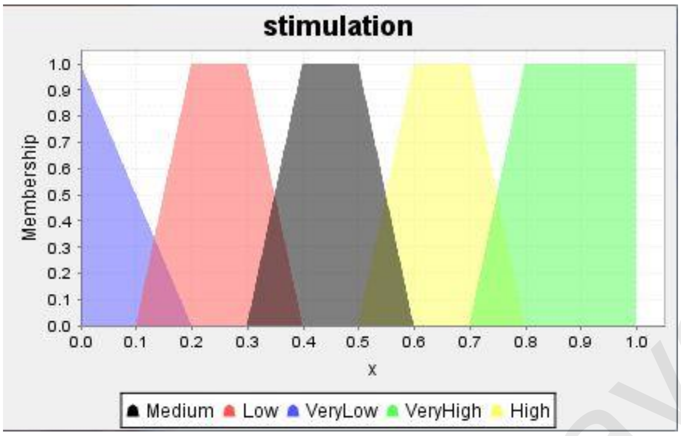

**Figure 4.6: Membership Function for Stimulation**

Values for ARB.stim, on the x-axis, are between 0 and 1, input membership functions determines its membership value.

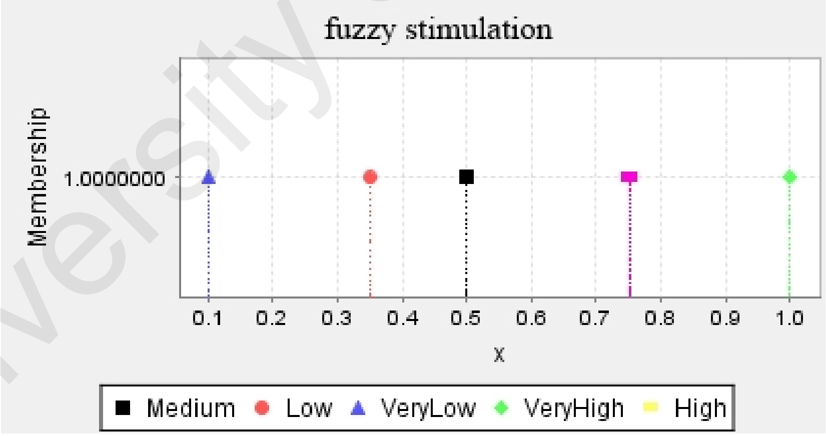

**Figure 4.7: Membership Function for Fuzzy Stimulation**

Membership functions are used to calculate the amount of fuzzy-stimulation, which can be any number between 0 and 1 and it is represented on the x-axis, (see Figure 4.7). The FuzzyStimulation procedure returns a real-value, which is used for calculating the allocated resource, the formula for this calculation it is given in Equation (2.2).

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Evaluation of data reduction capabilities for both algorithms AIRS2 and FRA-AIRS2 are presented in subsection 4.6.3.3(a). There, we can see that for example, Liver Disorders data set consists of 345 instances and while AIRS2 reduces the data set to approximately 197 records, FRA-AIRS2 reduces it to around 103 instances.

This thesis uses the FRA in step 5 of the 3rd stage of FSR-AIRS2 algorithm (explained later in section 4.4.1) for refining resource allocation of ARBs.

## 4.3 Development of RRC-AIRS2

The difference between AIRS1 and AIRS2 is explained in detail in subsection 2.6.1. As explained there, Watkins modified the procedures responsible for maintaining the memory of system (resource management of AIRS2). AIRS1 used to generate clones of multiple classes however only clones of the same class as the antigen are used in the ARB pool (Brownlee, 2005), AIRS2 maintains only the ARBs of the same class and does not allow mutation of the class value (switching classes are not permitted) this is in contrast to how AIRS1 dealt with ARBs (Watkins, 2005).

While in AIRS1 a user has the ability to set the “mutate rate” parameter to control the degree to mutate a created clone, AIRS2 uses the notion of somatic hypermutation where the quantity of mutation of a produced clone is proportional to its affinity to the concerning antigen (Brownlee, 2005). Nevertheless, the problem with linearity still exists, and this issue has not been addressed in AIRS2 yet.

Tournament selection (TS) is one of useful, robust, and popular mechanism in genetic algorithm. The selection pressure of ‘tournament selection’ varies directly as the ‘tournament size’ varies. Whenever the amount of competitors rise, the resulting selection pressure rises too (Miller & Goldberg, 1995), and this leads to premature convergence (Ahn, 2006). TS is considered to be effective in keeping the selection noise as low as

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possible (Ahn, 2006). This study uses Real World Tournament Selection (RWTS) which has shown good result in connection with AIRS1 in the work of (Golzari et al., 2009a, 2009b).

Lee et al. compared conventional TS and RWTS mechanism and discovered that the later has a higher selection pressure with a higher sampling accuracy and relatively small loss of diversity than the former. Authors concluded that RWTS preserves more diversity than TS under similar selection pressure, and that sampling accuracy and higher pressure, improve the performance in a selection strategy (Lee, Soak, Kim, Park, & Jeon, 2008). Lee et al. also argued that excessive use of high pressure in a selection strategy is not appropriate because it may cause a situation of premature convergence. Their results showed that RWTS causes only a small loss of diversity and this is an indication that RWTS does not have an excessive high selection pressure (Lee et al., 2008).

RWTS is widely used to find a winner in a sport game. The players or teams are randomly grouped pair wise in sequence with a neighbor. If the number of players is an odd number, the last individual will be paired with someone from the same tournament level randomly, pairs compete and the winner of each pair goes to the next tournament level. In the next round this procedure repeats by building new pairs and starting the competition. At the end, one champion will be identified. The champion of the tournament is the player with the best fitness value among all participating players. For the resource competition, ARBs of each class represent individuals. ARBs enter the competition and each ARB competes with a neighbor. This algorithm considers ARB A as a neighbor of ARB B, if ARB B is the first ARB from the same class as ARB A, and it is generated in the system after ARB A. The competition depends on the amount of allocated resources for ARBs. This amount is calculated for each ARB during the resource allocation process.

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Figure 4.8 illustrates the pseudocode for RWTS-based Resource Competition method which will be used by RRC-AIRS2 and FSR-AIRS2 models which will be explained in sections 4.3.1 and section 4.4.1 respectively. This method is dubbed as RRC. In this method each ARB has to compete with its neighbour.

```
RRC (ARBPool){
Resources Allowed ← Total Resources
Stimulate (ARBs.Stim)
Allocate resources to ARBs based on their Stimulation value
Allocated Resource ← Sum of allocated resources of ARBs
Current pair ← first pair of ARBs
//Continue until the resources are below a threshold
DOWHILE (Allocated Resource > Allowed Resource)
    NumResToBeRemoved ← Allocated Resource – Resource Allowed
    FOR Current pair
        MinARB.resource ← ARB with the lower resource from the pair
        //Check if element can be removed
        IF MinARB.resource ≤ NumResToBeRemoved
            Delete MinARB.resource from the population
            Allocated Resource ← Allocated Resource –
                    MinARB.resource
        ELSE
            //Decrement resources
            MinARB.resource ← MinARB.resource –
                    NumResToBeRemoved
            Allocated Resource ← Allocated Resource –
                    NumResToBeRemoved
        ENDIF
        IF current pair is last ARB pair
    GOTO first ARB pair
        ELSE
    GOTO next ARB pair
        ENDIF
    ENDFOR
ENDDOWHILE
//Compare Allocated Resources of ARBs
//The best ARB is always the one with the most resources
BestARB ← ARB with the most Allocated Resources
Return BestARB
}
```

**Figure 4.8: Pseudocode for RWTS-Resource Competition (RRC)**

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As it can be seen from the Figure 4.8, in line 1 the algorithm determines the number of allowed resources, which is set by the user, then ARBs are stimulated (line2) and resources are allocated to ARBs, based on their fuzzy stimulation value (lines 3-4) and then pairs of ARBs are built as described above and the first pair is selected (line 5), all pairs undergo a competition (lines 9-25) and the process of competition for resources continuous (lines 7-26) until the resources are below a threshold. In line 10 the algorithm verifies which of the pair has lower resources allocated to it, the one with the lowest resource will be removed from the population (line 13) and the winner will go to the next level. The competition between remaining pairs continuous until allowed resources will become either equal to the sum of allocated resources of remaining ARBs or equal to the sum of allocated resources of all in the competition participating ARBs. If for all ARBs that participate in the competition their sum of allocated resources is still higher than the amount of allowed resources, the tournament goes to the next level. The same competition rules exist across all levels of the tournament. The competition continuous until the sum of allocated resources becomes equal or less than the amount of allowed resources. The amount of allocated resources will be reduced by the amount of resources that was allocated by the looser (line 14). In lines 16-18 the amount of resources will be decreased and recalculated. The algorithm verifies whether or not other pairs exist (lines 20-24), if exist, the process of competition between pairs repeats otherwise it goes to next level and starts building new pairs with the winners of previous level and new competition starts. At the end the strongest ARB (the one with the most resources) will survive (lines 27-30).

The concept of RRC is illustrated in the following examples. Let us assume to have 10 ARBs and each ARB is denoted as $x_i$, where *i* = 1, 2,…,10. Each ARB has been allocated resources as follows: $x_1 = 3, x_2 = 6,\ x_3 = 2,\ x_4 = 4,\ x_5 = 1, x_6 = 10,\ x_7 = 8,\ x_8 = 5,\ x_9 = 7,\ x_{10} = 9$. Figure 4.9 illustrates the RRC process of the above mentioned

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ARBs. Assuming that total allowed resources (TAR=37), total allocated resources (TA) for all ARBs equals 55 (=1+2+3+...+9+10) which is greater than the TAR of 37, therefore competition for resources start between neighbors as it is illustrated in the Figure 4.9, the winner of each pair is the one with the highest resource allocated to it.

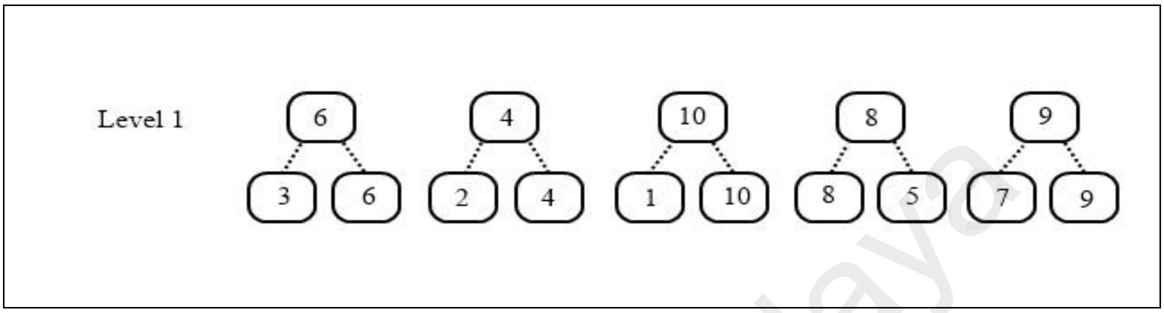

**Figure 4.9: RRC One Level**

For example the winner between $x_1 = 3\ and\ x_2 = 6$ is $x_2 = 6$ which goes to the next level (level 1), now TA = 55 – 3 = 52 which is still higher than TAR, and since we still have other pairs of ARBs, the competition continues between $x_3 = 2\ and\ \ x_4 = 4$ where the winner $x_4 = 4$ goes to level 1, now TA = 52 – 2 = 50 which is still higher than TAR=37, and the process of competition continues until all paired ARBs have competed against each other and TA becomes 37 or less. Looking at ARBs at level 1, their sum of allocated resource (TA = 37) is equal to TAR, and at this point the stop condition has been reached and ARBs with 6, 4, 10, 8, and 9 resources are allowed to go through next step of FSR-AIRS2 (step 6 of the pseudocode for FSR-AIRS2, that is explained later).

Figure 4.10 presents another example for RRC, here TAR is assumed to be 25. In order to satisfy the stop condition, the competition continues from level 1 to level 2, and at the end the ARBs with 6, 10, and 9 resources will be taken to the next step of FSR-AIRS2 (step 6 of pseudocode for FSR-AIRS2, that is explained later).

This thesis uses the RRC method, in step 5 of the 3rd stage of RRC-AIRS2 and FSR-AIRS2 algorithms (explained in sections 4.3.1 and 4.4.1 respectively) in order to

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determine and remove the weak cells during resource competition (it is a process for population control of memory cell pool).

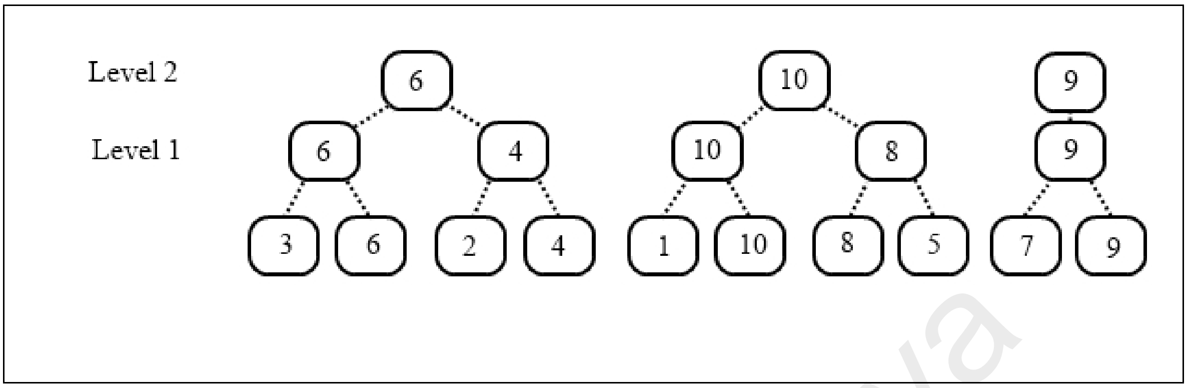

**Figure 4.10: RRC Two Levels**

Results of the evaluation of these algorithms are presented in sections 4.6.2.1 and 4.6.3.1.

### 4.3.1 Pseudocode for RRC-AIRS2

This section introduces a new algorithm. This model uses the RRC method that was introduced above and implements it in the AIRS2, the resulting algorithm is dubbed as the RRC-AIRS2. The goal of introducing this algorithm is to evaluate the application of the RRC method and verify whether or not this method improves the performance of the AIRS2.

Figure 4.11 illustrates the pseudocode for RRC-AIRS2 algorithm. Similar to the AIRS2, (introduced in section 2.6), RRC-AIRS2 consists of four stages: in the first stage data is normalized and initialized. In the second stage a memory cell is identified and ARB is generated. In the third stage the algorithm deals with competition for resources, here it uses the RRC method in the development process of a candidate memory cell. In the fourth stage of the algorithm the potential candidate memory cell is introduced into the set of already established memory cells.

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In step 5 of the 3rd stage, RRC-AIRS2 uses RRC for determining and removing the weak cells during resource competition (population control of memory cell pool).

In stage 4, the algorithm passes the memory cell pool **M** to the KNN for classification.

```
I. Initialize and normalize dataset
II. Seed the memory cell pool (M), if desired.
III. For each training example (antigen) do the following:
        1. If M is empty, add antigen to M.
        2. Select the memory cell (mc) in M of the same classification
        having the highest affinity to antigen.
        3. Clone mc in proportion to its affinity to antigen.
        4. Mutate each clone and add to the B-cell pool (ARB).
        5. Allocate resources to ARB
        Use RRC (RWTS-mechanism) for removing the weak cells
        (population control of ARB).
        6. Calculate the average stimulation of ARB to antigen and
        check for termination. If the termination condition is
        satisfied, goto step 9.
        7. Clone and mutate a random selection of B-cells in
        ARB based upon their stimulation.
        8. Loop back to step 5.
        9. Select the B-cell in ARB with the highest affinity to
        antigen (candidate). If candidate has a higher affinity to
        antigen than mc add candidate  to M. If mc and candidate are sufficiently
        similar, then remove mc from M.
return M
IV. Perform KNN classification using M.
```

**Figure 4.11: Pseudocode for RRC-AIRS2**

Evaluation of the model RRC-AIRS2 and its comparison with the AIRS2 is presented in section 4.6.2.1. There, for instance, we can see from the Table 4.6 that the degree of classification accuracy is statistically significantly increased from 88.24% (obtained with the AIRS2) to 89.23% (obtained with the RRC-AIRS2) for the “Statlog (Image Segmentation)” data set.

## 4.4 Development of FSR-AIRS2

Support vector machine (SVM) is originated from advanced statistical learning theory (SVMS.org, 2010) it is recognised as a robust and state-of-the-art classification technique. SVM is able to maximize the predictive accuracy of a model without overfitting the

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training instances. SVM is mainly suitable for analyzing data with very large numbers of predictor fields. SVM has found many applications in various disciplines, including bio sequence analysis, bioinformatics, classification, concept extraction, customer relationship management, character recognition, text mining, and speech and voice recognition.

Vapnik et al. introduced SVM in 1995, and later the “soft margin” SVM was presented by Cortes and Vapnik (Cortes & Vapnik, 1995).

SVM’s goal is to find an optimal hyperplanes in a multi-dimensional space, so that different classes are separated. Through an iterative training algorithm, an ideal hyperplane can be constructed. Cortes et al. have shown that constructing the optimal hyperplane which separates a set of training data has to satisfy (Cortes & Vapnik, 1995):

$$\hat{y} = \text{f(x,w,b)} = w^T.\text{x} + \text{ b} = 0 \qquad (4.4)$$

where ŷ is the predicted output, x is the input pattern, w is the weight vector, whereby w is orthogonal to the hyperplane, and b is the bias. Values for w and b must be set during the training process. Ideally no data points should fall into the margin, in this case the optimal margin hyperplane coincide with constructed hyperplane (Cortes & Vapnik, 1995). In many cases, it is not possible to separate training data without error, in such cases SVM allows a minimal number of errors, these errors are known as classification errors. In other words, the goal is to determine the optimum balance between a maximum margin and minimum classification error. To express this problem a slack variable ξ is introduced and now SVM tries to minimize the functional 4.5:

$$\Phi(\xi) = \sum_{i=1}^{n} \xi_i^{\sigma} \qquad (4.5)$$

for small $\sigma > 0$ , subject to the constraints

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$$\mathrm{y_i(w^T.x_i \;+\; b\,) \geq 1 - \xi_i}$$

$$\text{for all i = 1, …, n and } \xi_i \geq 0 \tag{4.6}$$

If σ is small enough, the functional (4.5) represents the number of training errors. SVM looks now for some minimal subset of training errors and attempts to exclude them from the training set. The part of the dataset that is error-free can be separated without errors. For separating the remaining part of the training data, SVM constructs an optimal hyperplane by solving the following optimization problem for w and b (Cortes & Vapnik, 1995):

$$min_w \ \frac{1}{2}||w||^2 + \mathrm{C}\ F(\textstyle\sum_{i=1}^{n} \xi_i^{\sigma}) \tag{4.7}$$

subject to:

$$\begin{aligned} &y_i(w^T.x_i \;+\; \mathrm{b}\,) \geq 1 - \xi_i, && \text{for all i = 1, …, n} \\ &\xi_i \geq 0, && \text{for all i = 1, …, n} \end{aligned} \tag{4.8}$$

where C is a user defined constant, also known as the tuning parameter, it weights in-sample classification errors and therefore controls the generalization ability of an SVM. C controls the trade-off between the frequency of the error and complexity of the decision rule (Cortes & Vapnik, 1995). If C increases, the classification accuracy for the training data improves too; however this may cause overfitting. Cortes et al. demonstrated that for solving this optimization problem, the saddle point of Lagrangian function can be used. This function has to be minimized with respect to w, b, and ξ , and maximized with respect to Lagrange multipliers ∝ (Cortes & Vapnik, 1995).

$$\mathrm{L(w,b,\propto)} = min_{w,b}max_{\propto}\{\frac{1}{2}\left||w|\right|^2 - \textstyle\sum_{i=1}^{n} \propto_i [y_i(w.x_i + b) - 1]\} \tag{4.9}$$

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This is a classical optimization problem. To solve this problem, standard Quadratic Programming (QP) techniques are used. It should be noted that only a few training vectors$x_i$ with $\propto_{\mathrm{i}}$ greater than zero have an effective contribution to the sum (4.9) (Cortes & Vapnik, 1995). Cortes et al. used Kuhn-Tucker theorem and showed that the corresponding $x_i$ lie on the margin and satisfy (Cortes & Vapnik, 1995):

$$y_i(w.x_i + b) = 1 \tag{4.10}$$

These points ($x_i$), whose $\propto_{\mathrm{i}} \neq 0$, are called support vectors (SV). They are relevant for the calculation of w, and the hyperplane is determined by SV. SVs lie either on the margin boundaries or, for non-perfectly separable data, within the margin. The complexity of calculations does not depend on the dimension of the input space but on the number of support vectors, which is a minor subdivision of the training vector (Laura Auria, 2008).

The decision or classification function $g(x)$ can be written as follows:

$$g(x) = sign\left(\sum_{i=1}^{n} \propto_i y_i K(x_i, x_j) + b\right) \tag{4.11}$$

where $K(x_i, x_j)$ is the value of a kernel function satisfying the Mercer theorem. Functions that satisfy Mercer's theorem ensure that inner (dot) products can be used as kernels (Laura Auria, 2008). SVM models can use a number of Kernels, including linear, polynomial, sigmoid, and radial basis function (RBF) (Statsoft, 2013):

**Kernel Functions:**

$$K(x_i, x_j) = \begin{cases} x_i x_i & Linear \\ (\gamma x_i\, x_j + coefficient)^d & Polynomial \\ \exp\left(-\gamma \left|x_i - x_j\right|^2\right) & Radial\ Basis\ Function\ (RBF) \\ \tanh(\gamma x_i\, x_j + coefficient) & Sigmoid \end{cases} \tag{4.12}$$

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where $\gamma$ is a kernel parameter. If the value of $\gamma$ increases, the classification accuracy improves, however this may cause overfitting too.

### 4.4.1 Pseudocode of FSR-AIRS2

This section introduces a new artificial immune system based hybrid algorithm. This model uses the FRA, RRC, and SVM methods that were introduced in sections 4.2, and 4.3, and implements them in the AIRS2; the resulting algorithm is dubbed as the FSR-AIRS2. Figure 4.12 illustrates the pseudocode for FSR-AIRS2 algorithm that is used in this study.

```
I. Initialize and normalize dataset
II. Seed the memory cell pool (M), if desired.
III. For each training example (antigen) do the following:
        1. If M is empty, add antigen to M.
        2. Select the memory cell (mc) in M of the same classification
        having the highest affinity to antigen.
        3. Clone mc in proportion to its affinity to antigen.
        4. Mutate each clone and add to the B-cell pool (ARB).
        5. Use FRA (Fuzzy-logic) to allocate resources to ARB
        Use RRC (RWTS-mechanism) for removing the weak cells
        (population control of ARB).
        6. Calculate the average stimulation of ARB to antigen and
        check for termination. If the termination condition is
        satisfied, goto step 9.
        7. Clone and mutate a random selection of B-cells in
        ARB based upon their stimulation.
        8. Loop back to step 5.
        9. Select the B-cell in ARB with the highest affinity to
        antigen (candidate). If candidate has a higher affinity to
        antigen than mc add candidate  to M. If mc and candidate are sufficiently
        similar, then remove mc from M.
return M
//prepare content of M for SVM
IV. Transfer M to SVM format
//run SVM as classifier
V. Perform SVM classification using M.
```

**Figure 4.12: Pseudocode for FSR-AIRS2**

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Similar to AIRS2, (introduced in section 2.5), there are five stages in FSR-AIRS2: the first stage consists of data normalization and initialization; also in this stage, optionally memory cell pool can be seeded. The second stage is where, a memory cell is identified and ARB is generated. The third stage handles competition for resources, and the development process for a candidate memory cell happens here. In the fourth stage of the algorithm, the potential candidate memory cell is introduced into the set of already established memory cells. In step 5 of the 3rd stage, FSR-AIRS2 uses FRA (explained in section 4.2) to refine resource allocation for ARBs and then it uses RRC (explained in section 4.3) for determining and removing the weak cells during resource competition (population control of memory cell pool).

In stage 4, the proposed algorithm formats the content of **M** so that it is prepared for the SVM. In the stage 5, this algorithm passes **M** to the SVM for classification.

This research used WLSVM (EL-Manzalawy & Honavar, 2005) which is a wrapper of LibSVM (Chang & Lin, 2011) inside WEKA (Mark Hall et al., 2009) to address classification problems. The LibSVM supports multi-class classification and both “one-against-one” and “one-against-the rest” multi-class strategies are part of the implementation.

## 4.5 Experimental Setup

The goal of the experiment is to evaluate the performance of FSR-AIRS2 in a real-world application setting. Details about data sets, performance and evaluation measurements were discussed in Chapter 3.

Performance of other developed algorithms the FRA-AIRS2 and RRC-AIRS2 are also evaluated.

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## 4.6 Results and Discussion

This section evaluates the behaviour of the current implementation of the FRA-AIRS2, RRC-AIRS2, and FSR-AIRS2 on some machine learning data sets. The standard machine learning data sets employed in this section have been used to investigate the performance of many different classification systems. This section compares the accuracy of the current implementation with the accuracy of other classifiers using the mentioned data sets. Table 4.2 presents the optimized parameter settings used to run AIRS2, FRA-AIRS2, and RRC-AIRS2 on the standard machine learning data sets as well as the classification accuracy obtained with AIRS2; the standard deviations are shown in parenthesis. The parameters that were used include Affinity Threshold Scalar (ATS), Clonal Rate (CR), Hypermutation Rate (HR), K-value for KNN classifier, Seed cells (S), Stimulation Value (St), and number of Resources (NR).

**Table 4.2: Parameter Settings used for AIRS2, FRA-AIRS2, and RRC-AIRS2.**

| Training Set | ATS | CR | HR | K | S | St | NR |
|---|---|---|---|---|---|---|---|
| Balance Scale | 0.2 | 10 | 0.5 | 10 | 1 | 0.9 | 150 |
| Breast Cancer Wisconsin (Diagnostic) | 0.2 | 10 | 6.0 | 3 | 1 | 0.9 | 150 |
| Contact Lenses | 0.1 | 10 | 2.7 | 4 | 1 | 0.9 | 150 |
| Ionosphere | 0.2 | 10 | 2.0 | 3 | 1 | 0.9 | 350 |
| Iris | 0.2 | 10 | 2.0 | 3 | 1 | 0.9 | 150 |
| Liver Disorders | 0.2 | 10 | 2.0 | 3 | 1 | 0.9 | 150 |
| Lung Cancer | 0.2 | 10 | 0.2 | 4 | 1 | 0.9 | 150 |
| Pima Indians | 0.2 | 10 | 1.4 | 15 | 1 | 0.9 | 150 |
| Statlog (Heart) | 0.2 | 10 | 0.2 | 5 | 1 | 0.9 | 150 |
| Statlog (Image Segmentation) | 0.2 | 10 | 2.0 | 2 | 1 | 0.9 | 150 |
| Statlog (Vehicle Silhouettes) | 0.2 | 10 | 2.9 | 4 | 1 | 0.9 | 150 |
| Sonar, Mines vs. Rocks | 0.2 | 10 | 2.0 | 2 | 1 | 0.9 | 150 |
| Vertebral Column_2C | 0.2 | 10 | 2.0 | 3 | 1 | 0.9 | 150 |
| Vertebral Column_3C | 0.2 | 10 | 2.0 | 3 | 1 | 0.9 | 150 |
| Wisconsin Breast Cancer Data Set (WBCD) (Original) | 0.2 | 10 | 3 | 5 | 2 | 0.9 | 200 |

Similar to the work of (Hamaker & Boggess, 2004) we did the following to determine the parameters for AIRS2.

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First we used the default values and ran 10 runs of 10-fold cross validation and noted the average classification value, and compared it with other results obtained from variations of the parameters.

We varied ATS from 0 to 1 by 0.1, after the best value for ATS was determined, we used it for the rest of experiment with that data set. Then we varied CR from 0 to 10 by 1, after the best value for CR was determined, we used it for the rest of experiment with that data set.

Then we varied HR from 0 to 7 by 0.1, after the optimal value for HR was determined, we used it for the rest of experiment with that data set. Then we varied the seed between 1 and 2, because we wanted AIRS2 to regulate the number of memory cells by itself, after the optimal value for the seed was determined, we used it for the rest of experiment with that data set.

Then we varied the Stim from 0 to 1 by 0.1, after the optimal value for the Stim was determined, we used it for the rest of experiment with that data set. Then we varied the number of resources from 50 to 400 by 50, after determining the optimal value for the number of resources, we used it for the rest of experiment with that data set.

Then we varied the k for KNN from 1 to 20 by 1, after determining the optimal value for the k we used it for the rest of experiment with that data set. Through experiments, we found that two parameters (HR and K) played greater role in optimizing the result, and other parmeters could be kept constant.

Table 4.3 presents the optimized parameter settings used to run FSR-AIRS2 on the standard machine learning data sets as well as the classification accuracy obtained with FSR-AIRS2; the standard deviations are shown in parenthesis.

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**Table 4.3: Parameter Settings used for FSR-AIRS2**

| Training Set | ATS | CR | HR | S | St | R | C | γ | Kernel |
|---|---|---|---|---|---|---|---|---|---|
| Balance Scale | 0.1 | 10 | 0.2 | 1 | 0.2 | 150 | 7 | 1 | RBF |
| Breast Cancer Wisconsin (Diagnostic) | 0.2 | 10 | 0.15 | 1 | 0.9 | 150 | 7 | 1 | RBF |
| Contact Lenses | 0.2 | 10 | 0.5 | 1 | 0.9 | 150 | 7 | 1 | RBF |
| Ionosphere | 0.2 | 10 | 0.2 | 1 | 0.9 | 300 | 7 | 1 | RBF |
| Iris | 0.2 | 10 | 2.0 | 1 | 0.9 | 150 | 7 | 1 | RBF |
| Liver Disorders | 0.2 | 10 | 0.5 | 1 | 0.9 | 150 | 7 | 1 | RBF |
| Lung Cancer | 0.2 | 10 | 0.5 | 1 | 0.9 | 150 | 7 | 1 | RBF |
| Pima Indians | 0.2 | 10 | 0.5 | 1 | 0.9 | 150 | 7 | 1 | RBF |
| Statlog (Heart) | 0.2 | 10 | 0.2 | 1 | 0.9 | 150 | 7 | 1 | RBF |
| Statlog (Image Segmentation) | 0.2 | 10 | 0.3 | 50 | 0.9 | 150 | 7 | 1 | RBF |
| Statlog (Vehicle Silhouettes) | 0.2 | 10 | 0.2 | 1 | 0.9 | 300 | 7 | 1 | RBF |
| Sonar, Mines vs. Rocks | 0.2 | 10 | 0.3 | 1 | 0.9 | 150 | 7 | 1 | RBF |
| Vertebral Column_2C | 0.2 | 10 | 2.0 | 1 | 0.9 | 150 | 7 | 1 | RBF |
| Vertebral Column_3C | 0.2 | 10 | 2.0 | 1 | 0.9 | 150 | 7 | 1 | RBF |
| Wisconsin Breast Cancer Data Set (WBCD) (Original) | 0.2 | 10 | 2.0 | 1 | 0.9 | 150 | 7 | 1 | RBF |

The parameters that were used include Affinity Threshold Scalar (ATS), Clonal Rate (CR), Hypermutation Rate (HR), Seed cells (S), Stimulation Value (St), Resources (R), SVM Constant C, kernel parameter γ, and Kernel Function.

Similar to the work of (Hamaker & Boggess, 2004) we did the following to determine the parameters for FSR-AIRS2. First we used the default values and ran 10 runs of 10-fold cross validation and noted the average classification value, and compared it with other results obtained from variations of the parameters.

We varied ATS from 0 to 1 by 0.1, after the best value for ATS was determined, we used it for the rest of experiment with that data set. Then we varied CR from 0 to 10 by 1, after the best value for CR was determined, we used it for the rest of experiment with that data set.

Then we varied HR from 0 to 7 by 0.1, after the optimal value for HR was determined, we used it for the rest of experiment with that data set. Then we varied the seed between 1 and 2, because we wanted AIRS2 to regulate the number of memory cells by itself, after

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the optimal value for the seed was determined, we used it for the rest of experiment with that data set. Then we varied the Stim from 0 to 1 by 0.1, after the optimal value for the Stim was determined, we used it for the rest of experiment with that data set. Then we varied the number of resources from 50 to 400 by 50, after determining the optimal value for the number of resources, we used it for the rest of experiment with that data set. One exception was in case of the Statlog (Image Segmentation) data set, where we found seed =50 as optimal value. For the SVM, we used RBF as the kernel function, as it is a reasonable choice for linear and non-linear problems, and most importantly, it has only two parameters to be set (C and **γ)** (Hsu, Chang, & Lin, 2003). This study used the default values C = 7, **γ =** 1, which were given in LibSVM (Chang & Lin, 2011; EL-Manzalawy & Honavar, 2005).

### 4.6.1 Evaluation of FRA-AIRS2

This section compares the results obtained from AIRS (AIRS2) and the FRA-AIRS2. Since AIRS2 has been a successful classifier, it is important to verify whether or not the changes to the algorithm have improved the classification accuracy.

#### 4.6.1.1 Classification Accuracy of FRA-AIRS2 versus AIRS2

Table 4.4 shows the best average test set accuracies, together with the standard deviations (given in parenthesis), obtained from AIRS2 and FRA-AIRS2 on the benchmark data sets and p-value results of the student t-test comparing the mean accuracies for AIRS2 and FRA-AIRS2.

All experiments utilized 10 fold cross validation and were averaged over 10 runs. The Student’s t-test, as described in section 3.4.7, is used for testing the statistical significance between the mean of the two results.

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**Table 4.4: Comparative Average Accuracies FRA-AIRS2 versus AIRS2**

| Training Set | AIRS2 (STD) | FRA-AIRS2 (STD) | p-value |
|---|---|---|---|
| Balance Scale | 86.83% (3.14) | 90.54% (2.49) | p < 0.05 |
| Breast Cancer Wisconsin (Diagnostic) | 96.17% (2.32) | 98.08% (1.16) | p < 0.05 |
| Contact Lenses | 82.83% (22.53) | 83.00% (15.81) | 0.92 |
| Ionosphere | 86.04% (4.84) | 93.02% (2.41) | p < 0.05 |
| Iris | 94.67% (5.36) | 96.33% (4.26) | 0.89 |
| Liver Disorders | 59.80% (8.18) | 69.48% (6.3) | p < 0.05 |
| Lung Cancer | 41.83% (26.64) | 49.50% (25.90) | p < 0.05 |
| Pima Indians | 74.41% (5.11) | 86.97% (2.62) | p < 0.05 |
| Statlog (Heart) | 77.48% (8.42) | 80.96% (6.48) | p < 0.05 |
| Statlog (Image Segmentation) | 88.24% (2.35) | 89.65% (4.98) | p < 0.05 |
| Statlog (Vehicle Silhouettes) | 62.56% (4.64) | 71.18% (4.72) | p < 0.05 |
| Sonar, Mines vs. Rocks | 65.60% (10.48) | 72.46% (8.97) | p < 0.05 |
| Vertebral Column_2C | 76.23% (8.70) | 82.79% (5.33) | p < 0.05 |
| Vertebral Column_3C | 72.84% (8.32) | 80.01% (5.26) | p < 0.05 |
| Wisconsin Breast Cancer Data Set (WBCD) (Original) | 96.58% (2.19) | 98.29% (1.09) | p < 0.05 |

Table 4.4 shows that the changes made to the AIRS2 algorithm have improved the classification accuracy. Results show that the differences in accuracy for almost all benchmark are significant at the 95% significant level (α = 0.05) based on a two-tailed student’s t-test as described in section 3.4.7.

When we compare the mean classification accuracy for the Balance Scale data set obtained with the AIRS2 ($n_1$ =100, *M*=86.83%, *SD*=3.14) to the one obtained with FRA-AIRS2 ($n_2$ =100, *M*=90.54%, *SD*=2.49) *p<.05* the results show that the differences are statistically significant at the 95% significant level (α = 0.05) for this data set. The FRA-AIRS2 achieved significantly higher classification accuracy.

Comparing the mean classification accuracy for the Breast Cancer Wisconsin (Diagnostic) data set obtained with AIRS2 ($n_1$ =100, *M*=96.17%, *SD*=2.32) to the one obtained with the FRA-AIRS2 ($n_2$ =100, *M*=98.08%, *SD*=1.16) *p*<.05 the results show that the differences are statistically significant at the 95% significant level (α = 0.05) for this data set and the FRA-AIRS2 achieved significantly higher classification accuracy.

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In the case of Contact Lenses data set, the comparison of the mean classification accuracy obtained with the AIRS2 ($n_1$ =100, *M*=82.83%, *SD*=22.53) to the one obtained with the FRA-AIRS2 ($n_2$ =100, *M*=83.0%, *SD*=15.81) *p*=.92 shows that the differences are statistically insignificant at the 95% significant level (α = 0.05) for this data set.

When we compare the mean classification accuracy for the Ionosphere data set obtained with the AIRS2 ($n_1$ =100, *M*=86.04%, *SD*=4.84) to the one obtained with the FRA-AIRS2 ($n_2$ =100, *M*=93.02%, *SD*=2.41) *p*<.05 the results show that the differences are statistically significant at the 95% significant level (α = 0.05) for this data set and the FRA-AIRS2 achieved significantly higher classification accuracy.

Comparing the mean classification accuracy for the Iris data set obtained with the AIRS2 ($n_1$ =100, *M*=94.67%, *SD*=5.36) to the one obtained with the FRA-AIRS2 ($n_2$ =100, *M*=96.33%, *SD*=4.26) *p*<.05 the results show that the differences are statistically insignificant at the 95% significant level (α = 0.05) for this data set. However, the FRA-AIRS2 achieved slightly higher classification accuracy.

In the case of Liver Disorders data set, the comparison of the mean classification accuracy obtained with the AIRS2 ($n_1$ =100, *M*=59.8%, *SD*=8.18) to the one obtained with the FRA-AIRS2 ($n_2$ =100, *M*=69.48%, *SD*=6.3) *p*<.05 the results show that the differences are statistically significant at the 95% significant level (α = 0.05) for this data set and the FRA-AIRS2 achieved significantly higher classification accuracy.

When we compare the mean classification accuracy for the Lung Cancer data set obtained with the AIRS2 ($n_1$ =100, *M*=41.83%, *SD*=26.64) to the one obtained with FRA-AIRS2 ($n_2$ =100, *M*=49.5%, *SD*=25.9) *p*<.05 the results show that the differences are statistically significant at the 95% significant level (α = 0.05) for this data set and the FRA-AIRS2 achieved significantly higher classification accuracy.

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Comparing the mean classification accuracy for the Pima Indians data set obtained with AIRS2 ($n_1$ =100, *M*=74.41%, *SD*=5.11) to the one obtained with FRA-AIRS2 ($n_2$ =100, *M*=86.97%, *SD*=2.62) *p*<.05 the results show that the differences are statistically significant at the 95% significant level (α = 0.05) for this data set and the FRA-AIRS2 achieved significantly higher classification accuracy.

In the case of Statlog (Heart) data set, the comparison of the mean classification accuracy obtained with the AIRS2 ($n_1$ =100, *M*=77.48%, *SD*=8.42) to the one obtained with the FRA-AIRS2 ($n_2$ =100, *M*=80.96%, *SD*=6.48) *p*<.05 the results show that the differences are statistically significant at the 95% significant level (α = 0.05) for this data set and the FRA-AIRS2 achieved significantly higher classification accuracy.

When we compare the mean classification accuracy for the Statlog (Image Segmentation) data set obtained with the AIRS2 ($n_1$ =100, *M*=88.24%, *SD*=2.35) to the one obtained with the FRA-AIRS2 ($n_2$ =100, *M*=89.65%, *SD*=4.98) *p*<.05 the results show that the differences are statistically significant at the 95% significant level (α = 0.05) for this data set and the FRA-AIRS2 achieved significantly higher classification accuracy.

Comparing the mean classification accuracy for the Statlog (Vehicle Silhouettes) data set obtained with AIRS2 ($n_1$ =100, *M*=62.56%, *SD*=4.64) to the one obtained with the FSR-AIRS2 ($n_2$ =100, *M*=71.18%, *SD*=4.72) *p*<.05 the results show that the differences are statistically significant at the 95% significant level (α = 0.05) for this data set and the FRA-AIRS2 achieved significantly higher classification accuracy.

In the case of Sonar, Mines vs. Rocks data set, the comparison of the mean classification accuracy obtained with the AIRS2 ($n_1$ =100, *M*=65.6%, *SD*=10.48) to the one obtained with the FRA-AIRS2 ($n_2$ =100, *M*=72.46%, *SD*=4.55) *p*<.05 the results

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show that the differences are statistically significant at the 95% significant level (α = 0.05) for this data set and the FRA-AIRS2 achieved significantly higher classification accuracy.

When we compare the mean classification accuracy for the Vertebral Column_2C data set obtained with the AIRS2 ($n_1$ =100, *M*=76.23%, *SD*=8.7) to the one obtained with the FRA-AIRS2 ($n_2$ =100, *M*=82.79%, *SD*=5.33) *p*<.05 the results show that the differences are statistically significant at the 95% significant level (α = 0.05) for this data set and the FRA-AIRS2 achieved significantly higher classification accuracy.

Comparing the mean classification accuracy for the Vertebral Column_3C data set obtained with AIRS2 ($n_1$ =100, *M*=72.84%, *SD*=8.32) to the one obtained with the FSR-AIRS2 ($n_2$ =100, *M*=80.01%, *SD*=5.26) *p*<.05 the results show that the differences are statistically significant at the 95% significant level (α = 0.05) for this data set and the FRA-AIRS2 achieved significantly higher classification accuracy.

In the case of Wisconsin Breast Cancer Data Set (WBCD) (Original) data set, the comparison of the mean classification accuracy obtained with the AIRS2 ($n_1$ =100, *M*=96.58%, *SD*=2.19) to the one obtained with the FRA-AIRS2 ($n_2$ =100, *M*=98.29%, *SD*=1.09) *p*<.05 the results show that the differences are statistically significant at the 95% significant level (α = 0.05) for this data set and the FRA-AIRS2 achieved significantly higher classification accuracy.

In general, since α ≥ p on almost all benchmark data sets, it can be concluded that modifications introduced in FRA-AIRS2 appear to have positive effect on the classification accuracy of the classifier. The comparison with AIRS2 shows that FRA-AIRS2 has statistically significantly increased the classification accuracy on almost all (13 out of 15) benchmark data sets.

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Figure 4.13 illustrates a graphical comparison of classification accuracy on benchmark data sets obtained with AIRS2 and FRA-AIRS2 algorithms.

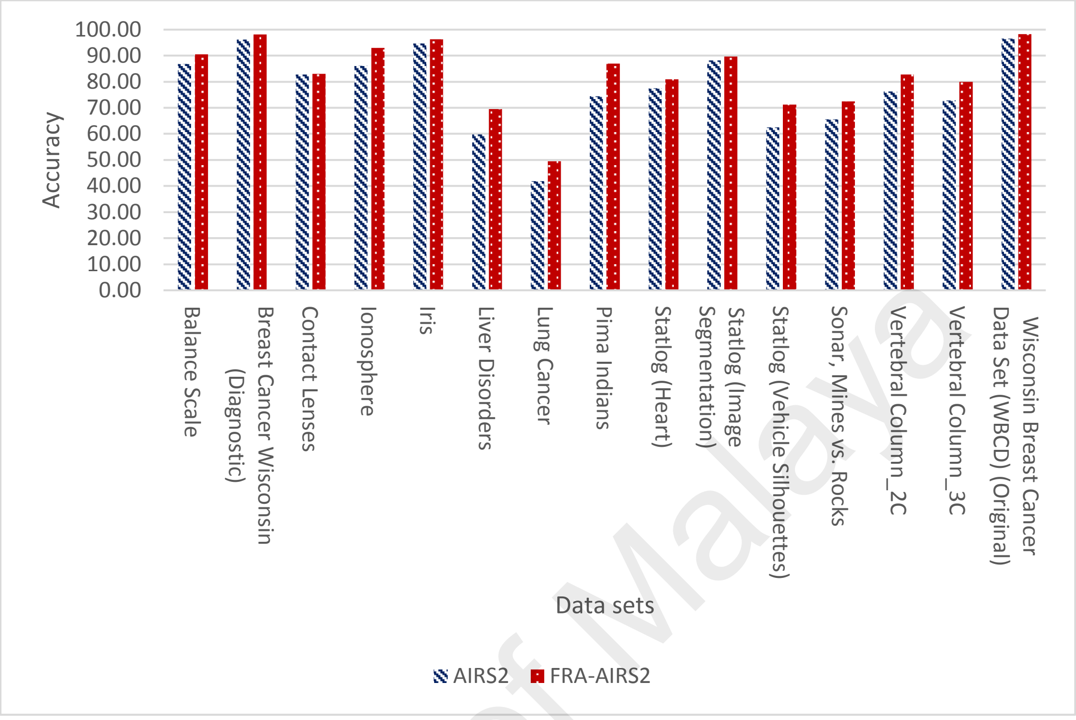

**Figure 4.13: Comparison of Classification Accuracy AIRS2 versus FRA-AIRS2 on benchmark data sets**

Figure 4.13 shows that FRA-AIRS2 has achieved higher classification accuracy than AIRS2 on 13 out of 15 benchmark data sets.

#### 4.6.1.2 Comparing Running Time of FRA-AIRS2 and AIRS2 on benchmark data sets

This section compares the running time results obtained from AIRS2 and the FRA-AIRS2. Since AIRS2 has been a successful classifier, it is important to verify whether or not the changes to the algorithm have improved the running time. Table 4.5 shows the best average test set running time, together with the standard deviations (given in parenthesis), obtained from AIRS2 and FRA-AIRS2 on the benchmark data sets and p-

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value results of the student t-test comparing the mean running time for AIRS2 and FRA-AIRS2.

**Table 4.5: Comparing Running Time of AIRS2 versus FRA-AIRS2**

| **Dataset** | **AIRS2 (STD)** | **FRA-AIRS2 (STD)** | **p-value** |
|---|---|---|---|
| Balance Scale | 0.0933 (0.03) | 0.0636 (0.01) | p <.05 |
| Breast Cancer Wisconsin (Diagnostic) | 0.2192 (0.03) | 0.1099 (0.01) | p <.05 |
| Contact Lenses | 0.0069 (0.01) | 0.0039 (0.01) | 0.026 |
| Ionosphere | 0.1103 (0.04) | 0.1046 (0.02) | p <.05 |
| Iris | 0.0133 (0.01) | 0.0087 (0.01) | p <.05 |
| Liver Disorders | 0.0448 (0.03) | 0.0242 (0.02) | p <.05 |
| Lung Cancer | 0.0036 (0.01) | 6.0254 (2.03) | p <.05 |
| Pima Indians | 0.1137 (0.03) | 0.0610 (0.01) | p <.05 |
| Statlog (Heart) | 0.0206 (0.02) | 0.0157 (0.01) | p <.05 |
| Statlog (Image Segmentation) | 0.6123 (0.04) | 0.3156 (0.02) | p <.05 |
| Statlog (Vehicle Silhouettes) | 0.2265 (0.03) | 0.1230 (0.02) | p <.05 |
| Sonar, Mines vs. Rocks | 0.0780 (0.02) | 20.5522 (2.22) | p <.05 |
| Vertebral Column_2C | 0.0360 (0.03) | 0.0197 (0.02) | p <.05 |
| Vertebral Column_3C | 0.0287 (0.01) | 0.0164 (0.01) | p <.05 |
| Wisconsin Breast Cancer Data set (WBCD) (Original) | 0.1424 (0.03) | 0.0742 (0.02) | p <.05 |

All experiments utilized 10 fold cross validation and were averaged over 10 runs. The Student's t-test, as described in section 3.4.7, is used for testing the statistical significance between the mean of the two results. As it was described in section 3.4.5, the overall runtime is defined as the sum of CPU training time and the CPU testing time. In all of our tests, CPU testing time were neglect able small and are not included in the overall runtime. When looking at the Table 4.5 we can see mixed results; while in case of following data sets (Lung Cancer and Sonar, Mines vs. Rocks) FRA-AIRS2 required higher running time for the classification, it performed well in all other 13 out of 15 cases. This is of course encouraging, because it shows that new implementations made in FRA-AIRS2 did not negatively affect the running time of the classifier.

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### 4.6.2 Evaluation of RRC-AIRS2

This section compares the results obtained from AIRS2 and the proposed RRC-AIRS2. Since AIRS2 has been a successful classifier, it is important to verify whether or not the changes to the algorithm have improved the classification accuracy.

#### 4.6.2.1 Classification Accuracy of RRC-AIRS2 versus AIRS2

Table 4.6 shows the best average test set accuracies, together with the standard deviations (given in parenthesis), obtained from AIRS2 and RRC-AIRS2 on the benchmark data sets and p-value results of the student t-test comparing the mean accuracies for AIRS2 and RRC-AIRS2. All experiments utilized 10 fold cross validation and were averaged over 10 runs. The Student's t-test, as described in section 3.4.7, is used for testing the statistical significance between the mean of the two results. Table 4.6 shows that the changes made to the AIRS2 algorithm have improved the classification accuracy. Results show that the differences in accuracy for some benchmark are significant at the 95% significant level ($\alpha = 0.05$) based on a two-tailed student's t-test.

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**Table 4.6: Comparative Average Accuracies AIRS2 versus RRC-AIRS2**

| Training Set | AIRS2 (STD) | RRC-AIRS2 (STD) | p-value |
|---|---|---|---|
| Balance Scale | 86.83% (3.14) | 86.9% (2.81) | 0.74 |
| Breast Cancer Wisconsin (Diagnostic) | 96.17% (2.32) | 96.82% (2.24) | 0.94 |
| Contact Lenses | 82.83% (22.53) | 82.17% (22.88) | 0.47 |
| Ionosphere | 86.04% (4.82) | 86.61% (4.9) | 0.21 |
| Iris | 94.67% (5.36) | 95.69% (4.98) | 0.08 |
| Liver Disorders | 59.80% (8.18) | 60.03% (9.05) | 0.80 |
| Lung Cancer | 41.83% (26.64) | 47.22% (26.59) | 0.09 |
| Pima Indians | 74.41% (5.11) | 73.00% (4.76) | $p < 0.05$ |
| Statlog (Heart) | 77.48% (8.42) | 79.76% (7.67) | $p < 0.05$ |
| Statlog (Image Segmentation) | 88.24% (2.35) | 89.32% (2.44) | $p < 0.05$ |
| Statlog (Vehicle Silhouettes) | 62.56% (4.64) | 63.09% (5.71) | 0.36 |
| Sonar, Mines vs. Rocks | 65.60% (10.48) | 69.28% (11.49) | $p < 0.05$ |
| Vertebral Column_2C | 76.23% (8.70) | 78.01% (7.56) | $p < 0.05$ |
| Vertebral Column_3C | 72.84% (8.32) | 74.23% (8.61) | 0.1 |
| Wisconsin Breast Cancer Data Set (WBCD) (Original) | 96.58% (2.19) | 96.56% (2.24) | 0.93 |

When we compare the mean classification accuracy for the Balance Scale data set obtained with the AIRS2 ($n_1$ =100, *M*=86.83%, *SD*=3.14) to the one obtained with RRC-AIRS2 ($n_2$ =100, *M*=86.9%, *SD*=2.81) *p*=.74 the results show that the differences are statistically insignificant at the 95% significant level (α = 0.05) for this data set. However, the RRC-AIRS2 achieved slightly higher classification accuracy.

Comparing the mean classification accuracy for the Breast Cancer Wisconsin (Diagnostic) data set obtained with the AIRS2 ($n_1$ =100, *M*=96.17%, *SD*=2.32) to the one obtained with the RRC-AIRS2 ($n_2$ =100, *M*=96.82%, *SD*=2.24) *p*=.94 the results show that the differences are statistically insignificant at the 95% significant level (α = 0.05) for this data set. However, the RRC-AIRS2 achieved slightly higher classification accuracy.

In the case of Contact Lenses data set, the comparison of the mean classification accuracy obtained with the AIRS2 ($n_1$ =100, *M*=82.83%, *SD*=22.53) to the one obtained with the RRC-AIRS2 ($n_2$ =100, *M*=82.17%, *SD*=22.88) *p*=.47 shows that the differences are statistically insignificant at the 95% significant level (α = 0.05) for this data set. However, the RRC-AIRS2 achieved slightly lower classification accuracy.

When we compare the mean classification accuracy for the Ionosphere data set obtained with the AIRS2 ($n_1$ =100, *M*=86.04%, *SD*=4.82) to the one obtained with the RRC-AIRS2 ($n_2$ =100, *M*=86.61%, *SD*=4.9) *p*=.21 the results show that the differences are statistically insignificant at the 95% significant level (α = 0.05) for this data set. However, the RRC-AIRS2 achieved slightly higher classification accuracy.

Comparing the mean classification accuracy for the Iris data set obtained with the AIRS2 ($n_1$ =100, *M*=94.67%, *SD*=5.36) to the one obtained with the RRC-AIRS2 ($n_2$ =100, *M*=95.69%, *SD*=4.98) *p*=.0.08 the results show that the differences are

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statistically insignificant at the 95% significant level (α = 0.05) for this data set. However, the RRC-AIRS2 achieved higher classification accuracy.

Compared to the mean classification accuracy obtained with the AIRS2 using the Liver Disorders data set, the mean classification accuracy obtained with the AIRS2 ($n_1$ =100, *M*=59.8%, *SD*=8.18) and the one obtained with the RRC-AIRS2 ($n_2$ =100, *M*=60.03%, *SD*=9.05) *p*=.8 the differences are statistically insignificant at the 95% significant level (α = 0.05) for this data set. However, the RRC-AIRS2 achieved slightly higher classification accuracy.

When we compare the mean classification accuracy for the Lung Cancer data set obtained with the AIRS2 ($n_1$ =100, *M*=41.83%, *SD*=26.64) to the one obtained with RRC-AIRS2 ($n_2$ =100, *M*=47.22%, *SD*=26.59) *p*=.09 the results show that the differences are statistically insignificant at the 95% significant level (α = 0.05) for this data set. However, the RRC-AIRS2 achieved higher classification accuracy.

Comparing the mean classification accuracy for the Pima Indians data set obtained with AIRS2 ($n_1$ =100, *M*=74.41%, *SD*=5.11) to the one obtained with RRC-AIRS2 ($n_2$ =100, *M*=73.05%, *SD*=4.76) *p*<0.05 the results show that the differences are statistically significant at the 95% significant level (α = 0.05) for this data set. Moreover, the AIRS2 achieved higher classification accuracy.

In the case of Statlog (Heart) data set, the comparison of the mean classification accuracy obtained with the AIRS2 ($n_1$ =100, *M*=77.48%, *SD*=8.42) to the one obtained with the RRC-AIRS2 ($n_2$ =100, *M*=79.76%, *SD*=7.67) *p*<.05 shows that the differences are statistically significant at the 95% significant level (α = 0.05) for this data set. The RRC-AIRS2 achieved higher classification accuracy.

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When we compare the mean classification accuracy for the Statlog (Image Segmentation) data set obtained with the AIRS2 ($n_1$ =100, *M*=88.24%, *SD*=2.35) to the one obtained with the RRC-AIRS2 ($n_2$ =100, *M*=89.32%, *SD*=2.44) *p*<.05 the results show that the differences are statistically significant at the 95% significant level (α = 0.05) for this data set, and the RRC-AIRS2 achieved higher classification accuracy.

Comparing the mean classification accuracy for the Statlog (Vehicle Silhouettes) data set obtained with AIRS2 ($n_1$ =100, *M*=62.56%, *SD*=4.64) to the one obtained with the RRC-AIRS2 ($n_2$ =100, *M*=63.09%, *SD*=5.71) *p*=0.36 the results show that the differences are statistically insignificant at the 95% significant level (α = 0.05) for this data set. And the RRC-AIRS2 achieved higher classification accuracy.

In the case of Sonar, Mines vs. Rocks data set, the comparison of the mean classification accuracy obtained with the AIRS2 ($n_1$ =100, *M*=65.6%, *SD*=10.48) to the one obtained with the RRC-AIRS2 ($n_2$ =100, *M*=69.28%, *SD*=11.49) *p*<.05 shows that the differences are statistically significant at the 95% significant level (α = 0.05) for this data set. The RRC-AIRS2 achieved higher classification accuracy.

When we compare the mean classification accuracy for the Vertebral Column_2C data set obtained with the AIRS2 ($n_1$ =100, *M*=76.23%, *SD*=8.7) to the one obtained with the RRC-AIRS2 ($n_2$ =100, *M*=78.01%, *SD*=7.56) *p*<.05 the results show that the differences are statistically significant at the 95% significant level (α = 0.05) for this data set, and the RRC-AIRS2 achieved higher classification accuracy.

Comparing the mean classification accuracy for the Vertebral Column_3C data set obtained with AIRS2 ($n_1$ =100, *M*=72.84%, *SD*=8.32) to the one obtained with the RRC-AIRS2 ($n_2$ =100, *M*=74.23%, *SD*=8.61) *p*=0.1 the results show that the differences are

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statistically insignificant at the 95% significant level (α = 0.05) for this data set. However the RRC-AIRS2 achieved higher classification accuracy.

In the case of Wisconsin Breast Cancer Data Set (WBCD) (Original) data set, the comparison of the mean classification accuracy obtained with the AIRS2 ($n_1$ =100, *M*=96.58%, *SD*=2.19) to the one obtained with the RRC-AIRS2 ($n_2$ =100, *M*=96.56%, *SD*=2.24) *p=0.93* shows that the differences are statistically significant at the 95% significant level (α = 0.05) for this data set. The AIRS2 achieved higher classification accuracy.

Figure 4.14 illustrates a graphical comparison of classification accuracy on benchmark data sets obtained with AIRS2 and RRC-AIRS2 algorithms. As it can be seen, RRC-AIRS2 has increased the classification accuracy on 12 out of 15 benchmark data sets.

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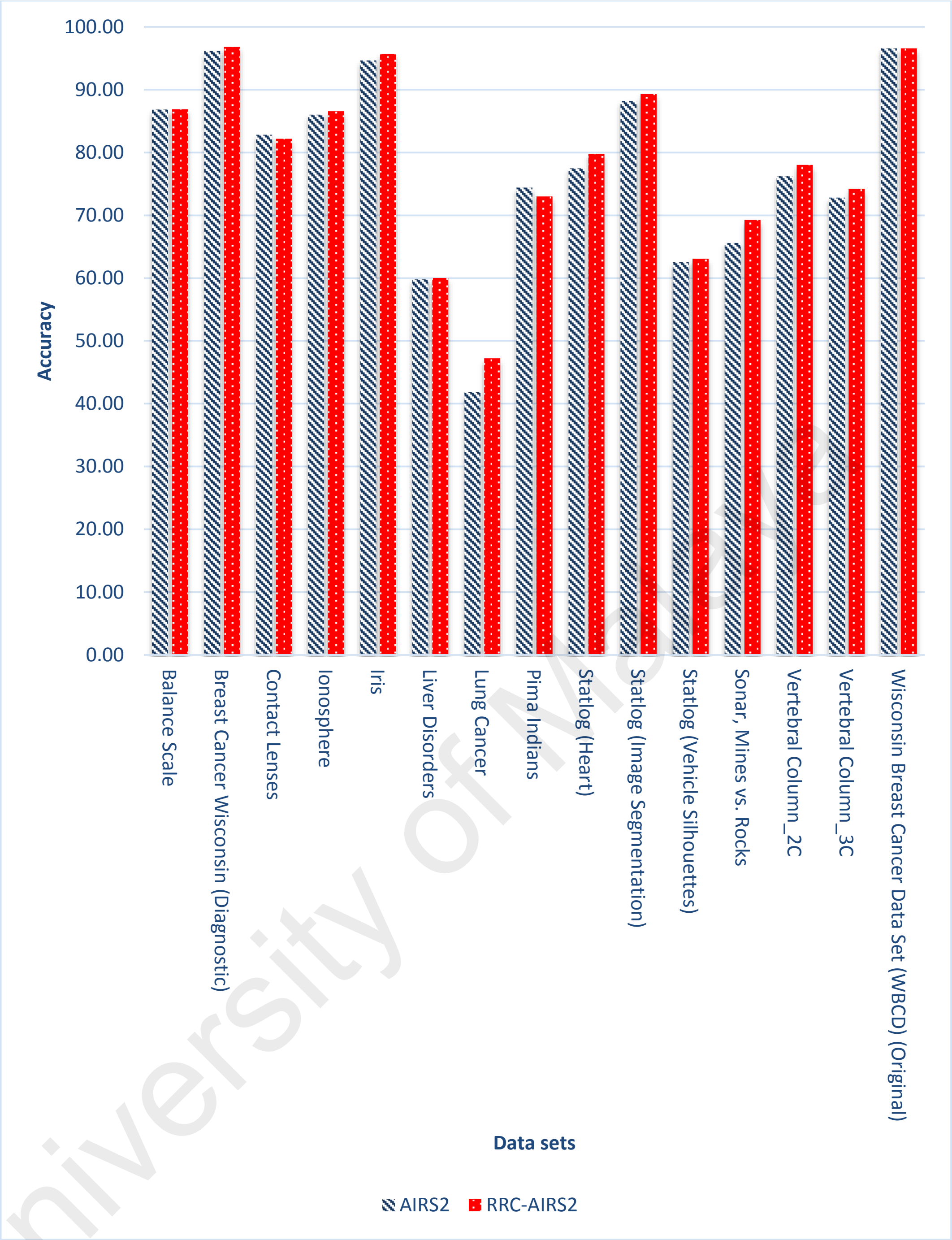

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**Figure 4.14: Comparison of Classification Accuracy AIRS2 versus RRC-AIRS2 on benchmark data sets**

In general we can conclude that RRC-AIRS2 has achieved higher classification accuracy than the AIRS2 on almost all (12 out of 15) benchmark data sets. Only in four cases the differences are statistically significant in favour of RRC-AIRS2, while in other cases the differences are statistically insignificant.

#### 4.6.2.2 Comparing Running Time of RRC-AIRS2 and AIRS2 on benchmark data sets

This section compares the running time results obtained from AIRS2 and the FRA-AIRS2. Since AIRS2 has been a successful classifier, it is important to verify whether or not the changes to the algorithm have improved the running time. Table 4.7 shows the best average test set running time, together with the standard deviations (given in parenthesis), obtained from AIRS2 and RRC-AIRS2 on the benchmark data sets and p-value results of the student t-test comparing the mean running time for AIRS2 and RRC-AIRS2.

**Table 4.7: Comparing Running Time of AIRS2 versus RRC-AIRS2**

| Dataset | AIRS2 (STD) | RRC-AIRS2 (STD) | p-value |
|---|---|---|---|
| Balance Scale | 0.0933 (0.03) | 0.1830 (0.03) | p <.05 |
| Breast Cancer Wisconsin (Diagnostic) | 0.2192 (0.03) | 15.0713 (0.13) | p <.05 |
| Contact Lenses | 0.0069 (0.01) | 32.5766(45.23) | 0.026 |
| Ionosphere | 0.1103 (0.04) | 0.2939 (0.01) | p <.05 |
| Iris | 0.0133 (0.01) | 0.0287 (0.01) | p <.05 |
| Liver Disorders | 0.0448 (0.03) | 0.1108 (0.01) | p <.05 |
| Lung Cancer | 0.0036 (0.01) | 0.0608 (0.01) | p <.05 |
| Pima Indians | 0.1137 (0.03) | 0.3022 (0.02) | p <.05 |
| Statlog (Heart) | 0.0206 (0.02) | 0.15 (0.01) | p <.05 |
| Statlog (Image Segmentation) | 0.6123 (0.04) | 4.6988 (0.06) | p <.05 |
| Statlog (Vehicle Silhouettes) | 0.2265 (0.03) | 0.6240 (0.05) | p <.05 |
| Sonar, Mines vs. Rocks | 0.0780 (0.02) | 0.4161 (0.02) | p <.05 |
| Vertebral Column_2C | 0.0360 (0.03) | 0.3401 (0.02) | p <.05 |
| Vertebral Column_3C | 0.0287 (0.01) | 0.7076 (0.04) | p <.05 |
| Wisconsin Breast Cancer Data set (WBCD) (Original) | 0.1424 (0.03) | 0.0047 (0.01) | p <.05 |

All experiments utilized 10 fold cross validation and were averaged over 10 runs. The Student’s t-test, as described in section 3.4.7, is used for testing the statistical significance between the mean of the two results. As it was described in section 3.4.5, the overall runtime is defined as the sum of CPU training time and the CPU testing time. In all of our tests, CPU testing time were neglect able small and are therefore not included in the overall runtime. When looking at the Table 4.7 we can see very interesting but not

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surprising results; while only in case of (Wisconsin Breast Cancer Data set (WBCD) (Original)) RRC-AIRS2 required lower running time for the classification, it required higher running time in all other 14 out of 15 cases.

The results are not surprising, because when we look at Table 4.6 in section 4.6.2.1, we can see that RRC-AIRS2 was able to achieve higher classification accuracy than AIRS2 in 13 out of 15 cases, whereby the results were statistically significant only in 5 cases. It is well known that the price for higher classification is usually higher running time.

### 4.6.3 Evaluation of FSR-AIRS2

This section compares the results obtained from AIRS (AIRS2) and the FSR-AIRS2. Since AIRS2 has been a successful classifier, it is important to verify whether or not the changes to the algorithm have improved the classification accuracy.

#### 4.6.3.1 Classification Accuracy of FSR-AIRS2 versus AIRS2

Table 4.8 shows the best average test set accuracies, together with the standard deviations (given in parenthesis), obtained from AIRS2 and FSR-AIRS2 on the benchmark data sets and p-value results of the student t-test comparing the mean accuracies for AIRS2 and FSR-AIRS2.

All experiments utilized 10 fold cross validation and were averaged over 10 runs. The Student’s t-test, as described in section 3.4.7, is used for testing the statistical significance between the mean of the two results.

Table 4.8 shows that the changes made to the AIRS2 algorithm have improved the classification accuracy. Results show that the differences in accuracy for almost all benchmark are significant at the 95% significant level ($\alpha = 0.05$) based on a two-tailed student’s t-test as described in section 3.4.7.

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**Table 4.8: Comparative Average Accuracies**

| Training Set | AIRS2 (STD) | FSR-AIRS2 (STD) | p-value |
|---|---|---|---|
| Balance Scale | 86.83% (3.14) | 94.25% (3.30) | p < 0.05 |
| Breast Cancer Wisconsin (Diagnostic) | 96.17% (2.32) | 100% (0.00) | p < 0.05 |
| Contact Lenses | 82.83% (22.53) | 83.17% (22.79) | 0.92 |
| Ionosphere | 86.04% (4.84) | 100% (0.00) | p < 0.05 |
| Iris | 94.67% (5.36) | 98.00% (6.03) | p < 0.05 |
| Liver Disorders | 59.80% (8.18) | 79.17% (9.49) | p < 0.05 |
| Lung Cancer | 41.83% (26.64) | 96.00% (12.34) | p < 0.05 |
| Pima Indians | 74.41% (5.11) | 99.54% (1.64) | p < 0.05 |
| Statlog (Heart) | 77.48% (8.42) | 84.44% (9.71) | p < 0.05 |
| Statlog (Image Segmentation) | 88.24% (2.35) | 91.05% (9.40) | p < 0.05 |
| Statlog (Vehicle Silhouettes) | 62.56% (4.64) | 79.79% (9.21) | p < 0.05 |
| Sonar, Mines vs. Rocks | 65.60% (10.48) | 98.08% (4.55) | p < 0.05 |
| Vertebral Column_2C | 76.23% (8.70) | 89.36% (6.06) | p < 0.05 |
| Vertebral Column_3C | 72.84% (8.32) | 87.19% (8.08) | p < 0.05 |
| Wisconsin Breast Cancer Data Set (WBCD) (Original) | 96.58% (2.19) | 100% (0.00) | p < 0.05 |

When we compare the mean classification accuracy for the Balance Scale data set obtained with the AIRS2 ($n_1$ =100, *M*=86.83%, *SD*=3.14) to the one obtained with FSR-AIRS2 ($n_2$ =100, *M*=94.5%, *SD*=3.3) *p<.05* the results show that the differences are statistically significant at the 95% significant level (α = 0.05) for this data set. The FSR-AIRS2 achieved significantly higher classification accuracy.

Comparing the mean classification accuracy for the Breast Cancer Wisconsin (Diagnostic) data set obtained with AIRS2 ($n_1$ =100, *M*=96.17%, *SD*=2.32) to the one obtained with the FSR-AIRS2 ($n_2$ =100, *M*=100%, *SD*=0.0) *p*<.05 the results show that the differences are statistically significant at the 95% significant level (α = 0.05) for this data set and the FSR-AIRS2 achieved significantly higher classification accuracy.

In the case of Contact Lenses data set, the comparison of the mean classification accuracy obtained with the AIRS2 ($n_1$ =100, *M*=82.83%, *SD*=22.53) to the one obtained with the FSR-AIRS2 ($n_2$ =100, *M*=83.17%, *SD*=22.79) *p*=.92 shows that the differences

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are statistically insignificant at the 95% significant level (α = 0.05) for this data set. However, the FSR-AIRS2 achieved slightly higher classification accuracy.

When we compare the mean classification accuracy for the Ionosphere data set obtained with the AIRS2 ($n_1$ =100, *M*=86.04%, *SD*=4.84) to the one obtained with the FSR-AIRS2 ($n_2$ =100, *M*=100%, *SD*=0.0) *p*<.05 the results show that the differences are statistically significant at the 95% significant level (α = 0.05) for this data set and the FSR-AIRS2 achieved significantly higher classification accuracy.

Comparing the mean classification accuracy for the Iris data set obtained with the AIRS2 ($n_1$ =100, *M*=94.67%, *SD*=5.36) to the one obtained with the FSR-AIRS2 ($n_2$ =100, *M*=98.00%, *SD*=6.03) *p*<.05 the results show that the differences are statistically significant at the 95% significant level (α = 0.05) for this data set and the FSR-AIRS2 achieved significantly higher classification accuracy.

In the case of Liver Disorders data set, the comparison of the mean classification accuracy obtained with the AIRS2 ($n_1$ =100, *M*=59.8%, *SD*=8.18) to the one obtained with the FSR-AIRS2 ($n_2$ =100, *M*=79.17%, *SD*=9.49) *p*<.05 the results show that the differences are statistically significant at the 95% significant level (α = 0.05) for this data set and the FSR-AIRS2 achieved significantly higher classification accuracy.

When we compare the mean classification accuracy for the Lung Cancer data set obtained with the AIRS2 ($n_1$ =100, *M*=41.83%, *SD*=26.64) to the one obtained with FSR-AIRS2 ($n_2$ =100, *M*=96.00%, *SD*=12.34) *p*<.05 the results show that the differences are statistically significant at the 95% significant level (α = 0.05) for this data set and the FSR-AIRS2 achieved significantly higher classification accuracy.

Comparing the mean classification accuracy for the Pima Indians data set obtained with AIRS2 ($n_1$ =100, *M*=74.41%, *SD*=5.11) to the one obtained with FSR-AIRS2

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($n_2$ =100, *M*=99.54%, *SD*=1.64) *p*<.05 the results show that the differences are statistically significant at the 95% significant level (α = 0.05) for this data set and the FSR-AIRS2 achieved significantly higher classification accuracy.

In the case of Statlog (Heart) data set, the comparison of the mean classification accuracy obtained with the AIRS2 ($n_1$ =100, *M*=77.48%, *SD*=8.42) to the one obtained with the FSR-AIRS2 ($n_2$ =100, *M*=84.44%, *SD*=9.71) *p*<.05 the results show that the differences are statistically significant at the 95% significant level (α = 0.05) for this data set and the FSR-AIRS2 achieved significantly higher classification accuracy.

When we compare the mean classification accuracy for the Statlog (Image Segmentation) data set obtained with the AIRS2 ($n_1$ =100, *M*=88.24%, *SD*=2.35) to the one obtained with the FSR-AIRS2 ($n_2$ =100, *M*=91.05%, *SD*=9.40) *p*<.05 the results show that the differences are statistically significant at the 95% significant level (α = 0.05) for this data set and the FSR-AIRS2 achieved significantly higher classification accuracy.

Comparing the mean classification accuracy for the Statlog (Vehicle Silhouettes) data set obtained with AIRS2 ($n_1$ =100, *M*=62.56%, *SD*=4.64) to the one obtained with the FSR-AIRS2 ($n_2$ =100, *M*=79.79%, *SD*=9.21) *p*<.05 the results show that the differences are statistically significant at the 95% significant level (α = 0.05) for this data set and the FSR-AIRS2 achieved significantly higher classification accuracy.

In the case of Sonar, Mines vs. Rocks data set, the comparison of the mean classification accuracy obtained with the AIRS2 ($n_1$ =100, *M*=65.6%, *SD*=10.48) to the one obtained with the FSR-AIRS2 ($n_2$ =100, *M*=98.08%, *SD*=4.55) *p*<.05 the results show that the differences are statistically significant at the 95% significant level (α = 0.05) for this data set and the FSR-AIRS2 achieved significantly higher classification accuracy.

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When we compare the mean classification accuracy for the Vertebral Column_2C data set obtained with the AIRS2 ($n_1$ =100, *M*=76.23%, *SD*=8.7) to the one obtained with the FSR-AIRS2 ($n_2$ =100, *M*=89.36%, *SD*=6.06) *p*<.05 the results show that the differences are statistically significant at the 95% significant level (α = 0.05) for this data set and the FSR-AIRS2 achieved significantly higher classification accuracy.

Comparing the mean classification accuracy for the Vertebral Column_3C data set obtained with AIRS2 ($n_1$ =100, *M*=72.84%, *SD*=8.32) to the one obtained with the FSR-AIRS2 ($n_2$ =100, *M*=87.19%, *SD*=8.08) *p*<.05 the results show that the differences are statistically significant at the 95% significant level (α = 0.05) for this data set and the FSR-AIRS2 achieved significantly higher classification accuracy.

In the case of Wisconsin Breast Cancer Data Set (WBCD) (Original) data set, the comparison of the mean classification accuracy obtained with the AIRS2 ($n_1$ =100, *M*=96.58%, *SD*=2.19) to the one obtained with the FSR-AIRS2 ($n_2$ =100, *M*=100%, *SD*=0.0) *p*<.05 the results show that the differences are statistically significant at the 95% significant level (α = 0.05) for this data set and the FSR-AIRS2 achieved significantly higher classification accuracy.

In general, since α ≥ p on all bench mark data sets, it can be concluded that modifications introduced in FSR-AIRS2 appear to have positive effect on the classification accuracy of the classifier. The comparison with AIRS2 shows that FSR-AIRS2 has statistically significantly increased the classification accuracy on almost all (14 out of 15) benchmark data sets.

Figure 4.15 illustrates a graphical comparison of classification accuracy on benchmark data sets obtained with AIRS2 and FSR-AIRS2 algorithms. Figure 4.15 shows the superiority of FSR-AIRS2 over AIRS2.

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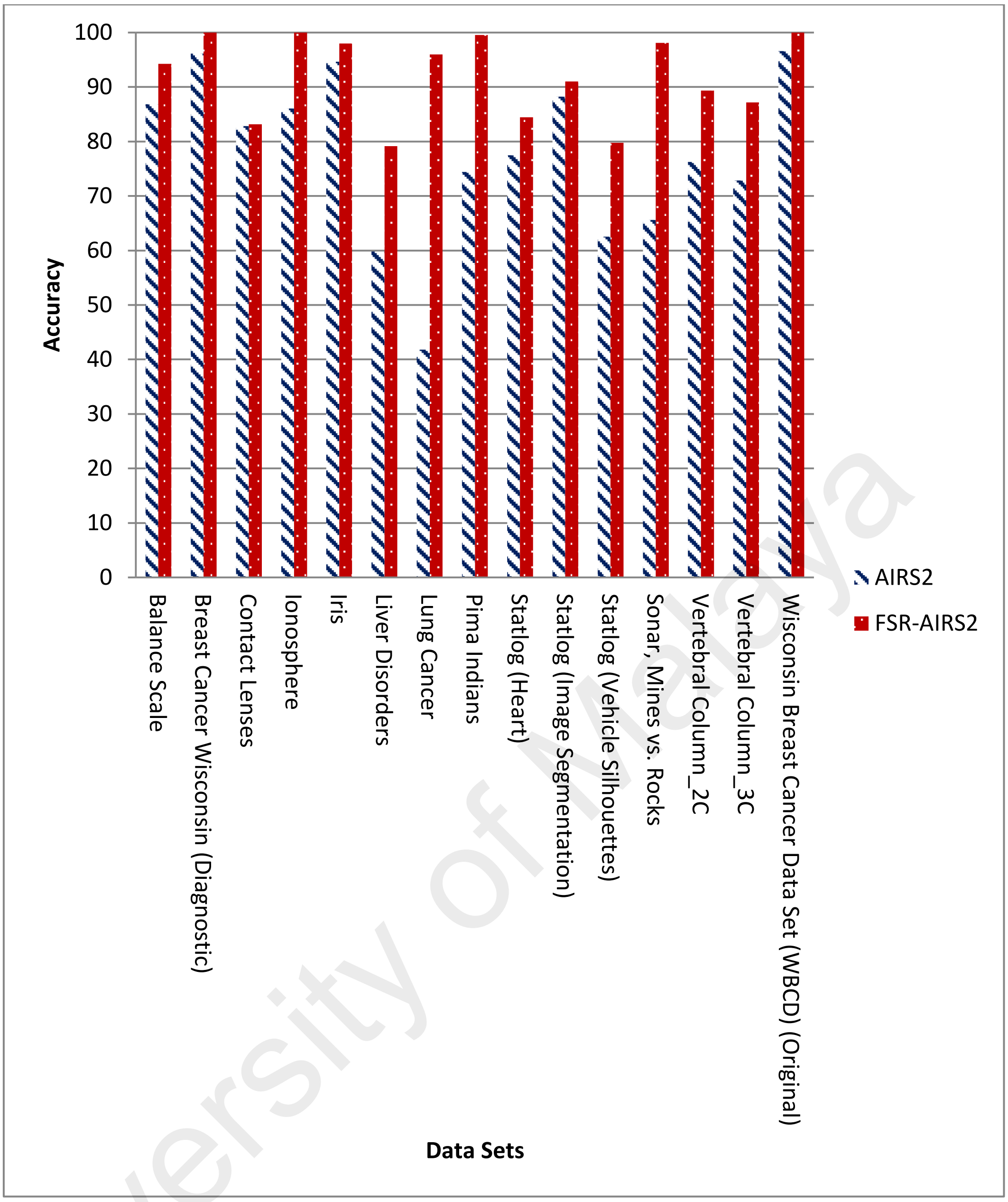

**Figure 4.15: Comparison of Classification Accuracy AIRS2 versus FSR-AIRS2 on benchmark data sets.**

#### 4.6.3.2 Classification Accuracy of FSR-AIRS2 versus Other Well-known Classifiers

Table 4.9 shows the best average test set accuracies, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Balance Scale data set.

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All experiments utilized 10 fold cross validation and were averaged over 10 runs. The top three classifiers for the data set are presented next.

Table 4.9: Comparison of Classification Results of FSR-AIRS2 and Benchmark Classifiers on Balance Scale Data Set

| **FSR-AIRS2** | **1KNN** | **7KNN** | **C4.5/J48** | **CLONALG** | **Immunos99** |
|---|---|---|---|---|---|
| **94.25**<br>(3.30) | 86.72<br>(2.71) | 89.71<br>(2.33) | 77.82<br>(3.42) | 77.46<br>(5.68) | 67.12<br>(9.59) |
| **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** | **SMO** |
| 89.87<br>(1.67) | 89.44<br>(3.29) | 90.69<br>(3.04) | 90.53<br>(1.67) | 86.18<br>(3.76) | 87.57<br>(2.49) |
| **SMO2** | | | | | |
| 91.38<br>(1.93) | | | | | |

Figure 4.16 illustrates a comparative graph of various classifiers on the Balance Scale data set. Results show that for this data set FSR-AIRS2 achieved the highest classification accuracy of 94.25% followed by SMO2 and MLP with 91.38% and 90.69% respectively. These results show that the proposed model compares well with other well-known classifiers on this data set.

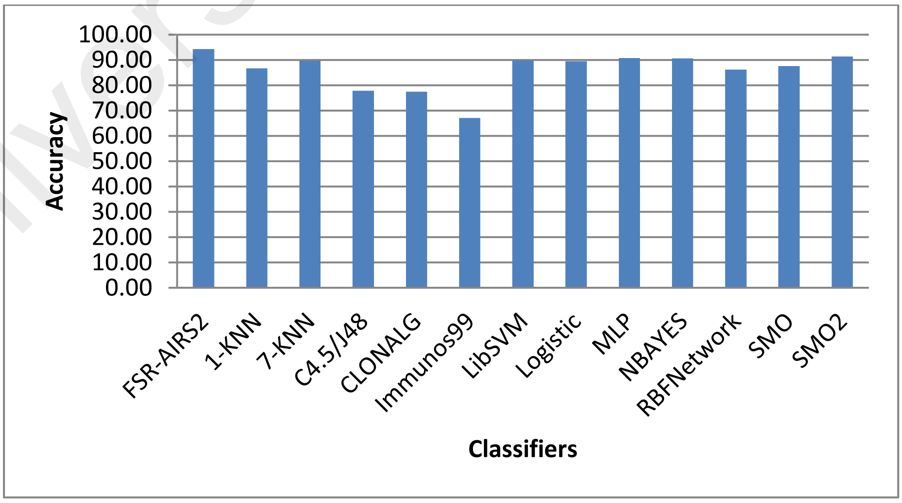

Figure 4.16: Comparison of Balance Scale Accuracy Results

Table 4.10 shows the best average test set accuracies, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known

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classifiers: 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Breast Cancer Wisconsin (Diagnostic) data sets.

All experiments utilized 10 fold cross validation and were averaged over 10 runs. The top three classifiers for the data set are presented next.

**Table 4.10: Comparison of Classification Results of FSR-AIRS2 and Benchmark Classifiers on Breast Cancer Wisconsin (Diagnostic) Data Set**

| **FSR-AIRS2** | **1KNN** | **7KNN** | **C4.5/J48** | **CLONALG** | **Immunos99** |
|---|---|---|---|---|---|
| **100.00**<br>(0.00) | 95.64<br>(2.32) | 97.19<br>(2.10) | 93.27<br>(3.55) | 88.82<br>(4.94) | 87.77<br>(4.10) |
| **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** | **SMO** |
| 62.74<br>(0.70) | 94.46<br>(3.53) | 96.61<br>(2.45) | 93.31<br>(3.30) | 94.22<br>(3.15) | 97.54<br>(1.85) |
| **SMO2** | | | | | |
| 98.00<br>(1.82) | | | | | |

Figure 4.17 illustrates a comparative graph of various classifiers on the Breast Cancer Wisconsin (Diagnostic) data set. Here, the highest accuracy was obtained by FSR-AIRS2 with 100% followed by SMO2 and SMO with 98% and 97.54% respectively.

These results show that the proposed model compares well with other well-known classifiers. These results show that the proposed model performs better or compares well with other well-known classifiers on this data set.

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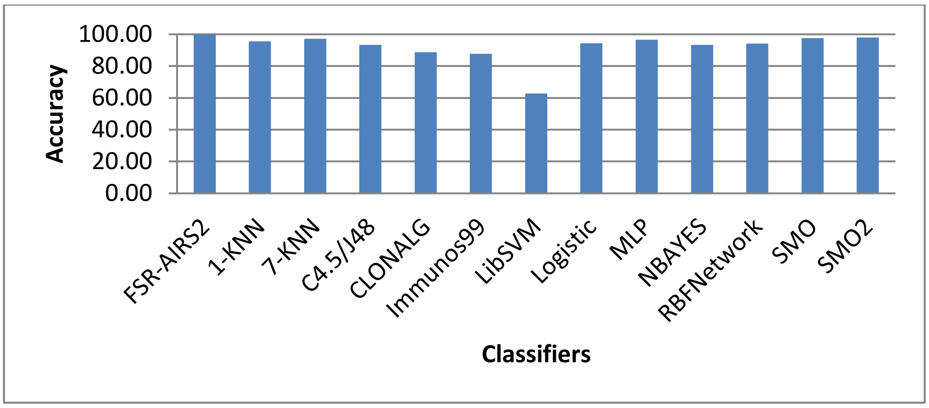

**Figure 4.17: Comparison of Breast Cancer Wisconsin (Diagnostic) Accuracy Results**

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Table 4.11 shows the best average test set accuracies, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Contact Lenses data sets. All experiments utilized 10 fold cross validation and were averaged over 10 runs. The top three classifiers for the data set are presented next.

**Table 4.11: Comparison of Classification Results of FSR-AIRS2 and Benchmark Classifiers on Contact Lenses Data Set**

| **FSR-AIRS2** | **1KNN** | **7KNN** | **C4.5/J48** | **CLONALG** | **Immunos99** |
|---|---|---|---|---|---|
| 83.17<br>(22.79) | 80.50<br>(25.19) | 63.33<br>(23.21) | 83.50<br>(22.42) | 65.67<br>(30.87) | 58.67<br>(31.74) |
| **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** | **SMO** |
| 63.83<br>(23.46) | 67.33<br>(30.05) | 74.50<br>(27.73) | 76.17<br>(25.54) | 76.67<br>(27.22) | 72.50<br>(26.42) |
| **SMO2** | | | | | |
| 76.50<br>(27.74) | | | | | |

Figure 4.18 illustrates a comparative graph of various classifiers on the Contact Lenses data set. C4.5/J48 achieved the highest classification accuracy of 83.50% for this data set, followed by FSR-AIRS2 and 1KNN with 83.17% and 80.5% respectively on the same

data set. The FSR-AIRS2 algorithm performs only slightly worse than the C4.5/J48. These results show that the proposed model compares well with other well-known classifiers.

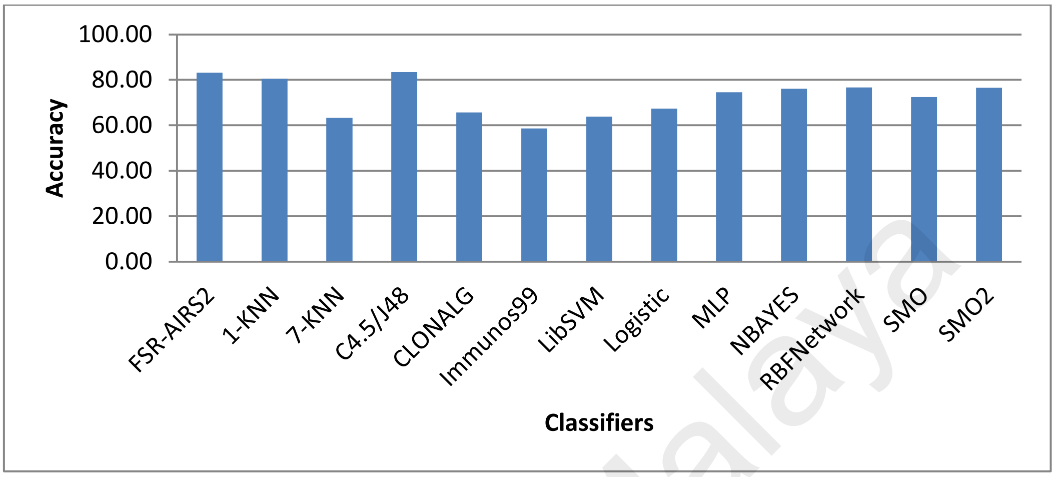

**Figure 4.18: Comparison of Contact Lenses Accuracy Results**

Table 4.12 shows the best average test set accuracies, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Ionosphere data set. All experiments utilized 10 fold cross validation and were averaged over 10 runs. The top three classifiers for the data set are presented next.

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**Table 4.12: Comparison of Classification Results of FSR-AIRS2 and Benchmark Classifiers on Ionosphere Data Set**

| **FSR-AIRS2** | **1KNN** | **7KNN** | **C4.5/J48** | **CLONALG** | **Immunos99** |
|---|---|---|---|---|---|
| **100.00**<br>(0.00) | 87.10<br>(5.12) | 84.30<br>(4.86) | 89.74<br>(4.38) | 77.22<br>(10.65) | 71.17<br>(4.16) |
| **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** | **SMO** |
| 93.05<br>(3.95) | 87.72<br>(5.57) | 91.06<br>(4.86) | 82.17<br>(6.14) | 91.74<br>(4.62) | 88.07<br>(5.32) |
| **SMO2** | | | | | |
| 90.69<br>(4.68) | | | | | |

Figure 4.19 illustrates a comparative graph of various classifiers on the Ionosphere data set. For this data set, the FSR-AIRS2 algorithm achieved the highest classification accuracy of 100% followed by LibSVM and RBF with 93.05% and 91.74% respectively. These results show that the proposed model performs better or compares well with other well-known classifiers on this data set.

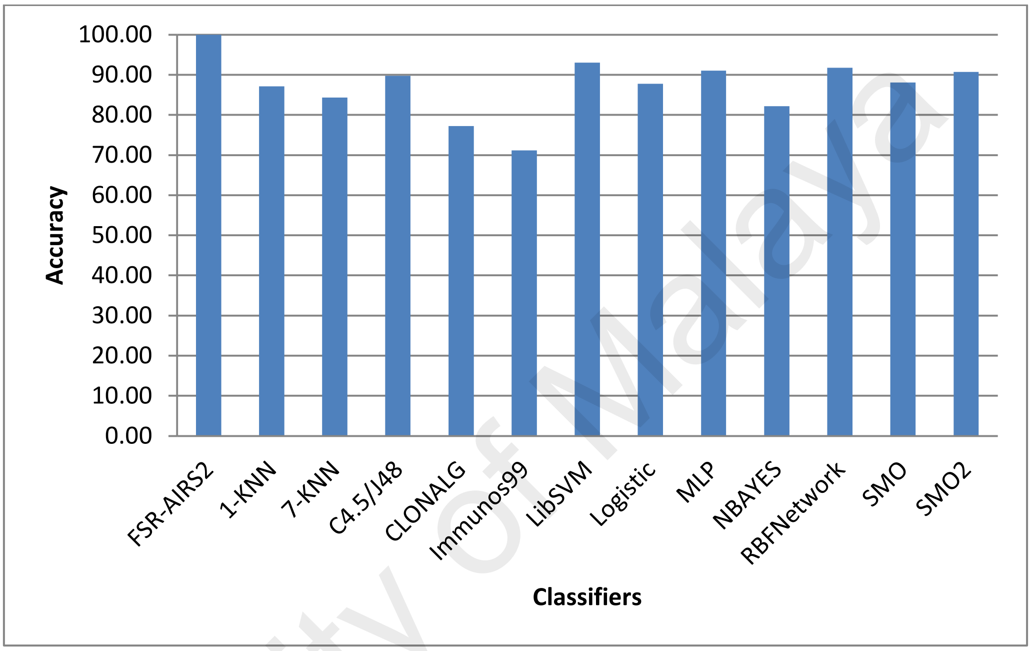

**Figure 4.19: Comparison of Ionosphere Accuracy Results**

Table 4.13 shows the best average test set accuracies, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Iris data set. All experiments utilized 10 fold cross validation and were averaged over 10 runs. The top three classifiers for the data set are presented next.

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**Table 4.13: Comparison of Classification Results of FSR-AIRS2 and Benchmark Classifiers on Iris Data Set**

| FSR-AIRS2 | 1KNN | 7KNN | C4.5/J48 | CLONALG | Immunos99 |
|---|---|---|---|---|---|
| **98.00**<br>(6.03) | 95.40<br>(4.80) | 96.40<br>(4.39) | 94.73<br>(5.30) | 95.00<br>(5.64) | 96.87<br>(4.39) |
| **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** | **SMO** |
| 97.67<br>(3.47) | 97.07<br>(4.77) | 96.93<br>(4.07) | 95.53<br>(5.02) | 96.00<br>(4.44) | 96.27<br>(4.58) |
| **SMO2** | | | | | |
| 95.53<br>(4.93) | | | | | |

Figure 4.20 illustrates a comparative graph of various classifiers on the Iris data set. For the Iris data set, which is also known as an easy classification task (Watkins, 2005), the highest accuracy was achieved by the FSR-AIRS2 algorithm with 98%, followed by LibSVM and Logistic with 97.67% and 97.07% respectively. These results show that the proposed model compares well with other well-known classifiers.

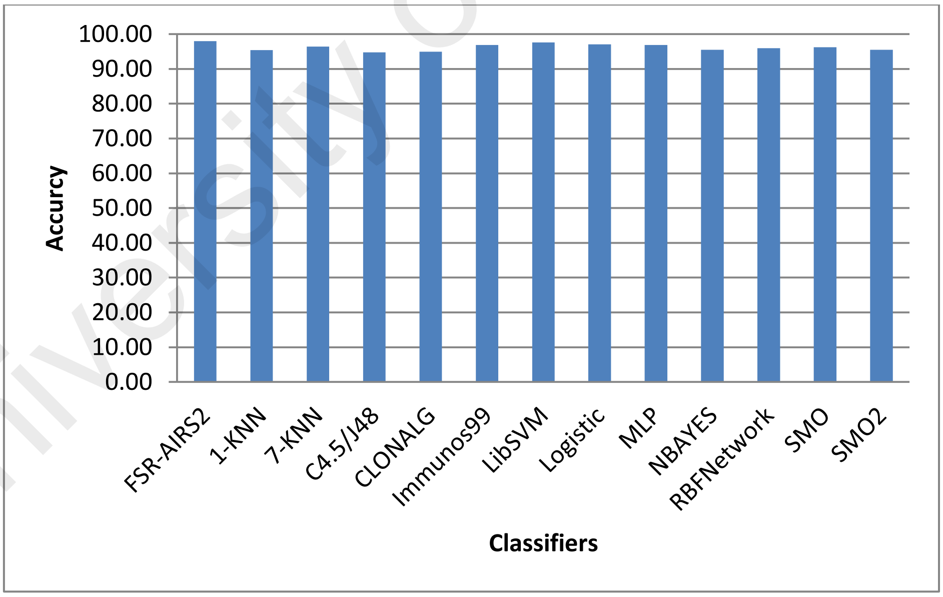

**Figure 4.20: Comparison of Iris Accuracy Results**

Table 4.14 shows the best average test set accuracies, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic,

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MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Liver Disorders data set. All experiments utilized 10 fold cross validation and were averaged over 10 runs. The top three classifiers for the data set are presented next.

**Table 4.14: Comparison of Classification Results of FSR-AIRS2 and Benchmark Classifiers on Liver Disorders Data Set**

| **FSR-AIRS2** | **1KNN** | **7KNN** | **C4.5/J48** | **CLONALG** | **Immunos99** |
|---|---|---|---|---|---|
| **79.17**<br>(9.49) | 62.22<br>(8.18) | 62.63<br>(7.92) | 65.84<br>(7.40) | 56.55<br>(8.19) | 51.34<br>(6.69) |
| **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** | **SMO** |
| 59.37<br>(2.28) | 68.72<br>(7.98) | 57.98<br>(0.84) | 54.89<br>(8.83) | 65.09<br>(8.88) | 57.98<br>(1.26) |
| **SMO2** | | | | | |
| 58.82<br>(3.11) | | | | | |

Figure 4.21 illustrates a comparative graph of various classifiers on the Liver Disorders data set. In case of Liver Disorders, the highest accuracy of 79.17% was obtained with FSR-AIRS2 followed by Logistic and C4.5/J48 with 68.72% and 65.84% respectively. These results show that the proposed model performed better other well-known classifiers on this data set.

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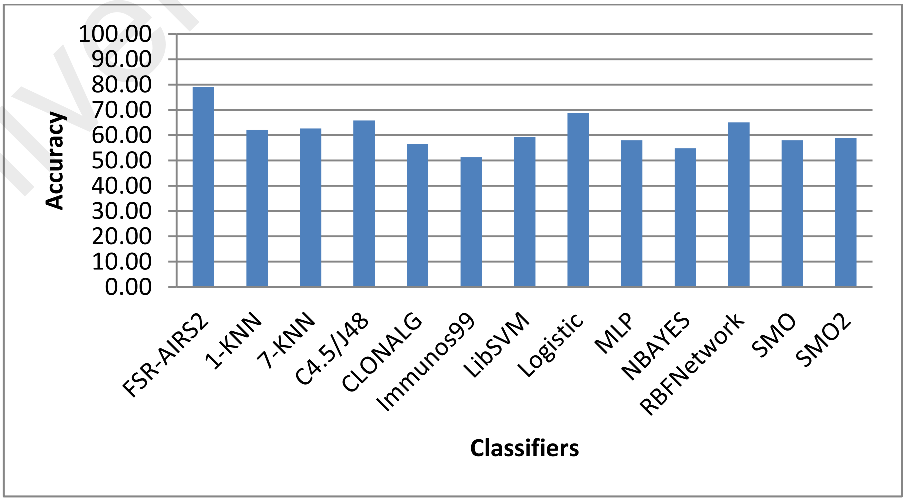

**Figure 4.21: Comparison of Liver Disorders Accuracy Results**

Table 4.15 shows the best average test set accuracies, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Lung Cancer data set.

All experiments utilized 10 fold cross validation and were averaged over 10 runs. The top three classifiers for the data set are presented next.

**Table 4.15: Comparison of Classification Results of FSR-AIRS2 and Benchmark Classifiers on Lung Cancer Data Set**

| **FSR-AIRS2** | **1KNN** | **7KNN** | **C4.5/J48** | **CLONALG** | **Immunos99** |
|---|---|---|---|---|---|
| **96.00**<br>(12.34) | 49.42<br>(25.41) | 41.75<br>(28.36) | 44.67<br>(24.52) | 52.83<br>(24.82) | 47.08<br>(25.50) |
| **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** | **SMO** |
| 51.17<br>(21.29) | 47.67<br>(25.63) | 33.92<br>(10.94) | 57.75<br>(26.96) | 54.58<br>(24.63) | 44.58<br>(26.52) |
| **SMO2** | | | | | |
| 46.33<br>(27.76) | | | | | |

Figure 4.22 illustrates a comparative graph of various classifiers on the Lung Cancer data set. For this data set, the FSR-AIRS2 algorithm achieved the highest classification accuracy of 96% followed by Naïve Bayes and RBF with 57.75% and 54.58% respectively.

These results show that the proposed model performs much better than other well-known classifiers on this data set.

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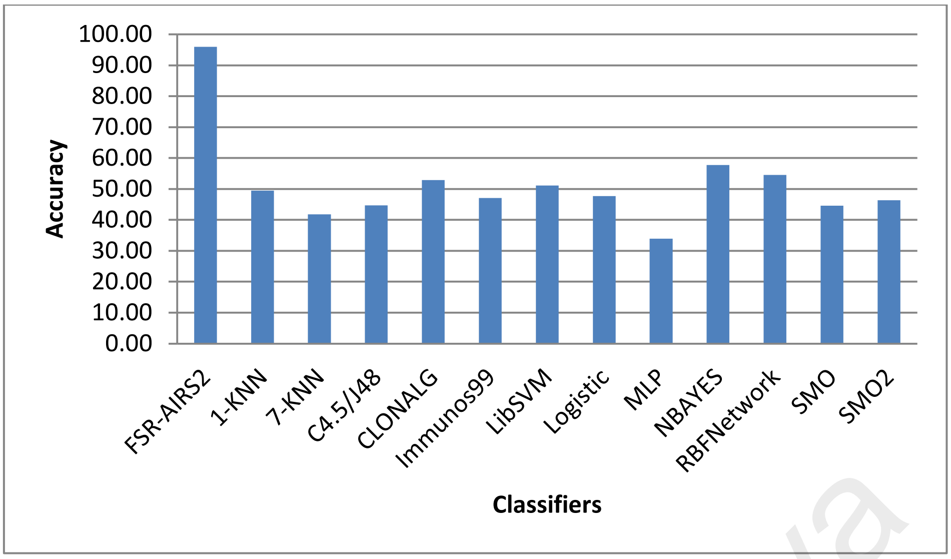

**Figure 4.22: Comparison of Lung Cancer Accuracy Results**

Table 4.16 shows the best average test set accuracies, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Pima Indians data set. All experiments utilized 10 fold cross validation and were averaged over 10 runs. The top three classifiers for the data set are presented next.

**Table 4.16: Comparison of Classification Results of FSR-AIRS2 and Benchmark Classifiers on Pima Indians Data Set**

| **FSR-AIRS2** | **1KNN** | **7KNN** | **C4.5/J48** | **CLONALG** | **Immunos99** |
|---|---|---|---|---|---|
| **99.54**<br>(1.64) | 70.62<br>(4.67) | 74.45<br>(4.66) | 74.49<br>(5.24) | 67.67<br>(5.68) | 62.74<br>(5.19) |
| **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** | **SMO** |
| 65.11<br>(0.34) | 77.47<br>(4.39) | 74.75<br>(4.87) | 75.75<br>(5.32) | 74.06<br>(4.93) | 76.80<br>(4.54) |
| **SMO2** | | | | | |
| 77.32<br>(4.46) | | | | | |

Figure 4.23 illustrates a comparative graph of various classifiers on the Pima Indians data set. The FSR-AIRS2 algorithm obtained an accuracy of 99.54% for this data set which is the highest, followed by Logistic and SMO2 with accuracies of 77.47% and

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77.32% respectively. These results show that the proposed model performs much better than other well-known classifiers on this data set.

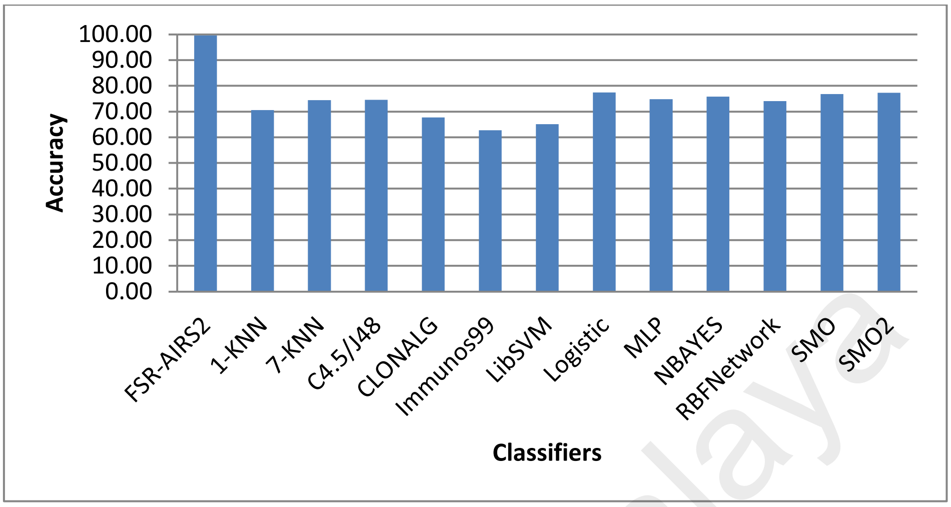

**Figure 4.23: Comparison of Pima Indians Accuracy Results**

Table 4.17 shows the best average test set accuracies, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Statlog (Heart) data set. All experiments utilized 10 fold cross validation and were averaged over 10 runs. The top three classifiers for the data set are presented next.

**Table 4.17: Comparison of Classification Results of FSR-AIRS2 and Benchmark Classifiers on Statlog (Heart) Data Set**

| **FSR-AIRS2** | **1KNN** | **7KNN** | **C4.5/J48** | **CLONALG** | **Immunos99** |
|---|---|---|---|---|---|
| **84.44**<br>(9.71) | 76.15<br>(8.46) | 80.81<br>(6.73) | 78.15<br>(7.42) | 63.26<br>(7.66) | 65.26<br>(8.61) |
| **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** | **SMO** |
| 55.93<br>(1.12) | 83.67<br>(6.43) | 55.56<br>(0.00) | 83.59<br>(5.98) | 83.11<br>(6.50) | 83.89<br>(6.62) |
| **SMO2** | | | | | |
| 81.22<br>(6.62) | | | | | |

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Figure 4.24 illustrates a comparative graph of various classifiers on the Statlog (Heart) data set. For the Statlog (Heart) data set the FSR-AIRS2 algorithm achieved the highest classification accuracy of 84.44% followed by SMO and Logistic with 83.89% and 83.67% respectively. These results show that the proposed model performs comparable with other well-known classifiers on this data set.

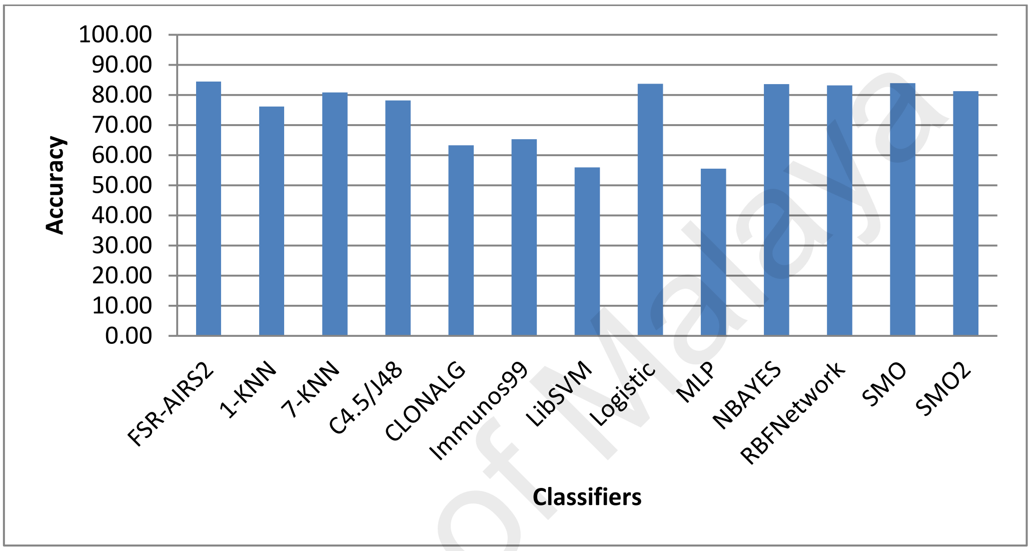

**Figure 4.24: Comparison of Statlog (Heart) Accuracy Results**

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Table 4.18 shows the best average test set accuracies, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Statlog (Image Segmentation) data set.

All experiments utilized 10 fold cross validation and were averaged over 10 runs. The top three classifiers for the data set are presented next.

**Table 4.18: Comparison of Classification Results of FSR-AIRS2 and Benchmark Classifiers on Statlog (Image Segmentation) Data Set**

| FSR-AIRS2 | 1KNN | 7KNN | C4.5/J48 | CLONALG | Immunos99 |
|---|---|---|---|---|---|
| 91.05 (9.40) | **97.15** (1.11) | 94.89 (1.37) | 96.79 (1.29) | 57.46 (6.11) | 54.17 (2.40) |
| **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** | **SMO** |
| 63.98 (3.47) | 95.61 (1.50) | 96.18 (1.17) | 80.17 (2.12) | 87.32 (2.15) | 92.92 (1.52) |
| **SMO2** | | | | | |
| 94.68 (1.50) | | | | | |

Figure 4.25 illustrates a comparative graph of various classifiers on the Statlog (Image Segmentation) data set. For this data set, the highest accuracy was obtained by 1KNN with 97.15% followed by C4.5/J48 and MLP with 96.79% and 96.18% respectively. These results show that the proposed model performs comparable with other well-known classifiers on this data set.

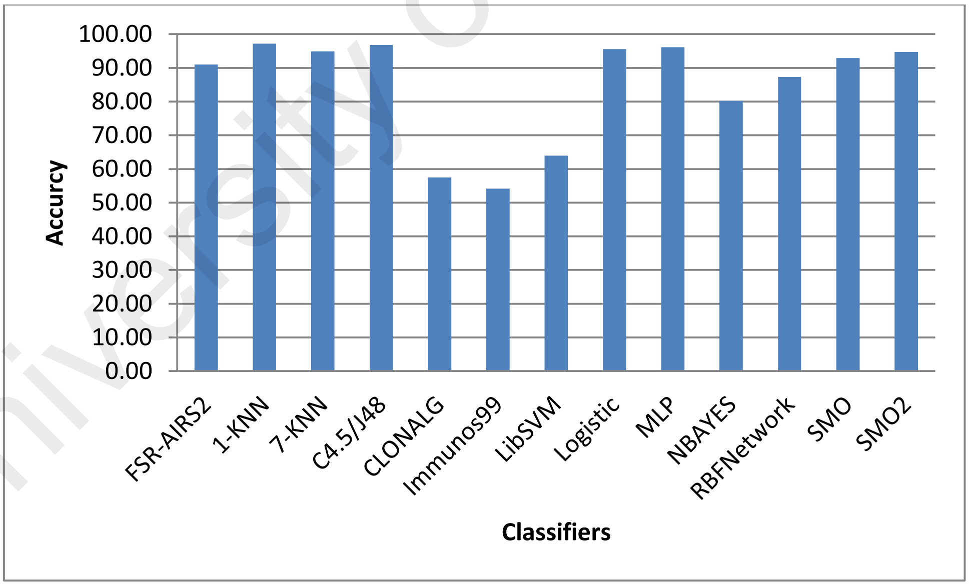

**Figure 4.25: Comparison of Statlog (Image Segmentation) Accuracy Results**

Table 4.19 shows the best average test set accuracies, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Statlog (Vehicle Silhouettes)

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data set. All experiments utilized 10 fold cross validation and were averaged over 10 runs. The top three classifiers for the data set are presented next.

**Table 4.19: Comparison of Classification Results of FSR-AIRS2 and Benchmark Classifiers on Statlog (Vehicle Silhouettes) Data Set**

| **FSR-AIRS2** | **1KNN** | **7KNN** | **C4.5/J48** | **CLONALG** | **Immunos99** |
|---|---|---|---|---|---|
| 79.79 (9.21) | 69.59 (3.77) | 70.55 (4.01) | 72.28 (4.32) | 42.22 (6.55) | 46.42 (4.98) |
| **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** | **SMO** |
| 30.06 (2.46) | 79.80 (4.03) | **81.11** (3.84) | 44.68 (4.59) | 65.34 (4.32) | 74.08 (3.82) |
| **SMO2** | | | | | |
| 80.26 (3.69) | | | | | |

Figure 4.26 illustrates a comparative graph of various classifiers on the Statlog (Vehicle Silhouettes) data set. The MLP obtained the highest accuracy of 81.11% for this data set, followed by SMO2 and Logistic with accuracies of 80.26% and 79.8% respectively. It should be noted that the MLP algorithm performs only slightly better than the FSR-AIRS2 on this data set.

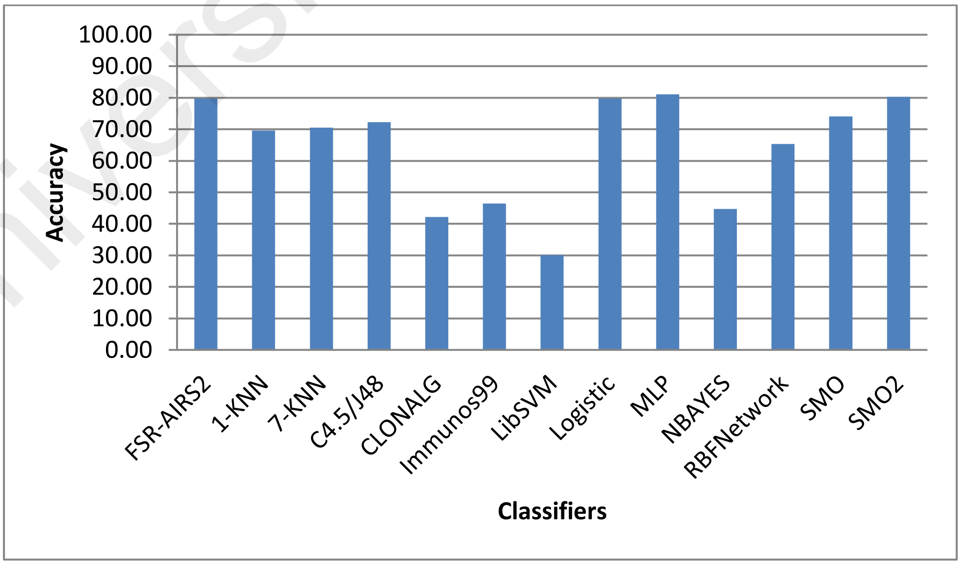

**Figure 4.26: Comparison of Statlog (Vehicle Silhouettes) Accuracy Results**

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Table 4.20 shows the best average test set accuracies, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Sonar, Mines vs. Rocks data set.

All experiments utilized 10 fold cross validation and were averaged over 10 runs. The top three classifiers for the data set are presented next.

**Table 4.20: Comparison of Classification Results of FSR-AIRS2 and Benchmark Classifiers on Sonar, Mines vs. Rocks Data Set**

| **FSR-AIRS2** | **1KNN** | **7KNN** | **C4.5/J48** | **CLONALG** | **Immunos99** |
|---|---|---|---|---|---|
| **98.08** (4.55) | 86.17 (8.45) | 79.10 (8.98) | 73.61 (9.34) | 63.41 (9.95) | 61.25 (9.60) |
| **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** | **SMO** |
| 64.99 (7.66) | 72.47 (8.90) | 81.61 (8.66) | 67.71 (8.66) | 72.62 (9.91) | 76.60 (8.27) |
| **SMO2** | | | | | |
| 83.80 (7.84) | | | | | |

Figure 4.27 illustrates a comparative graph of various classifiers on the Sonar, Mines vs. Rocks data set. For this data set, the FSR-AIRS2 algorithm achieved the highest classification accuracy of 98.08% followed by 1KNN and SMO2 with 86.17% and 83.8% respectively.

These results show that the proposed model performs much better than other well-known classifiers on this data set.

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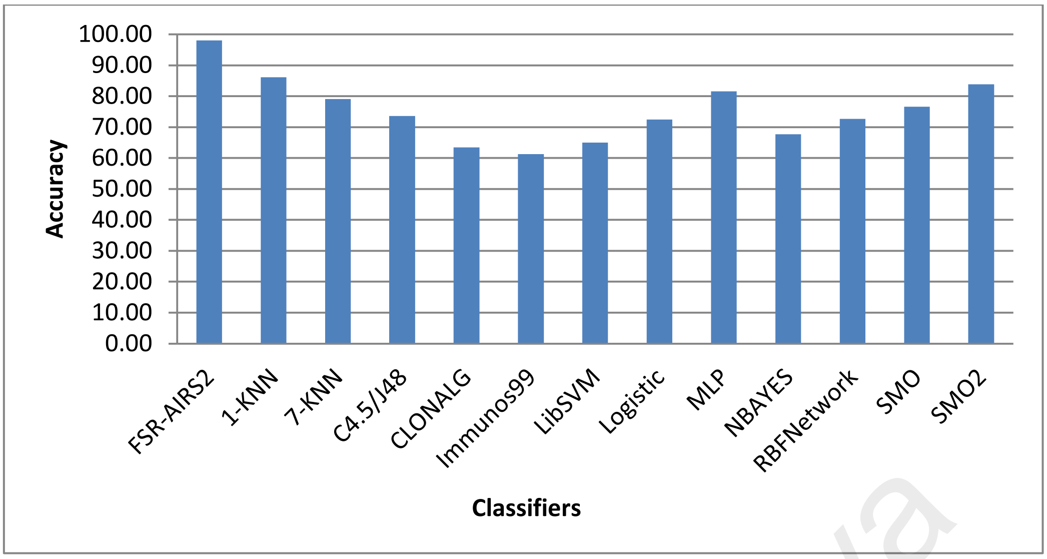

**Figure 4.27: Comparison of Sonar, Mines vs. Rocks Accuracy Results**

Table 4.21 shows the best average test set accuracies, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Vertebral Column_2C data set. All experiments utilized 10 fold cross validation and were averaged over 10 runs. The top three classifiers for the data set are presented next.

**Table 4.21: Comparison of Classification Results of FSR-AIRS2 and Benchmark Classifiers on Vertebral Column_2C Data Set**

| **FSR-AIRS2** | **1KNN** | **7KNN** | **C4.5/J48** | **CLONALG** | **Immunos99** |
|---|---|---|---|---|---|
| **89.36**<br>(6.06) | 81.06<br>(6.18) | 78.19<br>(6.27) | 81.39<br>(6.38) | 75.19<br>(7.82) | 72.97<br>(7.03) |
| **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** | **SMO** |
| 67.74<br>(0.00) | 85.06<br>(5.85) | 85.00<br>(6.24) | 77.87<br>(6.82) | 80.29<br>(6.72) | 78.90<br>(6.06) |
| **SMO2** | | | | | |
| 79.39<br>(6.05) | | | | | |

Figure 4.28 illustrates a comparative graph of various classifiers on the Vertebral Column_2C data set. The FSR-AIRS2 algorithm achieved the highest classification accuracy of 89.36% followed by Logistic and MLP with 85.06% and 85% respectively.

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These results show that the proposed model performs better or is comparable with other well-known classifiers on this data set.

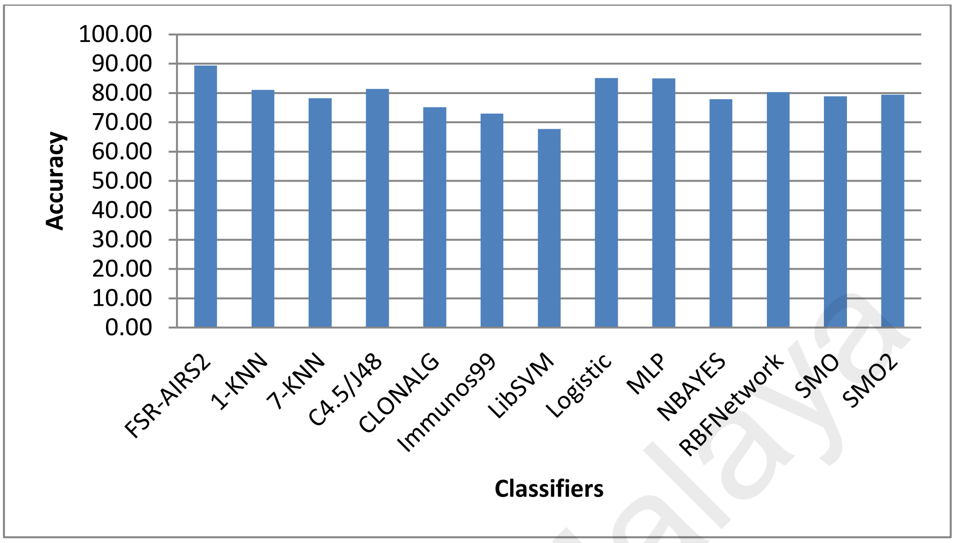

**Figure 4.28: Comparison of Vertebral Column_2C Accuracy Results**

Table 4.22 shows the best average test set accuracies, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Vertebral Column_3C data set. All experiments utilized 10 fold cross validation and were averaged over 10 runs. The top three classifiers for the data set are presented next.

**Table 4.22: Comparison of Classification Results of FSR-AIRS2 and Benchmark Classifiers on Vertebral Column_3C Data Set**

| FSR-AIRS2 | 1KNN | 7KNN | C4.5/J48 | CLONALG | Immunos99 |
|---|---|---|---|---|---|
| **87.19**<br>(8.08) | 76.74<br>(6.47) | 75.13<br>(7.50) | 81.55<br>(6.47) | 73.32<br>(7.16) | 73.06<br>(8.52) |
| **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** | **SMO** |
| 48.39<br>(0.00) | 85.94<br>(5.01) | 84.97<br>(5.77) | 82.58<br>(6.48) | 83.00<br>(6.27) | 76.10<br>(6.85) |
| **SMO2** | | | | | |
| 77.58<br>(7.08) | | | | | |

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Figure 4.29 illustrates a comparative graph of various classifiers on the Vertebral Column_3C data set. For this data set the FSR-AIRS2 algorithm achieved the highest classification accuracy of 87.19% followed by Logistic and MLP with 85.94% and 84.97% respectively.

These results show that the proposed model performs better or is comparable with other well-known classifiers on this data set.

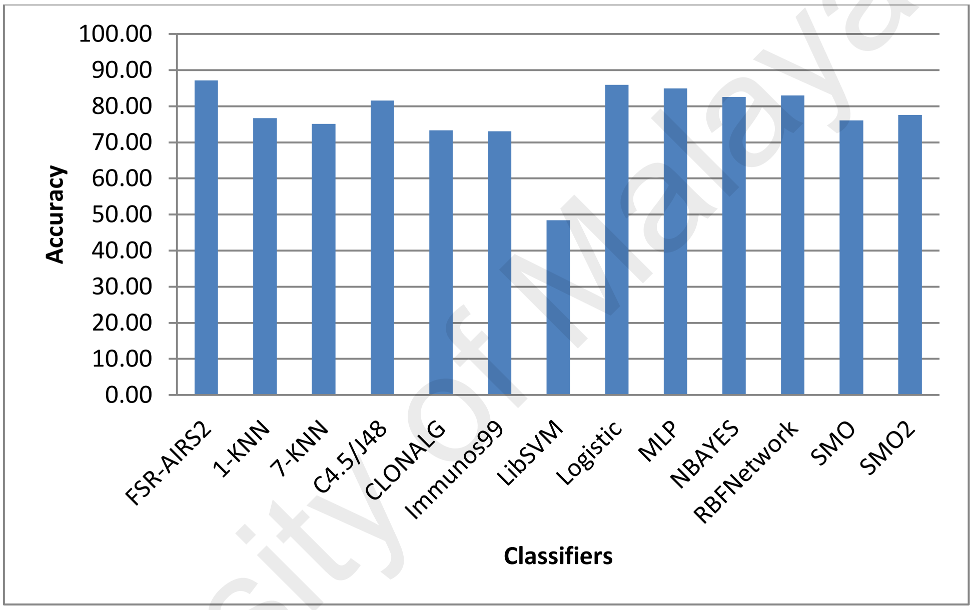

**Figure 4.29: Comparison of Vertebral Column_3C Accuracy Results**

Table 4.23 shows the best average test set accuracies, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Wisconsin Breast Cancer Data set (WBCD) (Original) data set.

All experiments utilized 10 fold cross validation and were averaged over 10 runs. The top three classifiers for the data set are presented next.

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**Table 4.23: Comparison of Classification Results of FSR-AIRS2 and Benchmark Classifiers on Wisconsin Breast Cancer Data set (WBCD) (Original) Data Set**

| FSR-AIRS2 | 1KNN | 7KNN | C4.5/J48 | CLONALG | Immunos99 |
|---|---|---|---|---|---|
| **100.00**<br>(0.00) | 95.18<br>(2.61) | 96.80<br>(2.06) | 94.58<br>(2.49) | 61.51<br>(6.84) | 67.90<br>(1.99) |
| **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** | **SMO** |
| 66.27<br>(0.98) | 96.48<br>(2.17) | 95.67<br>(2.21) | 95.99<br>(2.25) | 95.91<br>(2.48) | 96.61<br>(2.02) |
| **SMO2** | | | | | |
| 96.47<br>(2.20) | | | | | |

Figure 4.30 illustrates a comparative graph of various classifiers on the Wisconsin Breast Cancer Data Set (WBCD) (Original)  data set. In case of this data set the highest classification accuracy of 100% was obtained with the FSR-AIRS2 algorithm followed by 7KNN and SMO with 96.8% and 96.61% respectively. These results show that the proposed model performs better or is comparable with other well-known classifiers on this data set.

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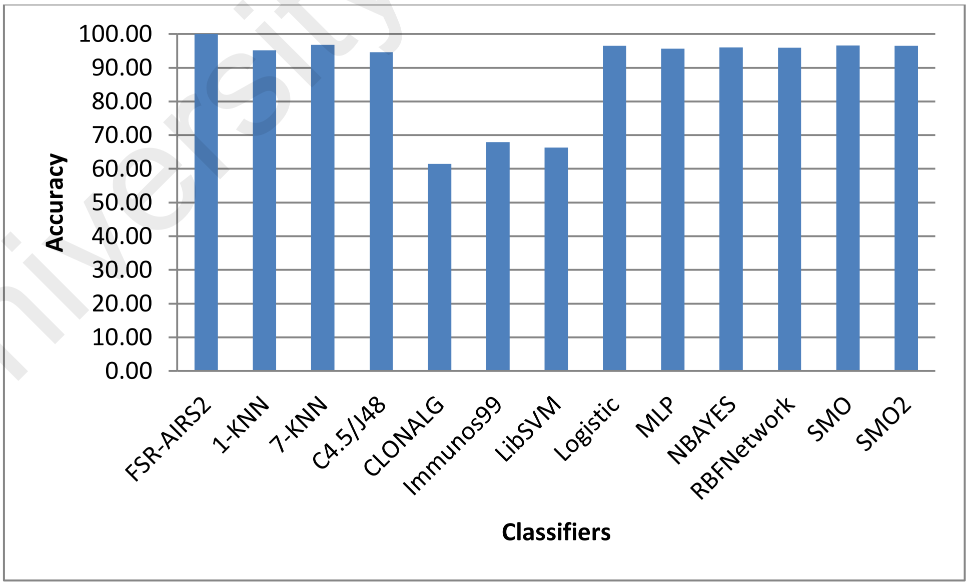

**Figure 4.30: Comparison of Wisconsin Breast Cancer Data Set (WBCD) (Original) Accuracy Results**

Results show that FSR-AIRS2 has achieved higher classification accuracy in 12 out of 15 cases and in one case it obtained the second highest accuracy on the benchmark data sets. Results show that the FSR-AIRS2 algorithm performs comparatively well in relation to other classifiers.

The results also suggest that the changes made in the proposed algorithm has contributed toward the power of AIRS2, as Goodman et al. said major source of power of the AIRS must lie in the way how it manages its memory cell population (Goodman et al., 2003). Changes to resource allocation and resource competition mechanism on one side and using a strong classifier such as SVM on the other hand have given the FSR-AIRS2 this strength.

#### 4.6.3.3 Data Reduction

One important feature of AIRS2 is its capability to perform the classification task with the reduced number of data instances. Thus, it is essential to validate the performance of the proposed algorithm.

(a) ***Comparison of Evolved Memory Cells through AIRS2 and FRA-AIRS2***

The goal of this section is to evaluate the application of the FRA method (introduced in section 4.2) and verify whether or not this method improves the performance of the AIRS2.

Table 4.24 presents the total number of instances, the best average test set evolved memory cells, together with the standard deviations (given in parenthesis) and p-values obtained from AIRS2 and FRA-AIRS2 on the benchmark data sets. All experiments utilized 10 fold cross validation and were averaged over 10 runs. The two algorithms were applied against fifteen data sets and the results are presented next. The results show the number of memory cells (recognizer records) that were used for the classification. The Goal of this evaluation is to verify which algorithm could do the classification task with

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fewer numbers of memory cells (that is: number of records that are used for classification).

**Table 4.24: Comparison of Memory Cells Evolved with AIRS2 and FRA-AIRS2**

| Training Set | Total Instances | AIRS2 (STD) | FRA-AIRS2 (STD) | p-value |
|---|---|---|---|---|
| Balance Scale | 625 | 248.68 (9.30) | 285.23 (9.79) | $p < 0.05$ |
| Breast Cancer Wisconsin (Diagnostic) | 569 | 237.09 (10.47) | 80.56 (5.60) | $p < 0.05$ |
| Contact Lenses | 24 | 21.28 (0.75) | 21.3 (0.75) | 0.77 |
| Ionosphere | 351 | 140.78 (6.53) | 55.75 (7.16) | $p < 0.05$ |
| Iris | 150 | 47.11 (2.84) | 42.36 (2.47) | $p < 0.05$ |
| Liver Disorders | 345 | 196.7 (5.84) | 102.95 (6.74) | $p < 0.05$ |
| Lung Cancer | 32 | 15.66 (2.09) | 20.51 (2.09) | $p < 0.05$ |
| Pima Indians | 768 | 378.04 (11.24) | 183.67 (11.17) | $p < 0.05$ |
| Statlog (Heart) | 270 | 50.37 (6.21) | 51.96 (6.02) | $p < 0.05$ |
| Statlog (Image Segmentation) | 2310 | 219.79 (11.71) | 107.77 (7.81) | $p < 0.05$ |
| Statlog (Vehicle Silhouettes) | 846 | 354.88 (12.30) | 132.94 (7.89) | $p < 0.05$ |
| Sonar, Mines vs. Rocks | 208 | 143.33 (8.76) | 61.69 (5.83) | $p < 0.05$ |
| Vertebral Column_2C | 310 | 151.75 (6.28) | 102.32 (9.26) | $p < 0.05$ |
| Vertebral Column_3C | 310 | 153.52 (6.43) | 104.51 (8.34) | $p < 0.05$ |
| Wisconsin Breast Cancer Data Set (WBCD) (Original) | 699 | 227.82 (6.60) | 214.74 (6.67) | $p < 0.05$ |

When we compare the mean evolved memory cells for the Balance Scale data set obtained from the AIRS2 ($n_1$ =100, *M*=248.68, *SD*=9.30) to the one obtained with the FRA-AIRS2 ($n_2$ =100, *M*=258.23, *SD*=9.79) the results show that the differences in average evolved memory cells are significant at the 95% significant level (α = 0.05) for this data set using student's t-test as described in section 3.4.7 The results suggest that applying the FRA method could reduce the size of data set that is needed for classification for this data set, however the AIRS2 performed slightly better.

When we compare the mean evolved memory cells for the Breast Cancer Wisconsin (Diagnostic) data set obtained from the AIRS2 ($n_1$ =100, *M*=237.09, *SD*=10.47) to the one obtained from the FRA-AIRS2 ($n_2$ =100, *M*=80.56, *SD*=5.60) the results show that

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the difference in average evolved memory cells is significant at the 95% significant level (α = 0.05) for this data set using student's t-test. The difference suggests that applying the FRA-AIRS2 algorithm causes a decrease of number of evolved memory cells and thus it can reduce the number of data sets needed for the classification; furthermore, it has also performed better than the AIRS2.

When we compare the mean evolved memory cells for the Contact Lenses data set obtained from the AIRS2 ($n_1$ =100, *M*=21.28, *SD*=0.75) to the one obtained with the FRA-AIRS2 ($n_2$ =100, *M*=21.3, *SD*=.75) the results show that the differences in average evolved memory cells are insignificant at the 95% significant level (α = 0.05) for this data set using student's t-test. However the difference is a small increase. Thus applying the FRA-AIRS2 algorithm on this data set reduced the number of data set needed for classification, but the AIRS2 performed slightly better.

Comparing the results for Ionosphere data set, the mean evolved memory cell obtained with AIRS2 ($n_1$ =100, *M*=140.78, *SD*=6.53) to the one obtained from the FRA-AIRS2 ($n_2$ =100, *M*=55.75, *SD*=7.16) the results show that the differences in average evolved memory cells are statistically significant at the 95% significant level (α = 0.05) using the student's t-test. The FRA-AIRS2 algorithm could reduce the data set that is needed for the classification task and its data reduction performance was better than the AIRS2.

Comparing the results for Iris data set, the mean evolved memory cell obtained with AIRS2 ($n_1$ =100, *M*=47.11, *SD*=2.84) to the one obtained from the FRA-AIRS2 ($n_2$ =100, *M*=42.36, *SD*=2.47) the results show that the differences in average evolved memory cells are statistically significant at the 95% significant level (α = 0.05) using the student's t-test. The FRA-AIRS2 algorithm was able to reduce the data set that is needed for classification task and its data reduction performance was better than AIRS2.

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When we compare the mean evolved memory cells for the Liver Disorders data set obtained from the AIRS2 ($n_1$ =100, *M*=196.7, *SD*=5.84) to the one obtained with the FRA-AIRS2 ($n_2$ =100, *M*=102.95, *SD*=6.74) the results show that the difference in average evolved memory cells is statistically significant at the 95% significant level (α = 0.05) for this data set using student's t-test. The difference suggests that applying the FRA-AIRS2 algorithm causes a decrease of evolved memory cells. The FRA-AIRS2 algorithm was able to reduce the data set that is needed for classification task and its data reduction performance was better than the AIRS2.

Comparing the results for Lung Cancer data set, the mean evolved memory cell obtained with the AIRS2 ($n_1$ =100, *M*=15.66, *SD*=2.09) to the one obtained from the FRA-AIRS2 ($n_2$ =100, *M*=20.51, *SD*=2.09) the results show that the differences in average evolved memory cells are statistically significant at the 95% significant level (α = 0.05) using the student's t-test. Results show that applying the FRA-AIRS2 algorithm on this data set reduced the number of data set needed for classification, however in comparison with the AIRS2, the FRA-AIRS2 algorithm increased the number of evolved memory cells and AIRS2 performed slightly better.

When we compare the mean evolved memory cells for the Pima Indians data set obtained from the AIRS2 ($n_1$ =100, *M*=378.04, *SD*=11.24) to the one obtained with the FRA-AIRS2 ($n_2$ =100, *M*=183.67, *SD*=11.17) the results show that the difference in average evolved memory cells is statistically significant at the 95% significant level (α = 0.05) for this data set using student's t-test. The results show that applying the FRA-AIRS2 method decreased the number of evolved memory cells for this data set, and it performed better than the AIRS2.

Comparing the results for Statlog (Heart) data set, the mean evolved memory cell obtained with the AIRS2 ($n_1$ =100, *M*=50.37, *SD*=6.21) to the one obtained from the

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FRA-AIRS2 ($n_2$ =100, *M*=51.96, *SD*=6.02) the results show that the differences in average evolved memory cells are statistically significant at the 95% significant level (α = 0.05) using the student's t-test. Results show that the FRA-AIRS2 algorithm decreased the number of evolved memory cells for this data set and its data reduction capability was better than that of the AIRS2.

When we compare the mean evolved memory cells for the Statlog (Image Segmentation) data set obtained from the AIRS2 ($n_1$ =100, *M*=219.79, *SD*=11.71) to the one obtained with the FRA-AIRS2 ($n_2$ =100, *M*=107.77, *SD*=7.81) the results show that the difference in average evolved memory cells is statistically significant at the 95% significant level (α = 0.05) for this data set using student's t-test. The results show that applying the FRA-AIRS2 algorithm decreased the number of evolved memory cells for this data set, and it performed better than the AIRS2.

Comparing the results for the Statlog (Vehicle Silhouettes) data set, the mean evolved memory cell obtained with the AIRS2 ($n_1$ =100, *M*=354.88, *SD*=12.30) to the one obtained from the FRA-AIRS2 ($n_2$ =100, *M*=132.94, *SD*=7.89) the results show that the differences in average evolved memory cells are statistically significant at the 95% significant level (α = 0.05) using the student's t-test. Results show that applying the FRA-AIRS2 algorithm on this data set reduced the number of data set needed for classification, and it performed better than the AIRS2.

When we compare the mean evolved memory cells for the Sonar data set obtained from the AIRS2 ($n_1$ =100, *M*=143.33, *SD*=8.76) to the one obtained with the FRA-AIRS2 ($n_2$ =100, *M*=61.69, *SD*=5.83) the results show that the difference in average evolved memory cells is statistically significant at the 95% significant level (α = 0.05) for this data set using student's t-test. The results show that applying the FRA-AIRS2 algorithm

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decreased the number of evolved memory cells for this data set, and it performed better than the AIRS2.

Comparing the results for the Vertebral Column_2C data set, the mean evolved memory cell obtained with the AIRS2 ($n_1$ =100, *M*=151.75, *SD*=6.28) to the one obtained from the FRA-AIRS2 ($n_2$ =100, *M*=102.32, *SD*=9.26) the results show that the differences in average evolved memory cells are statistically significant at the 95% significant level (α = 0.05) using the student's t-test. Results show that applying the FRA-AIRS2 algorithm on this data set reduced the number of data set needed for classification, and it performed better than the AIRS2.

When we compare the mean evolved memory cells for the Vertebral Column_3C data set obtained from the AIRS2 ($n_1$ =100, *M*=153.52, *SD*=6.43) to the one obtained with the FRA-AIRS2 ($n_2$ =100, *M*=104.51, *SD*=8.34) the results show that the difference in average evolved memory cells is statistically significant at the 95% significant level (α = 0.05) for this data set using student's t-test. The results show that applying the FRA-AIRS2 algorithm decreased the number of evolved memory cells for this data set, and it performed better than the AIRS2.

Comparing the results for the Vertebral Wisconsin Breast Cancer Data Set (WBCD) (Original) data set, the mean evolved memory cell obtained with the AIRS2 ($n_1$ =100, *M*=227.82, *SD*=6.60) to the one obtained from the FRA-AIRS2 ($n_2$ =100, *M*=214.74, *SD*=6.67) the results show that the differences in average evolved memory cells are statistically significant at the 95% significant level (α = 0.05) using the student's t-test. Results show that applying the FRA-AIRS2 algorithm on this data set reduced the number of data set needed for classification, and it performed better than the AIRS2.

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Figure 4.31 illustrates a graphical comparison of evolved memory cells obtained with AIRS2 and FRA-ARIS2 algorithms on benchmark data sets.

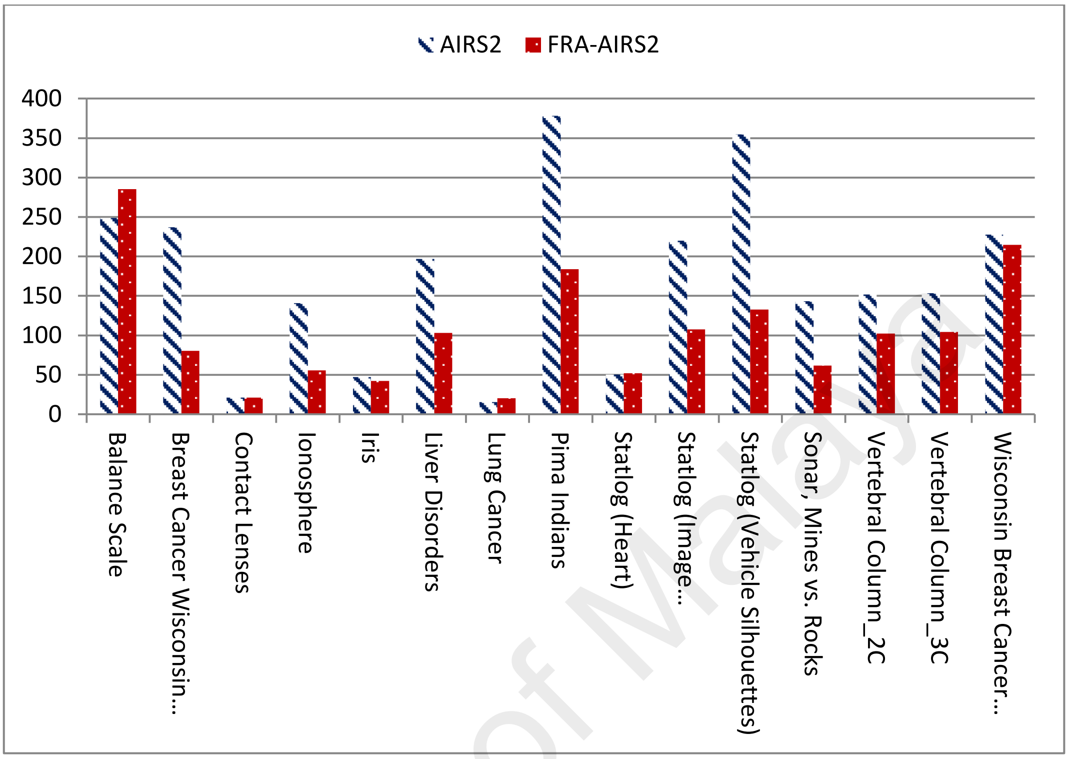

**Figure 4.31: Evolved Memory Cells Applying AIRS2 and FRA-AIRS2**

Results in Table 4.24 and Figure 4.31 show the application of FRA-AIRS2 and AIRS2 on fifteen benchmark data sets. These results show that both the AIRS2 and the FRA-AIRS2 algorithm could reduce the number of evolved memory cells, moreover FRA-AIRS2 performed better than the AIRS2 in eleven cases and in four cases data reduction capabilities are close to each other.

Therefore, we can conclude that using FRA algorithm inside AIRS2 not only reduces the number of data sets, but also improves the data reduction capability of AIRS2. Results also prove that linear resource allocation of AIRS2 causes higher number of evolved data sets and thus reduces its performance. Furthermore, the results show that FRA-method can solve the linearity problem associated with resource allocation and improve AIRS2's data reduction capabilities.

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(b) ***Comparison of Data Reduction Capabilities of FSR-AIRS2 and AIRS2***

Figure 4.32 illustrates a graphical comparison of data reduction obtained with AIRS2 and FSR-ARIS2 on benchmark data sets.

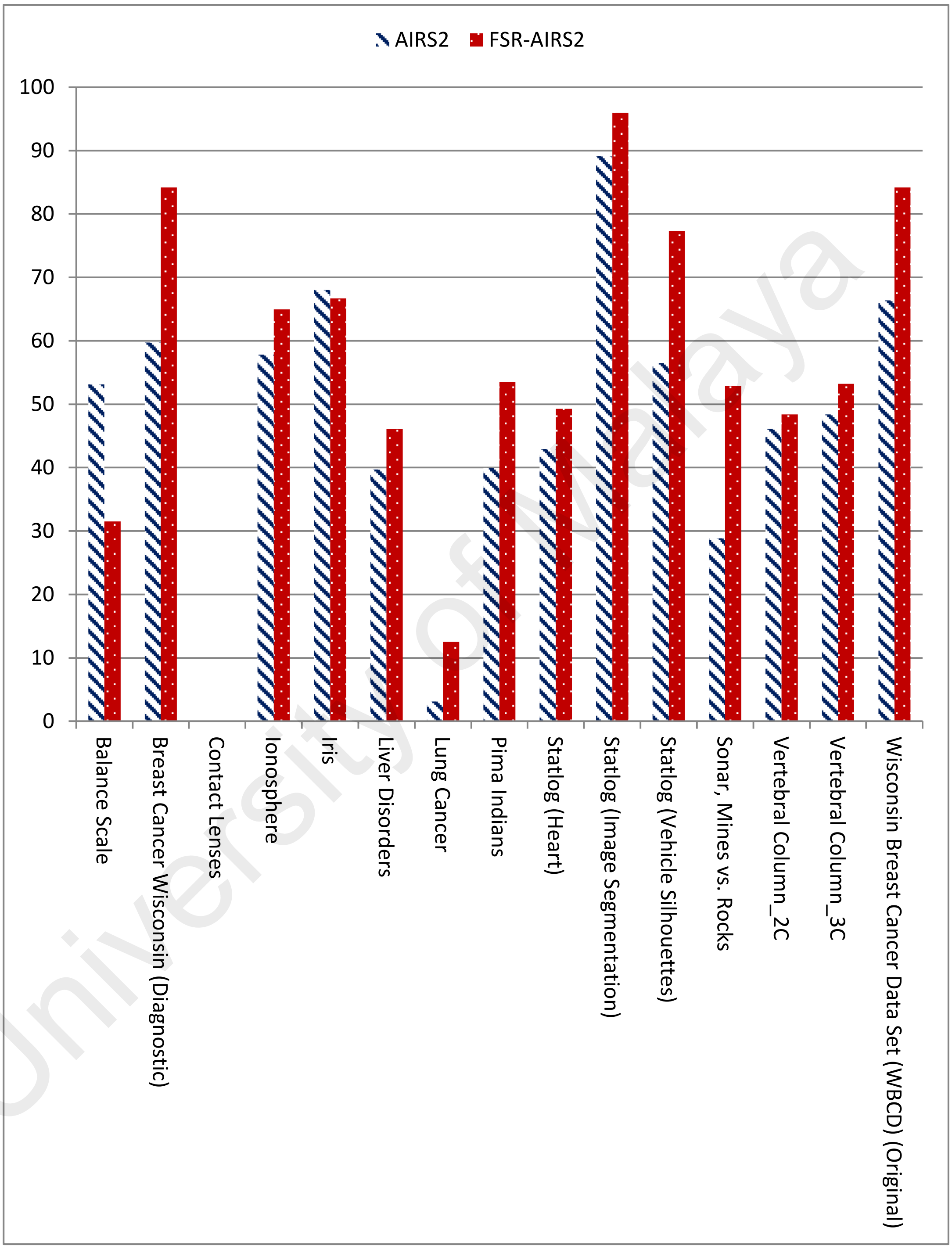

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**Figure 4.32: Comparison of Data Reduction between AIRS2 and FSR-AIRS2**

Table 4.25 presents total number of Instances for each data set, total evolved memory cells through each algorithm and the percentage of data reduction achieved by AIRS2 and FSR-AIRS2 on benchmark data sets.

**Table 4.25: Comparison of Data Reduction Capabilities of FSR-AIRS2 and AIRS2**

| | | AIRS2 | | FSR-AIRS2 | |
|---|---|---|---|---|---|
| **Training set** | **Total Instances** | **Total Memory Cell** | **Data Reduction Percentage** | **Total Memory Cell** | **Data Reduction Percentage** |
| Balance Scale | 625 | 293 | 53.12% | 428 | 31.52% |
| Breast Cancer Wisconsin (Diagnostic) | 569 | 229 | 59.75% | 90 | 84.18% |
| Contact Lenses | 24 | 24 | 0.00% | 24 | 0.00% |
| Ionosphere | 351 | 148 | 57.84% | 123 | 64.96% |
| Iris | 150 | 48 | 68.00% | 50 | 66.67% |
| Liver Disorders | 345 | 208 | 39.71% | 186 | 46.09% |
| Lung Cancer | 32 | 31 | 3.13% | 28 | 12.5% |
| Pima Indians | 768 | 461 | 39.97% | 357 | 53.52% |
| Statlog (Heart) | 270 | 154 | 42.96% | 137 | 49.26% |
| Statlog (Image Segmentation) | 2310 | 251 | 89.13% | 93 | 95.97% |
| Statlog (Vehicle Silhouettes) | 846 | 368 | 56.50% | 192 | 77.30% |
| Sonar, Mines vs. Rocks | 208 | 148 | 28.85% | 98 | 52.89% |
| Vertebral Column_2C | 310 | 167 | 46.13% | 160 | 48.39% |
| Vertebral Column_3C | 310 | 160 | 48.39% | 145 | 53.23% |
| Wisconsin Breast Cancer Data Set (WBCD) (Original) | 699 | 235 | 66.38% | 237 | 84.18% |

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Equation (3.3) is used to calculate the data reduction percentage; it compares the number of developed memory cells with the size of the training data sets. Results show that both AIRS2 and FSR-AIRS2 can reduce the data sets that are required to perform the classification tasks. The initial training records were used to create these reduced data sets, which are evolved memory cells. Results indicate that FSR-AIRS2 shows greater data reduction tendency than AIRS2. For most of the data sets the degree of data reduction is greatly increased: from 59.75% to 84.18% for Breast Cancer Wisconsin (Diagnostic) data, from 57.84% to 64.9% for Ionosphere data, from 39.71% to 46.09% for Liver Disorders data, from 3.13% to 12.5% for Lung Cancer data, from 39.97% to 53.52% for Pima Indians Diabetes data, from 42.96% to 49.26% for Statlog (Heart) data, from 89.13% to 95.97% for Statlog (Image Segmentation) data, from 56.5% to 77.3% for Statlog (Vehicle Silhouettes) data, from 28.85% to 52.89% for Sonar data, from 46.13% to 48.39% for Vertebral Column 2C data, from 48.39% to 53.23% for Vertebral Column 3C data, and from 66.38% to 84.18% for Wisconsin Breast Cancer Data Set (WBCD) (Original) data. Since the total instance of Contact Lenses is 24, both AIRS2 and FSR-AIRS2 could not perform classification with less than 24 instances, therefore the data reduction percentage for both models are 0.00%. It should also be noted that with few instances, there would not be enough records to perform the 10-fold cross validation. Many real-world data sets are large in size and any algorithm that can reduce the volumes of these data sets while maintaining the significant feature Using less of the data sets is useful. data instances for classification tasks reduces also the classification time. As we have seen in Table 4.8, FSR-AIRS2' classification accuracy was higher than that of AIRS2, this means that the proposed algorithm could reduce the volume of data sets without sacrificing the classification accuracy. Although FSR-AIRS2 has shown greater efficiency than AIRS2 without sacrificing accuracy, but it cannot be accepted blindly as a feature of FSR-AIRS2. Of course, data reduction depends on the domain, and there can be no assurance that FSR-AIRS2 would keep the trend for all data sets.

#### 4.6.3.4 Comparing Running Time of FSR-AIRS2 with that of benchmark algorithms

Table 4.26 illustrates the best average test set running time, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: AIRS2, 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM,

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Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Balance Scale data sets. All experiments utilized 10 fold cross validation and were averaged over 10 runs.

**Table 4.26: Running time measured in seconds [s] on Balance Scale Data Set**

| **FSR-AIRS2** | **AIRS2** | **1KNN** | **7KNN** | **C4.5/J48** | **CLONALG** |
|---|---|---|---|---|---|
| 0.016<br>(0.005) | 0.111<br>(0.011) | 0.0<br>(0.0) | 0.0<br>(0.0) | 0.012<br>(0.008) | 0.070<br>(0.008) |
| **Immunos99** | **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** |
| 0.127<br>(0.008) | 0.041<br>(0.008) | 0.020<br>(0.007) | 0.487<br>(0.014) | 0.0<br>(0.0) | 0.027<br>(0.007) |
| **SMO** | **SMO2** | | | | |
| 0.020<br>(0.007) | 0.096<br>(0.020) | | | | |

Figure 4.33 illustrate a comparative graph of various classifiers' running time on the Balance Scale data sets. By looking at this Figure and Table 4.26 we can see that 1KNN, 7KNN, and NBayes are clear winners; they perform much better than other classifiers, including FSR-AIRS2. However, FSR-AIRS2 performs better or is comparable with other well-known classifiers.

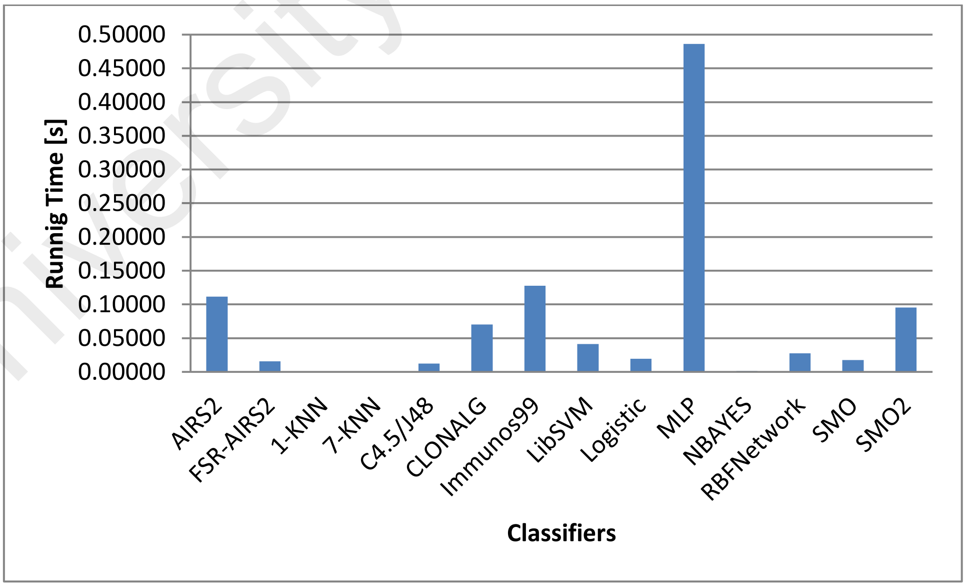

**Figure 4.33: Comparison of Balance Scale Running time Results**

Table 4.27 illustrates the best average test set running time, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known

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classifiers: AIRS2, 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Breast Cancer Wisconsin (Diagnostic) data sets.

All experiments utilized 10 fold cross validation and were averaged over 10 runs.

**Table 4.27: Running time measured in seconds [s] on Breast Cancer Wisconsin (Diagnostic) Data Set**

| **FSR-AIRS2** | **AIRS2** | **1KNN** | **7KNN** | **C4.5/J48** | **CLONALG** |
|---|---|---|---|---|---|
| 0.010<br>(0.012) | 0.210<br>(0.016) | 0.0<br>(0.0) | 0.0<br>(0.0) | 0.022<br>(0.011) | 0.192<br>(0.01) |
| **Immunos99** | **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** |
| 0.205<br>(0.012) | 0.215<br>(0.050) | 0.038<br>(0.009) | 3.471<br>(0.032) | 0.004<br>(0.009) | 0.053<br>(0.016) |
| **SMO** | **SMO2** | | | | |
| 0.007<br>(0.008) | 0.032<br>(0.006) | | | | |

Figure 4.34 illustrate a comparative graph of various classifiers' running time on the Breast Cancer Wisconsin (Diagnostic) data sets.

By looking at this Figure and Table 4.27 we can see that 1KNN, 7KNN, and NBayes are clear winners; they perform much better than other classifiers, including FSR-AIRS2. However, FSR-AIRS2 performs better or is comparable with other well-known classifiers.

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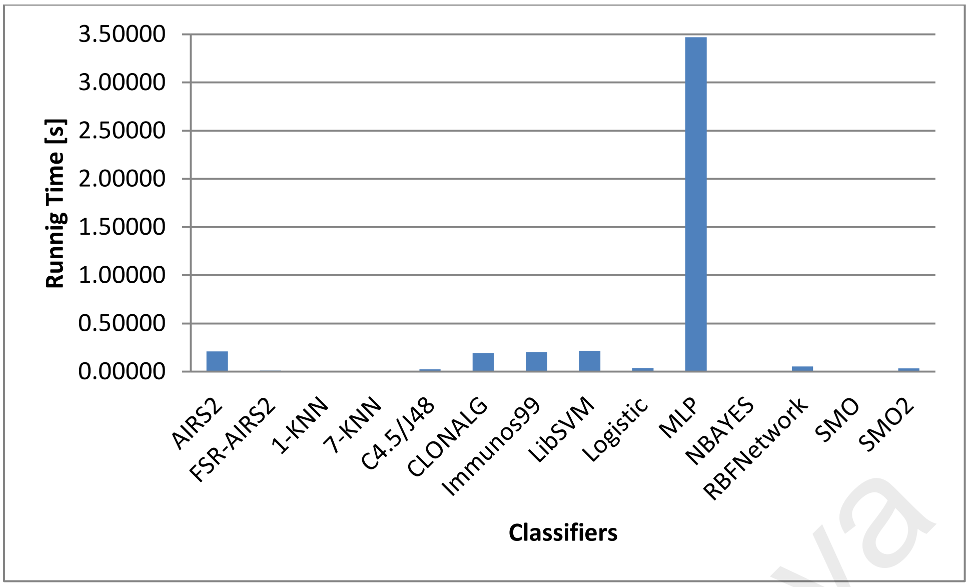

**Figure 4.34: Comparison of Breast Cancer Wisconsin (Diagnostic) Running time Results**

Table 4.28 illustrates the best average test set running time, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: AIRS2, 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Contact Lenses data sets. All experiments utilized 10 fold cross validation and were averaged over 10 runs.

**Table 4.28: Running time measured in seconds [s] on Contact Lenses Data Set**

| **FSR-AIRS2** | **AIRS2** | **1KNN** | **7KNN** | **C4.5/J48** | **CLONALG** |
|---|---|---|---|---|---|
| 0.004<br>(0.007) | 0.004<br>(0.007) | 0.0<br>(0.0) | 0.0<br>(0.0) | 0.0<br>(0.0) | 0.003<br>(0.006) |
| **Immunos99** | **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** |
| 0.0<br>(0.0) | 0.001<br>(0.004) | 0.0<br>(0.0) | 0.028<br>(0.007) | 0.0<br>(0.0) | 0.003<br>(0.006) |
| **SMO** | **SMO2** | | | | |
| 0.010<br>(0.008) | 0.011<br>(0.007) | | | | |

Figure 4.35 illustrate a comparative graph of various classifiers' running time on the Contact Lenses data sets. By looking at this Figure and Table 4.28 we can see that 1KNN, 7KNN, C4.5/J48, Immunos99, Logistic, and NBayes are clear winners; they perform

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much better than other classifiers, including FSR-AIRS2. However, FSR-AIRS2 performs better or is comparable with other well-known classifiers.

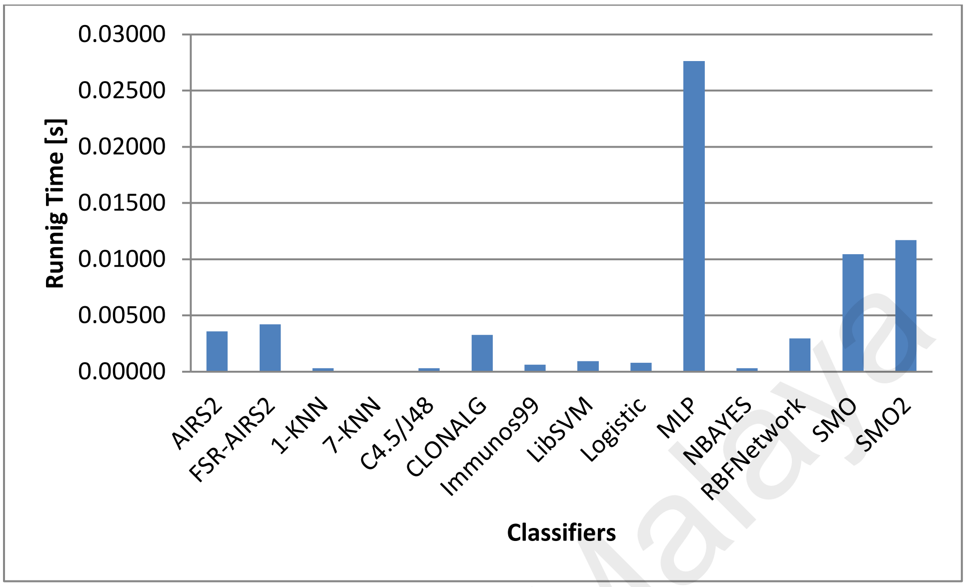

**Figure 4.35: Comparison of Contact Lenses Running time Results**

Table 4.29 illustrates the best average test set running time, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: AIRS2, 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Ionosphere data sets. All experiments utilized 10 fold cross validation and were averaged over 10 runs.

**Table 4.29: Running time measured in seconds [s] on Ionosphere Data Set**

| **FSR-AIRS2** | **AIRS2** | **1KNN** | **7KNN** | **C4.5/J48** | **CLONALG** |
|---|---|---|---|---|---|
| 0.011<br>(0.008) | 0.260<br>(0.033) | 0.0<br>(0.0) | 0.0<br>(0.0) | 0.027<br>(0.007) | 0.128<br>(0.009) |
| **Immunos99** | **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** |
| 0.083<br>(0.007) | 0.063<br>(0.007) | 0.026<br>(0.008) | 2.680<br>(0.026) | 0.005<br>(0.008) | 0.021<br>(0.008) |
| **SMO** | **SMO2** | | | | |
| 0.017<br>(0.004) | 0.078<br>(0.017) | | | | |

Figure 4.36 illustrate a comparative graph of various classifiers' running time on the Ionosphere data sets. By looking at this Figure and Table 4.29 we can see that 1KNN,

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7KNN, and NBayes are clear winners; they perform much better than other classifiers, including FSR-AIRS2. However, FSR-AIRS2 performs better or is comparable with other well-known classifiers.

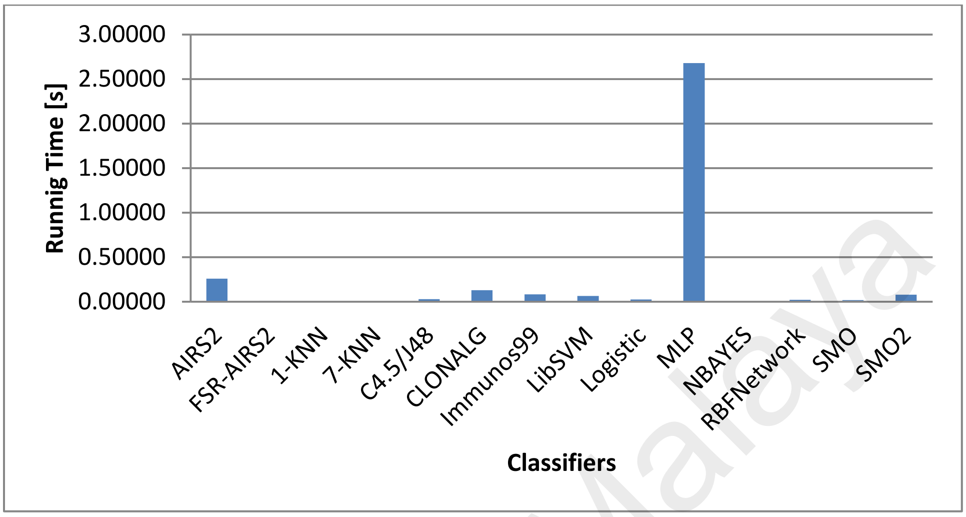

**Figure 4.36: Comparison of Ionosphere Running time Results**

Table 4.30 illustrates the best average test set running time, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: AIRS2, 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Iris  data sets. All experiments utilized 10 fold cross validation and were averaged over 10 runs.

**Table 4.30: Running time measured in seconds [s] on Iris Data Set**

| **FSR-AIRS2** | **AIRS2** | **1KNN** | **7KNN** | **C4.5/J48** | **CLONALG** |
|---|---|---|---|---|---|
| 0.001<br>(0.004) | 0.014<br>(0.006) | 0.0<br>(0.0) | 0.0<br>(0.0) | 0.0<br>(0.0) | 0.018<br>(0.005) |
| **Immunos99** | **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** |
| 0.005<br>(0.007) | 0.005<br>(0.007) | 0.007<br>(0.008) | 0.200<br>(0.097) | 0.001<br>(0.024) | 0.009<br>(0.008) |
| **SMO** | **SMO2** | | | | |
| 0.010<br>(0.007) | 0.012<br>(0.006) | | | | |

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Figure 4.37 illustrate a comparative graph of various classifiers' running time on the Iris data sets. By looking at this Figure and Table 4.30 we can see that 1KNN, 7KNN, and C4.5/J48 are clear winners; they perform much better than other classifiers, including FSR-AIRS2. However, FSR-AIRS2 performs better or is comparable with other well-known classifiers.

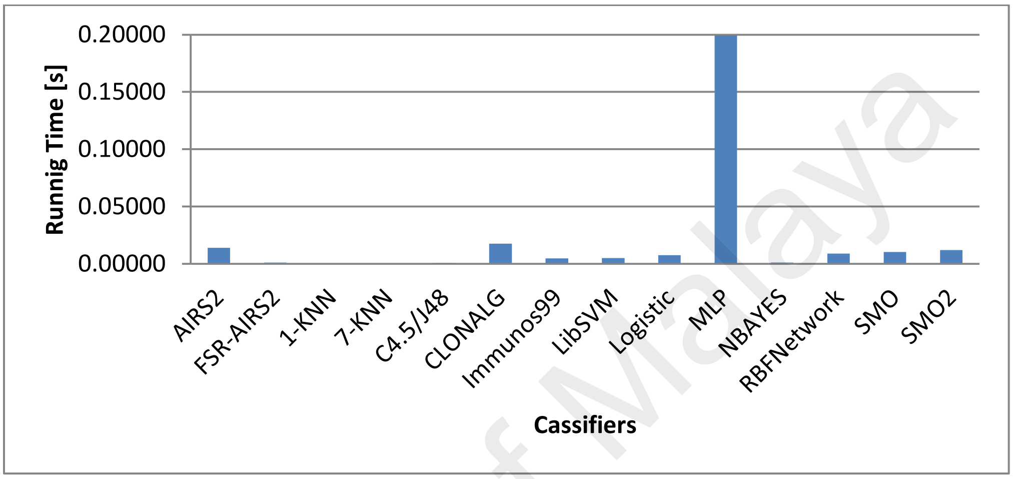

**Figure 4.37: Comparison of Iris Running time Results**

Table 4.31 illustrates the best average test set running time, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: AIRS2, 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Liver Disorders data sets. All experiments utilized 10 fold cross validation and were averaged over 10 runs.

**Table 4.31: Running time measured in seconds [s] on Liver Disorders Data Set**

| FSR-AIRS2 | AIRS2 | 1KNN | 7KNN | C4.5/J48 | CLONALG |
|---|---|---|---|---|---|
| 0.007<br>(0.008) | 0.062<br>(0.031) | 0.0<br>(0.0) | 0.0<br>(0.0) | 0.005<br>(0.007) | 0.042<br>(0.008) |
| **Immunos99** | **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** |
| 0.042<br>(0.007) | 0.029<br>(0.308) | 0.004<br>(0.007) | 0.085<br>(0.008) | 0.0<br>(0.0) | 0.008<br>(0.008) |
| **SMO** | **SMO2** | | | | |
| 0.005<br>(0.007) | 0.046<br>(0.014) | | | | |

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Figure 4.38 illustrate a comparative graph of various classifiers' running time on the Liver Disorders data sets. By looking at this Figure and Table 4.31 we can see that 1KNN, 7KNN, and NBayes are clear winners; they perform much better than other classifiers, including FSR-AIRS2. However, FSR-AIRS2 performs better or is comparable with other well-known classifiers.

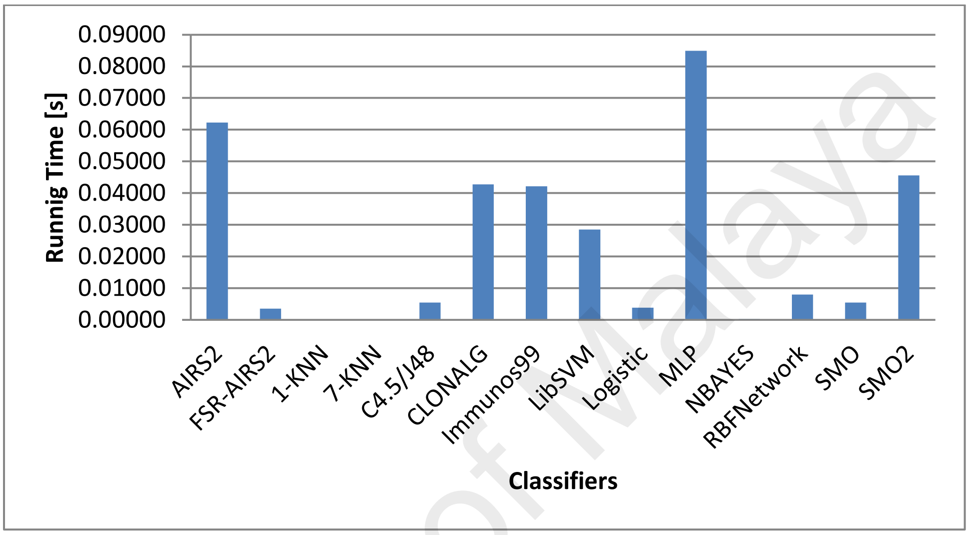

**Figure 4.38: Comparison of Liver Disorders Running time Results**

Table 4.32 illustrates the best average test set running time, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: AIRS2, 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Lung Cancer data sets. All experiments utilized 10 fold cross validation and were averaged over 10 runs.

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**Table 4.32: Running time measured in seconds [s] on Lung Cancer Data Set**

| FSR-AIRS2 | AIRS2 | 1KNN | 7KNN | C4.5/J48 | CLONALG |
|---|---|---|---|---|---|
| 0.004<br>(0.007) | 0.002<br>(0.005) | 0.0<br>(0.0) | 0.0<br>(0.0) | 0.002<br>(0.005) | 0.019<br>(0.007) |
| **Immunos99** | **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** |
| 0.001<br>(0.004) | 0.004<br>(0.007) | 0.018<br>(0.009) | 0.054<br>(0.009) | 0.0<br>(0.0) | 0.006<br>(0.008) |
| **SMO** | **SMO2** | | | | |
| 0.011<br>(0.007) | 0.012<br>(0.007) | | | | |

Figure 4.39 illustrate a comparative graph of various classifiers' running time on the Lung Cancer data sets. By looking at this Figure and Table 4.32 we can see that 1KNN, 7KNN, and NBayes are clear winners; they perform much better than other classifiers, including FSR-AIRS2. However, FSR-AIRS2 performs better or is comparable with other well-known classifiers.

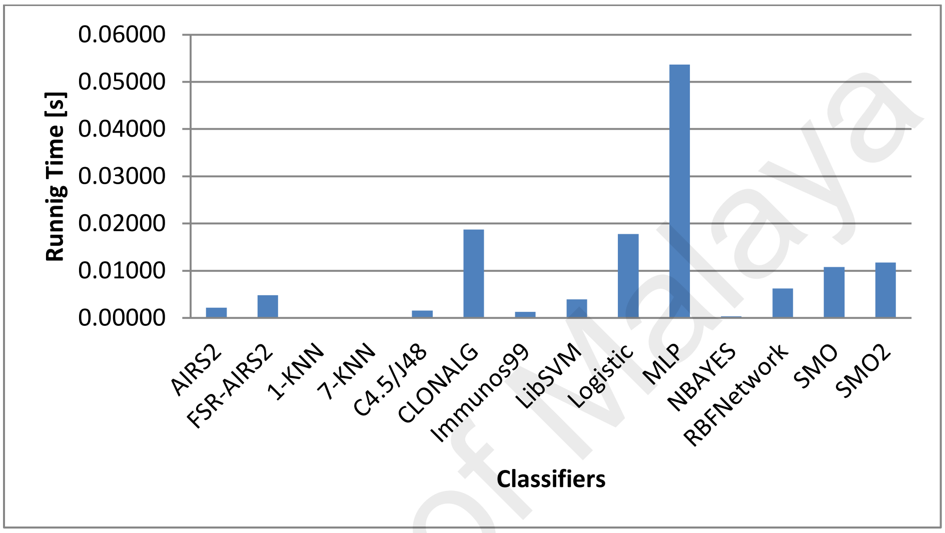

**Figure 4.39: Comparison of Lung Cancer Running time Results**

Table 4.33 illustrates the best average test set running time, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: AIRS2, 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Pima Indians data sets. All experiments utilized 10 fold cross validation and were averaged over 10 runs.

**Table 4.33: Running time measured in seconds [s] on Pima Indians Data Set**

| FSR-AIRS2 | AIRS2 | 1KNN | 7KNN | C4.5/J48 | CLONALG |
|---|---|---|---|---|---|
| 0.026<br>(0.010) | 0.130<br>(0.040) | 0.0<br>(0.0) | 0.0<br>(0.0) | 0.009<br>(0.008) | 0.113<br>(0.010) |
| **Immunos99** | **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** |
| 0.239<br>(0.012) | 0.125<br>(0.009) | 0.011<br>(0.007) | 0.100<br>(0.030) | 0.002<br>(0.008) | 0.020<br>(0.008) |
| **SMO** | **SMO2** | | | | |
| 0.011<br>(0.008) | 0.185<br>(0.029) | | | | |

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Figure 4.40 illustrate a comparative graph of various classifiers' running time on the Pima Indians data sets. By looking at this Figure and Table 4.33 we can see that 1KNN, and 7KNN are clear winners; they perform much better than other classifiers, including FSR-AIRS2. However, FSR-AIRS2 performs better or is comparable with other well-known classifiers.

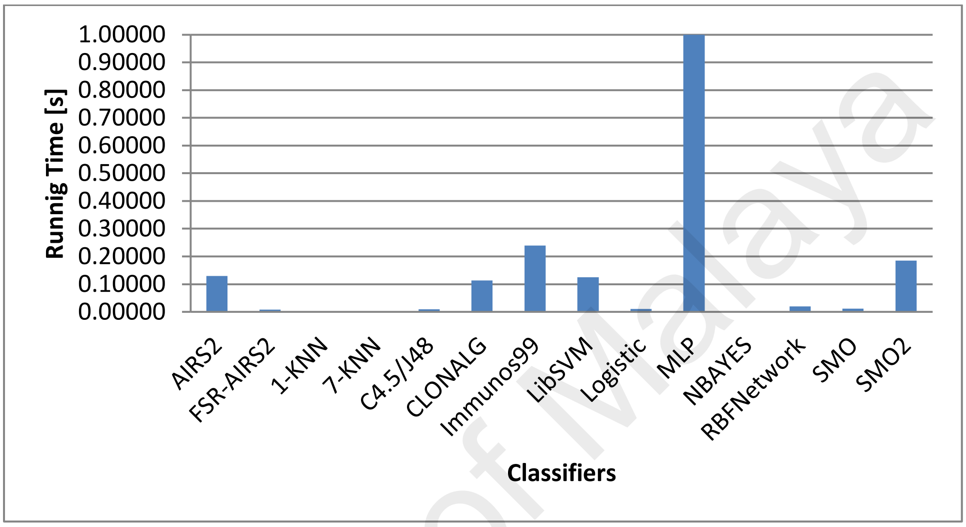

**Figure 4.40: Comparison of Pima Indians Running time Results**

Table 4.34 illustrates the best average test set running time, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: AIRS2, 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Statlog (Heart) data sets. All experiments utilized 10 fold cross validation and were averaged over 10 runs.

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**Table 4.34: Running time measured in seconds [s] on Statlog (Heart) Data Set**

| **FSR-AIRS2** | **AIRS2** | **1KNN** | **7KNN** | **C4.5/J48** | **CLONALG** |
|---|---|---|---|---|---|
| 0.026<br>(0.013) | 0.028<br>(0.021) | 0.0<br>(0.0) | 0.0<br>(0.0) | 0.005<br>(0.007) | 0.050<br>(0.009) |
| **Immunos99** | **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** |
| 0.031<br>(0.004) | 0.036<br>(0.008) | 0.005<br>(0.007) | 0.097<br>(0.009) | 0.0<br>(0.0) | 0.007<br>(0.008) |
| **SMO** | **SMO2** | | | | |
| 0.008<br>(0.008) | 0.032<br>(0.008) | | | | |

Figure 4.41 illustrate a comparative graph of various classifiers' running time on the Statlog (Heart) data sets.

By looking at this Figure and Table 4.34 we can see that 1KNN, 7KNN, and NBayes are clear winners; they perform much better than other classifiers, including FSR-AIRS2. However, FSR-AIRS2 performs better or is comparable with other well-known classifiers.

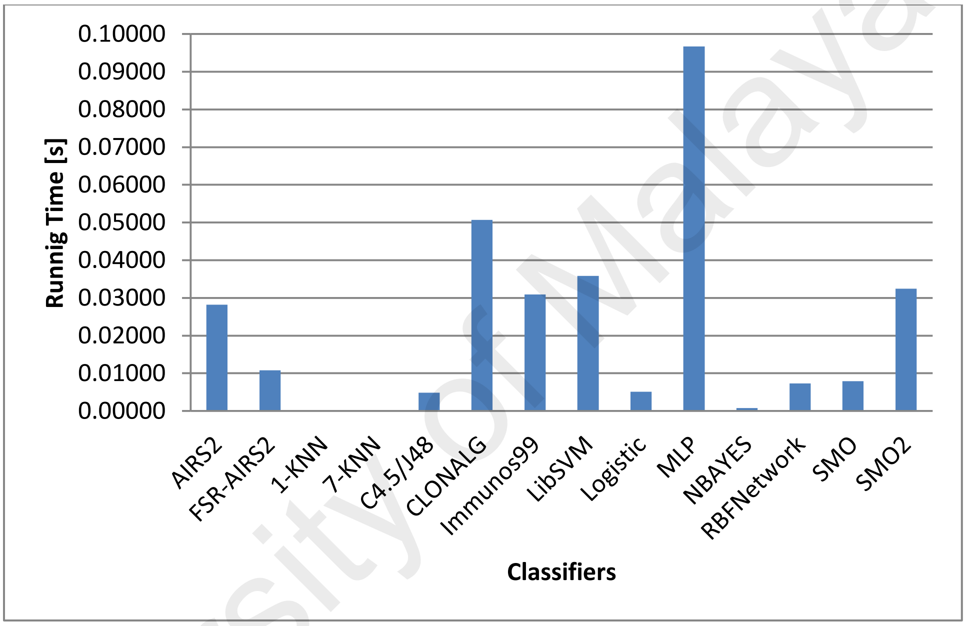

**Figure 4.41: Comparison of Statlog (Heart) Running time Results**

Table 4.35 illustrates the best average test set running time, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: AIRS2, 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Statlog (Image Segmentation) data sets.

All experiments utilized 10 fold cross validation and were averaged over 10 runs.

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**Table 4.35: Running time measured in seconds [s] on Statlog (Image Segmentation) Data Set**

| FSR-AIRS2 | AIRS2 | 1KNN | 7KNN | C4.5/J48 | CLONALG |
|---|---|---|---|---|---|
| 0.012<br>(0.007) | 1.320<br>(0.080) | 0.0<br>(0.0) | 0.0<br>(0.0) | 0.118<br>(0.010) | 0.560<br>(0.015) |
| **Immunos99** | **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** |
| 2.750<br>(0.027) | 3.191<br>(0.308) | 10.000<br>(0.017) | 12.390<br>(0.100) | 0.0<br>(0.0) | 4.034<br>(1.350) |
| **SMO** | **SMO2** | | | | |
| 0.164<br>(0.010) | 0.590<br>(0.034) | | | | |

Figure 4.42 illustrate a comparative graph of various classifiers' running time on the Statlog (Image Segmentation) data sets. By looking at this Figure and Table 4.35 we can see that 1KNN, 7KNN, and NBayes are clear winners; they perform much better than other classifiers, including FSR-AIRS2. However, FSR-AIRS2 performs better or is comparable with other well-known classifiers.

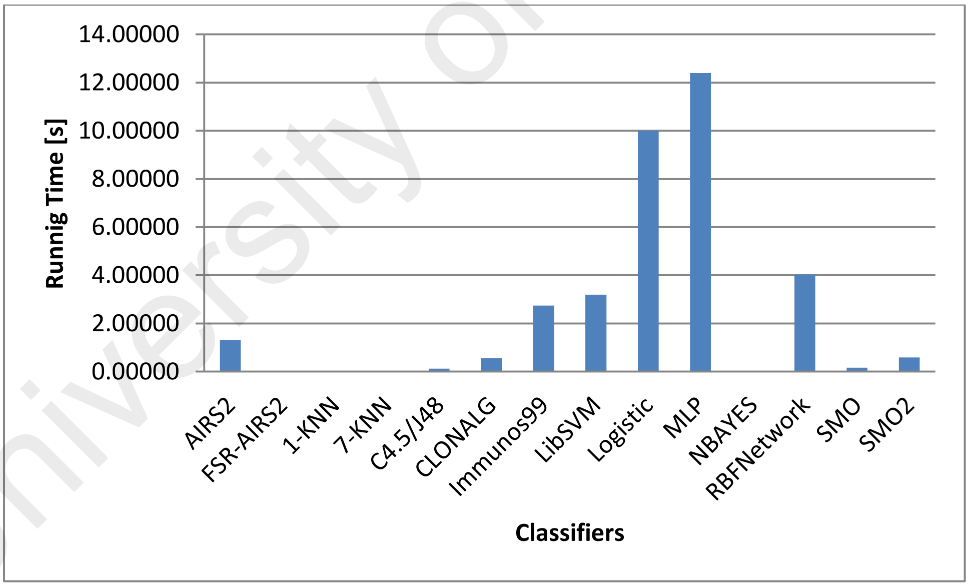

**Figure 4.42: Comparison of Statlog (Image Segmentation) Running time Results**

Table 4.36 illustrates the best average test set running time, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: AIRS2, 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Statlog (Vehicle

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Silhouettes) data sets. All experiments utilized 10 fold cross validation and were averaged over 10 runs.

**Table 4.36: Running time measured in seconds [s] on Statlog (Vehicle Silhouettes) Data Set**

| FSR-AIRS2 | AIRS2 | 1KNN | 7KNN | C4.5/J48 | CLONALG |
|---|---|---|---|---|---|
| 0.014<br>(0.004) | 0.221<br>(0.030) | 0.0<br>(0.0) | 0.0<br>(0.0) | 0.030<br>(0.007) | 0.187<br>(0.008) |
| **Immunos99** | **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** |
| 0.343<br>(0.012) | 0.472<br>(0.041) | 0.284<br>(0.074) | 4.428<br>(0.098) | 0.003<br>(0.006) | 0.155<br>(0.030) |
| **SMO** | **SMO2** | | | | |
| 0.066<br>(0.007) | 0.323<br>(0.022) | | | | |

Figure 4.43 illustrate a comparative graph of various classifiers' running time on the Statlog (Vehicle Silhouettes) data sets. By looking at this Figure and Table 4.36 we can see that 1KNN, 7KNN, and NBayes are clear winners; they perform much better than other classifiers, including FSR-AIRS2. However, FSR-AIRS2 performs better or is comparable with other well-known classifiers.

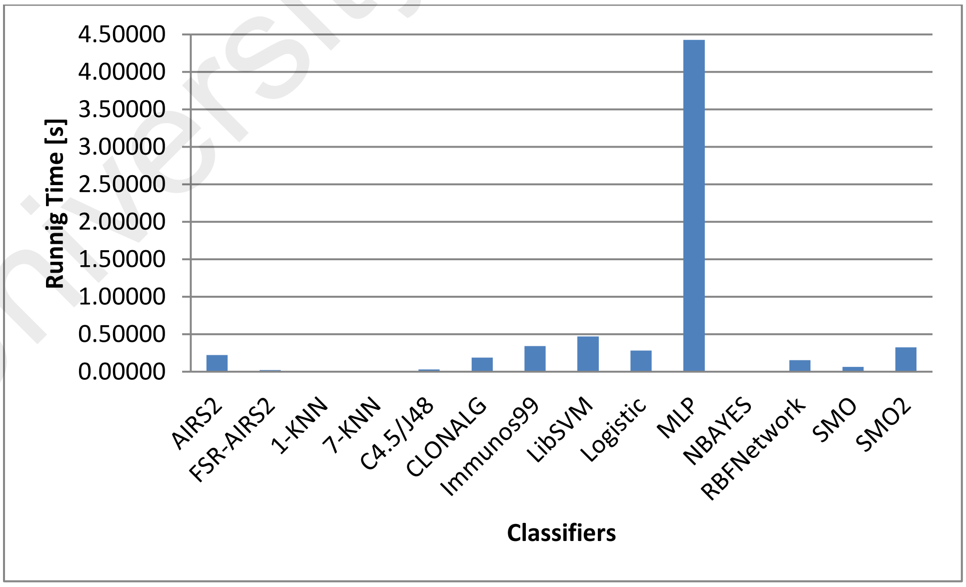

**Figure 4.43: Comparison of Statlog (Vehicle Silhouettes) Running time Results**

Table 4.37 illustrates the best average test set running time, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known

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classifiers: AIRS2, 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Sonar, Mines vs. Rocks data sets.

All experiments utilized 10 fold cross validation and were averaged over 10 runs.

**Table 4.37: Running time measured in seconds [s] on Sonar, Mines vs. Rocks Data Set**

| **FSR-AIRS2** | **AIRS2** | **1KNN** | **7KNN** | **C4.5/J48** | **CLONALG** |
|---|---|---|---|---|---|
| 0.040<br>(0.008) | 0.100<br>(0.010) | 0.0<br>(0.0) | 0.0<br>(0.0) | 0.040<br>(0.011) | 0.124<br>(0.010) |
| **Immunos99** | **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** |
| 0.044<br>(0.007) | 0.092<br>(0.012) | 0.017<br>(0.006) | 4.124<br>(0.042) | 0.006<br>(0.008) | 0.019<br>(0.007) |
| **SMO** | **SMO2** | | | | |
| 0.012<br>(0.006) | 0.057<br>(0.010) | | | | |

Figure 4.44 illustrate a comparative graph of various classifiers' running time on the Sonar data sets.

By looking at this Figure and Table 4.37 we can see that 1KNN, 7KNN, and NBayes are clear winners; they perform much better than other classifiers, including FSR-AIRS2. However, FSR-AIRS2 performs better or is comparable with other well-known classifiers.

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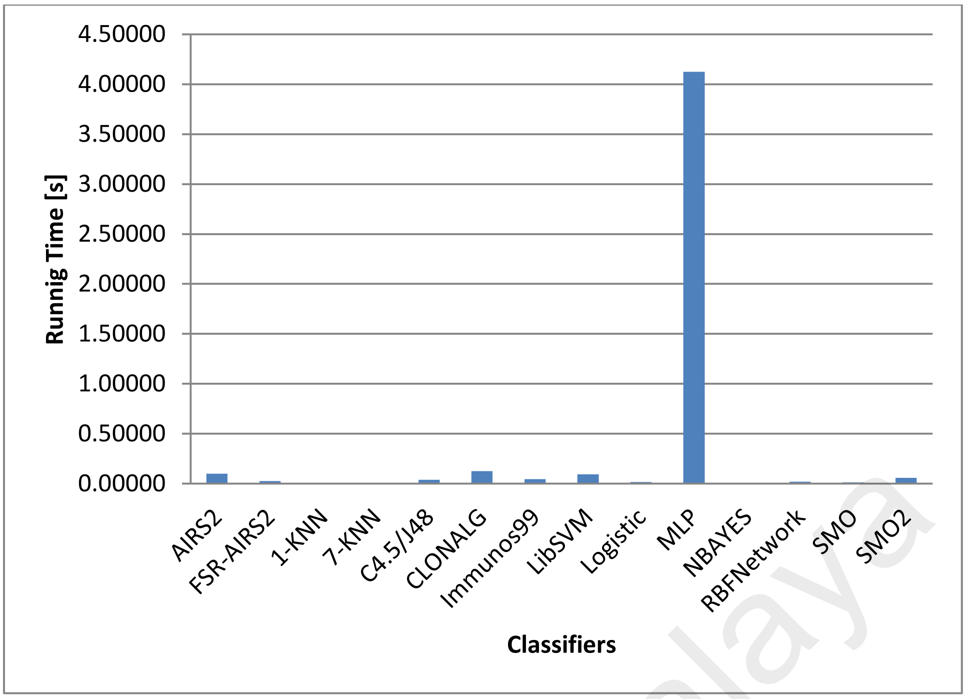

**Figure 4.44: Comparison of Sonar, Mines vs. Rocks Running time Results**

Table 4.38 illustrates the best average test set running time, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: AIRS2, 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Vertebral Column_2C data sets. All experiments utilized 10 fold cross validation and were averaged over 10 runs.

**Table 4.38: Running time measured in seconds [s] on Vertebral Column_2C Data Set**

| **FSR-AIRS2** | **AIRS2** | **1KNN** | **7KNN** | **C4.5/J48** | **CLONALG** |
|---|---|---|---|---|---|
| 0.003<br>(0.006) | 0.036<br>(0.030) | 0.0<br>(0.0) | 0.0<br>(0.0) | 0.004<br>(0.006) | 0.027<br>(0.007) |
| **Immunos99** | **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** |
| 0.021<br>(0.008) | 0.026<br>(0.014) | 0.004<br>(0.007) | 0.348<br>(0.089) | 0.0<br>(0.0) | 0.008<br>(0.008) |
| **SMO** | **SMO2** | | | | |
| 0.006<br>(0.009) | 0.024<br>(0.008) | | | | |

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Figure 4.45 illustrate a comparative graph of various classifiers' running time on the Vertebral Column_2C data sets.

By looking at this Figure and Table 4.38 we can see that 1KNN, 7KNN, and NBayes are clear winners; they perform much better than other classifiers, including FSR-AIRS2. However, FSR-AIRS2 performs better or is comparable with other well-known classifiers.

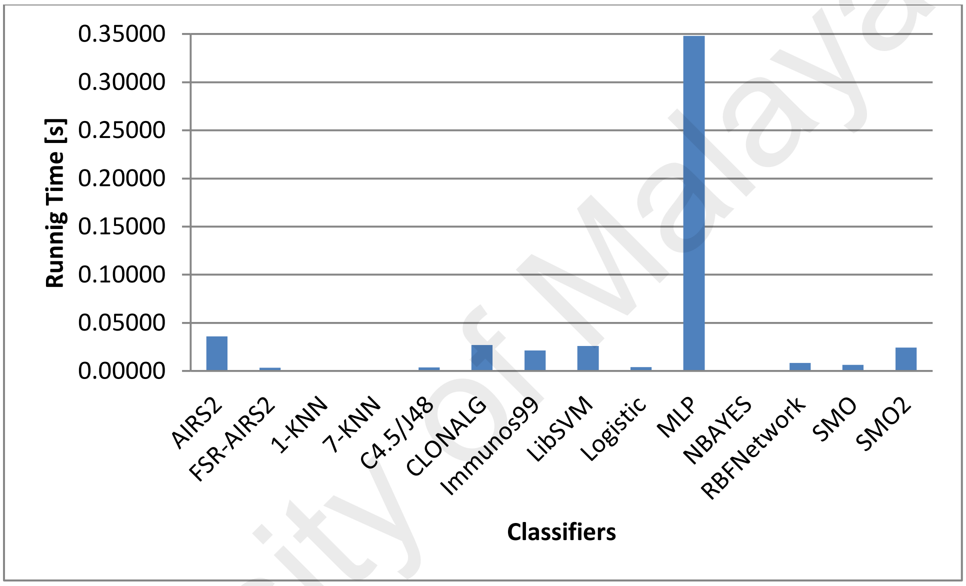

**Figure 4.45: Comparison of Vertebral Column_2C Running time Results**

Table 4.39 illustrates the best average test set running time, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: AIRS2, 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Vertebral Column_3C data sets.

All experiments utilized 10 fold cross validation and were averaged over 10 runs.

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**Table 4.39: Running time measured in seconds [s] on Vertebral Column_3C Data Set**

| FSR-AIRS2 | AIRS2 | 1KNN | 7KNN | C4.5/J48 | CLONALG |
|---|---|---|---|---|---|
| 0.003<br>(0.006) | 0.029<br>(0.007) | 0.0<br>(0.0) | 0.0<br>(0.0) | 0.005<br>(0.007) | 0.028<br>(0.010) |
| **Immunos99** | **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** |
| 0.019<br>(0.006) | 0.033<br>(0.006) | 0.010<br>(0.010) | 0.394<br>(0.014) | 0.0<br>(0.0) | 0.021<br>(0.009) |
| **SMO** | **SMO2** | | | | |
| 0.012<br>(0.007) | 0.030<br>(0.009) | | | | |

Figure 4.46 illustrate a comparative graph of various classifiers' running time on the Vertebral Column_3C data sets. By looking at this Figure and Table 4.39 we can see that 1KNN, 7KNN, and NBayes are clear winners; they perform much better than other classifiers, including FSR-AIRS2. However, FSR-AIRS2 performs better or is comparable with other well-known classifiers.

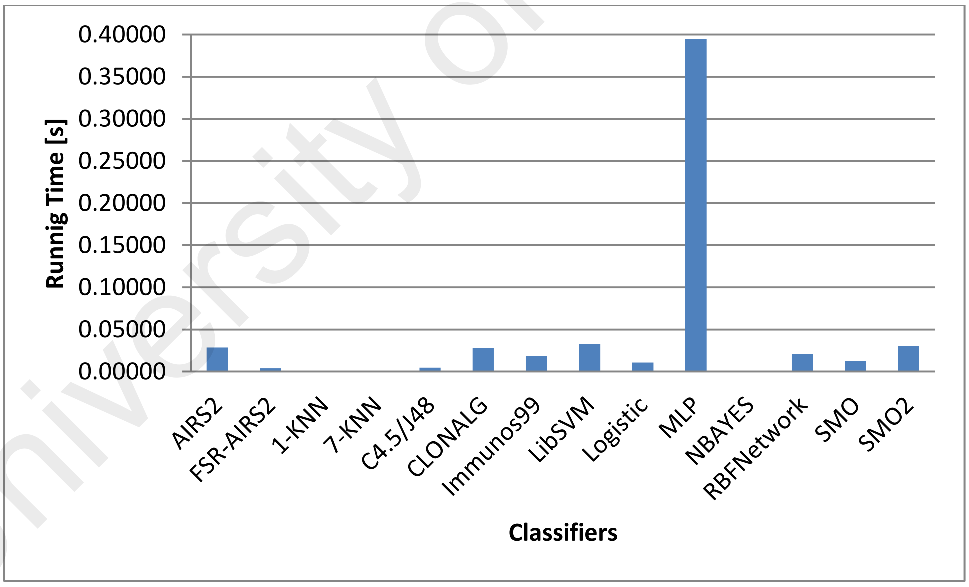

**Figure 4.46: Comparison of Vertebral Column_3C Running time Results**

Table 4.40 illustrates the best average test set running time, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: AIRS2, 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Wisconsin Breast

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Cancer Data set (WBCD) (Original). All experiments utilized 10 fold cross validation and were averaged over 10 runs.

**Table 4.40: Running time measured in seconds [s] on Wisconsin Breast Cancer Data Set (WBCD) Original**

| FSR-AIRS2 | AIRS2 | 1KNN | 7KNN | C4.5/J48 | CLONALG |
|---|---|---|---|---|---|
| 0.015<br>(0.008) | 0.141<br>(0.028) | 0.0<br>(0.0) | 0.0<br>(0.0) | 0.007<br>(0.010) | 0.11<br>(0.007) |
| **Immunos99** | **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** |
| 0.186<br>(0.007) | 0.110<br>(0.023) | 0.020<br>(0.009) | 1.177<br>(0.077) | 0.003<br>(0.007) | 0.029<br>(0.012) |
| **SMO** | **SMO2** | | | | |
| 0.007<br>(0.008) | 0.039<br>(0.009) | | | | |

Figure 4.47 illustrate a comparative graph of various classifiers' running time on the Wisconsin Breast Cancer Data Set (WBCD) (Original). By looking at this Figure and Table 4.40 we can see that 1KNN, 7KNN, and NBayes are clear winners; they perform much better than other classifiers, including FSR-AIRS2. However, FSR-AIRS2 performs better or is comparable with other well-known classifiers.

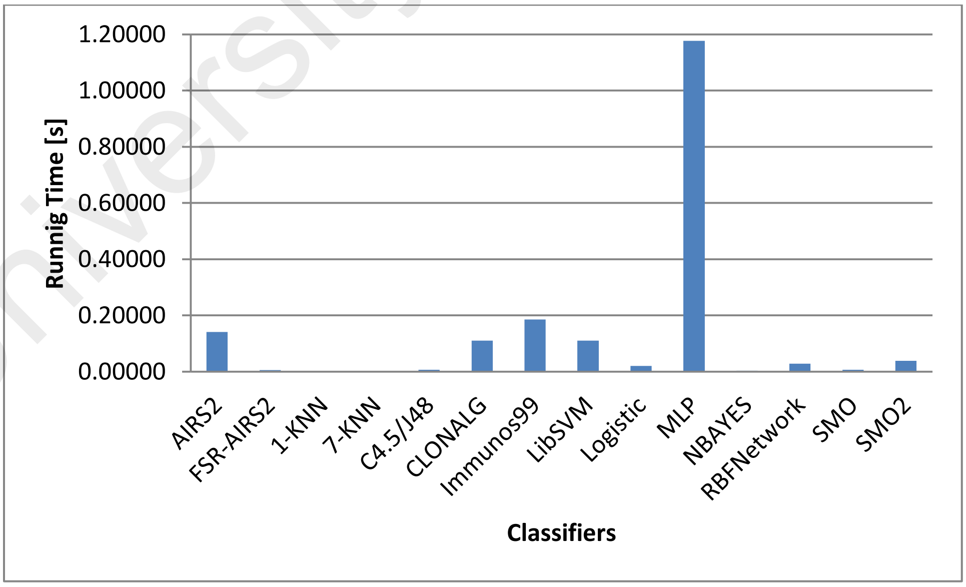

**Figure 4.47: Comparison of Wisconsin Breast Cancer Data Set (WBCD) (Original) Running time Results**

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The results show some interesting patterns. While 1-KNN and 7-KNN are the clear winner in terms of running time among all used classifiers, the running time of FSR-AIRS2 was on 12 benchmark data sets lower, thus better than that of AIRS2, there was one case where both of them were tie, and in 2 cases AIRS2 time was better than FSR-AIRS2. In average, the running time of FSR-AIRS2 and C4.5/J48 were tie, while FSR-AIRS2 performed faster than C4.5/J48 on 7 benchmark data sets, C4.5/J48 performed on other 7 bench mark data sets faster and in only on one data set they were equal. The running time of FSRARIS2 was lower than that of CLONALAG, MLP and SMO2 on all benchmark data sets. Comparison between FSR-AIRS2 and Immunos99, LibSVM, RBF Network, and SMO showed that in most cases, FSRARIS2 performed faster in the running time. However, the running time of Naïve Bayes was in most cases lower than FSR-AIRS2, only in one case FSR-AIRS2 performed faster.

While 3 classifiers performed faster in running time, FSR-AIRS2 was able to be faster in most cases on the same benchmark data sets. This is of course encouraging, because it shows that new implementations made in FSR-AIRS2 did not negatively affect the running time of the classifier. The results suggest that FSR-AIRS2 is comparable to other classifiers based on the running time.

#### 4.6.3.5 Area under the curve (AUC)

Table 4.41 presents the best average test set of the area under ROC, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: AIRS2, 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Balance Scale data sets. All experiments utilized 10 fold cross validation and were averaged over 10 runs.

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**Table 4.41: Comparison of FSR-AIRS2 and Other Classifiers' Area under ROC on Balance Scale Data Set**

| **FSR-AIRS2** | **AIRS2** | **1KNN** | **7KNN** | **C4.5/J48** | **CLONALG** |
|---|---|---|---|---|---|
| 0.981<br>(0.023) | 0.913<br>(0.034) | 0.978<br>(0.010) | 0.990<br>(0.006) | 0.845<br>(0.041) | 0.823<br>(0.054) |
| **Immunos99** | **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** |
| 0.814<br>(0.062) | 0.941<br>(0.024) | 0.981<br>(0.011) | 0.987<br>(0.014) | 0.993<br>(0.007) | 0.971<br>(0.020) |
| **SMO** | **SMO2** | | | | |
| 0.926<br>(0.024) | 0.959<br>(0.019) | | | | |

Figure 4.48 illustrate a comparative graph of various classifiers’ AUC on the Balance Scale data sets. For interpretation of the values of area under the curve, this thesis uses the grading point system that was discussed in section 3.4.6. By looking at Figure 4.48 and Table 4.41, we can see that AUCs of FSR-AIRS2 and ten other classifiers are above 0.9, which indicate that these classifiers perform excellent on this data set.  The complete interpretation is summarized in Table 4.56. The complete explanation is presented at the end of this section, just after Figure 4.62 and before Table 4.56.

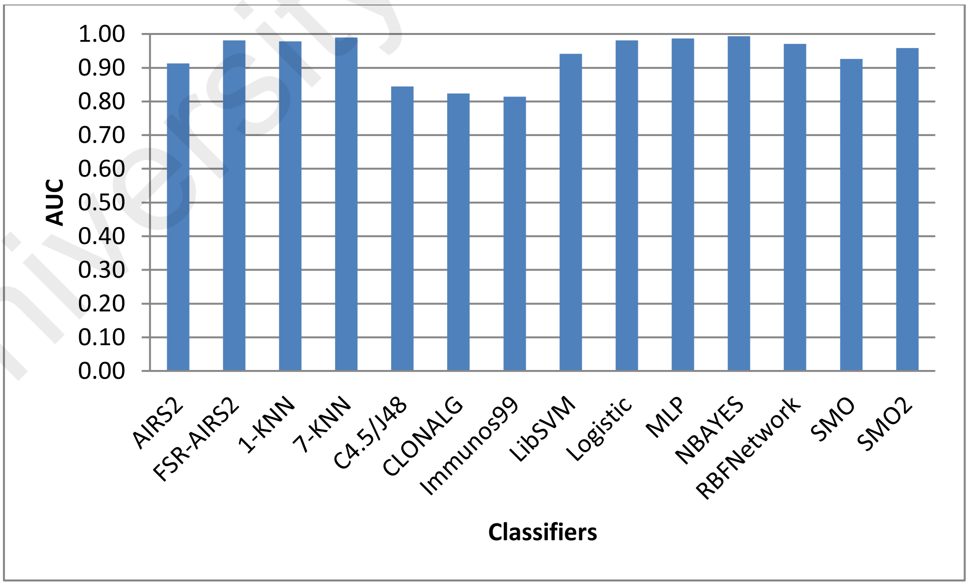

**Figure 4.48: Comparison of FSR-AIRS2 and Other Classifiers' Area under ROC on Balance Scale Data Sets**

Table 4.42 presents the best average test set of the area under ROC, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-

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known classifiers: AIRS2, 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Breast Cancer Wisconsin (Diagnostic) data sets. All experiments utilized 10 fold cross validation and were averaged over 10 runs.

**Table 4.42: Comparison of FSR-AIRS2 and Other Classifiers' Area under ROC on Breast Cancer Wisconsin (Diagnostic) Data Set**

| FSR-AIRS2 | AIRS2 | 1KNN | 7KNN | C4.5/J48 | CLONALG |
|---|---|---|---|---|---|
| 1.000<br>(0.0) | 0.955<br>(0.029) | 0.953<br>(0.025) | 0.990<br>(0.013) | 0.927<br>(0.042) | 0.869<br>(0.060) |
| **Immunos99** | **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** |
| 0.840<br>(0.055) | 0.500<br>(0.0) | 0.973<br>(0.023) | 0.992<br>(0.011) | 0.981<br>(0.019) | 0.981<br>(0.020) |
| **SMO** | **SMO2** | | | | |
| 0.969<br>(0.024) | 0.975<br>(0.023) | | | | |

Figure 4.49 illustrate a comparative graph of various classifiers' AUC on the Breast Cancer Wisconsin (Diagnostic) data sets. For interpretation of the values of area under the curve, this thesis uses the grading point system that was discussed in section 3.4.6.

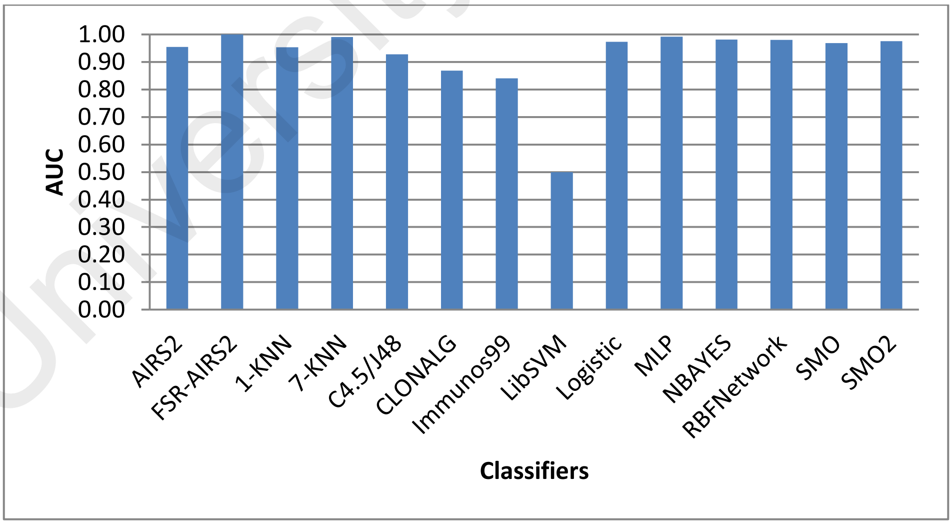

**Figure 4.49: Comparison of FSR-AIRS2 and Other Classifiers' Area under ROC on Breast Cancer Wisconsin (Diagnostic) Data Set**

By looking at Figure 4.49 and Table 4.42, we can see that AUCs of FSR-AIRS2 and ten other classifiers are above 0.9, which indicate that these classifiers perform excellent

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on this data set. Here, the AUC of FSR-AIRS2 is the highest of all. The complete interpretation is summarized in Table 4.56. The complete explanation is presented at the end of this section, just after Figure 4.62 and before Table 4.56.

Table 4.43 presents the best average test set of the area under ROC, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: AIRS2, 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Contact Lenses data sets. All experiments utilized 10 fold cross validation and were averaged over 10 runs.

**Table 4.43: Comparison of FSR-AIRS2 and Other Classifiers' Area under ROC on Contact Lenses Data Set**

| **FSR-AIRS2** | **AIRS2** | **1KNN** | **7KNN** | **C4.5/J48** | **CLONALG** |
|---|---|---|---|---|---|
| 1.000<br>(0.0) | 0.890<br>(0.203) | 0.955<br>(0.140) | 0.935<br>(0.158) | 0.945<br>(0.144) | 0.725<br>(0.249) |
| **Immunos99** | **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** |
| 0.655<br>(0.236) | 0.500<br>(0.0) | 0.840<br>(0.338) | 0.870<br>(0.313) | 0.950<br>(0.208) | 0.910<br>(0.280) |
| **SMO** | **SMO2** | | | | |
| 0.915<br>(0.172) | 0.845<br>(0.208) | | | | |

Figure 4.50 illustrate a comparative graph of various classifiers' AUC on the Contact Lenses data sets. For interpretation of the values of area under the curve, this thesis uses the grading point system that was discussed in section 3.4.6.

By looking at Figure 4.50 and Table 4.43, we can see that AUCs of FSR-AIRS2 and seven other classifiers are above 0.9, which indicate that these classifiers perform excellent on this data set. Here, the AUC of FSR-AIRS2 is the highest of all. The complete interpretation is summarized in Table 4.56. The complete explanation is presented at the end of this section, just after Figure 4.62 and before Table 4.56.

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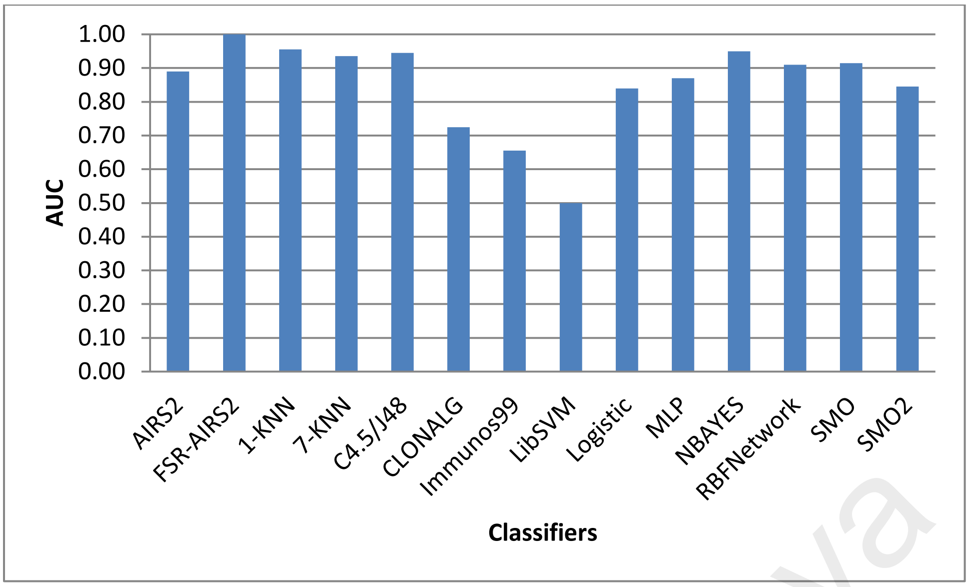

**Figure 4.50: Comparison of FSR-AIRS2 and Other Classifiers' Area under ROC on Contact Lenses Data Set**

Table 4.44 presents the best average test set of the area under ROC, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: AIRS2, 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Ionosphere data sets.

All experiments utilized 10 fold cross validation and were averaged over 10 runs.

**Table 4.44: Comparison of FSR-AIRS2 and Other Classifiers' Area under ROC on Ionosphere Data Set**

| **FSR-AIRS2** | **AIRS2** | **1KNN** | **7KNN** | **C4.5/J48** | **CLONALG** |
|---|---|---|---|---|---|
| 1.000<br>(0.0) | 0.816<br>(0.062) | 0.832<br>(0.067) | 0.924<br>(0.051) | 0.891<br>(0.060) | 0.736<br>(0.099) |
| **Immunos99** | **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** |
| 0.599<br>(0.057) | 0.907<br>(0.053) | 0.865<br>(0.081) | 0.919<br>(0.062) | 0.937<br>(0.037) | 0.954<br>(0.039) |
| **SMO** | **SMO2** | | | | |
| 0.845<br>(0.069) | 0.881<br>(0.062) | | | | |

Figure 4.51 illustrate a comparative graph of various classifiers’ AUC on the Ionosphere data sets. For interpretation of the values of area under the curve, this thesis

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uses the grading point system that was discussed in section 3.4.6. By looking at Figure 4.51 and Table 4.44, we can see that AUCs of FSR-AIRS2 and six other classifiers are above 0.9, which indicate that these classifiers perform excellent on this data set. Here, the AUC of FSR-AIRS2 is the highest of all.

The complete interpretation is summarized in Table 4.56. The complete explanation is presented at the end of this section, just after Figure 4.62 and before Table 4.56.

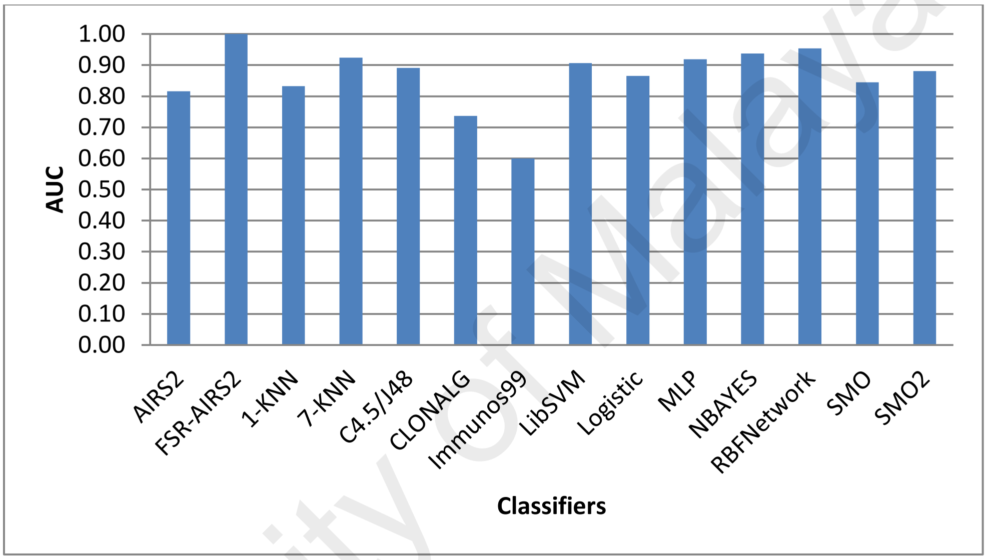

**Figure 4.51: Comparison of FSR-AIRS2 and Other Classifiers' Area under ROC on Ionosphere Data Set**

Table 4.45 presents the best average test set of the area under ROC, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: AIRS2, 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Iris data sets.

All experiments utilized 10 fold cross validation and were averaged over 10 runs.

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Table 4.45: Comparison of FSR-AIRS2 and Other Classifiers' Area under ROC on Iris Data Set

| FSR-AIRS2 | AIRS2 | 1KNN | 7KNN | C4.5/J48 | CLONALG |
|---|---|---|---|---|---|
| 1.000<br>(0.0) | 1.000<br>(0.0) | 1.000<br>(0.0) | 1.000<br>(0.0) | 0.990<br>(0.030) | 1.000<br>(0.0) |
| **Immunos99** | **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** |
| 1.000<br>(0.0) | 1.000<br>(0.0) | 1.000<br>(0.0) | 1.000<br>(0.0) | 1.000<br>(0.0) | 1.000<br>(0.0) |
| **SMO** | **SMO2** | | | | |
| 1.000<br>(0.0) | 1.000<br>(0.0) | | | | |

Figure 4.52 illustrate a comparative graph of various classifiers' AUC on the Iris data sets. For interpretation of the values of area under the curve, this thesis uses the grading point system that was discussed in section 3.4.6. By looking at Figure 4.52 and Table 4.45, we can see that AUCs of almost all classifiers equal 1.0, which indicate that these classifiers perform excellent on this data set.

The complete interpretation is summarized in Table 4.56. The complete explanation is presented at the end of this section, just after Figure 4.62 and before Table 4.56.

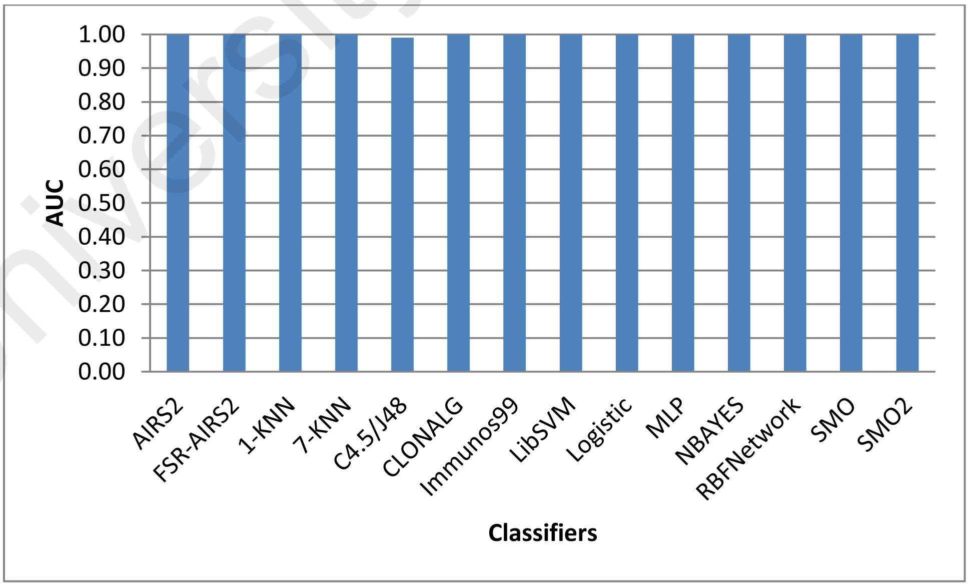

Figure 4.52: Comparison of FSR-AIRS2 and Other Classifiers' Area under ROC on Iris Data Set

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Table 4.46 presents the best average test set of the area under ROC, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: AIRS2, 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Liver Disorders data sets. All experiments utilized 10 fold cross validation and were averaged over 10 runs.

**Table 4.46: Comparison of FSR-AIRS2 and Other Classifiers' Area under ROC on Liver Disorders Data Set**

| **FSR-AIRS2** | **AIRS2** | **1KNN** | **7KNN** | **C4.5/J48** | **CLONALG** |
|---|---|---|---|---|---|
| 0.738<br>(0.109) | 0.585<br>(0.087) | 0.613<br>(0.083) | 0.638<br>(0.098) | 0.650<br>(0.090) | 0.534<br>(0.084) |
| **Immunos99** | **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** |
| 0.560<br>(0.067) | 0.517<br>(0.025) | 0.715<br>(0.091) | 0.500<br>(0.0) | 0.645<br>(0.096) | 0.680<br>(0.099) |
| **SMO** | **SMO2** | | | | |
| 0.500<br>(0.009) | 0.515<br>(0.032) | | | | |

Figure 4.53 illustrate a comparative graph of various classifiers' AUC on the Liver Disorders data sets. For interpretation of the values of area under the curve, this thesis uses the grading point system that was discussed in section 3.4.6. By looking at Figure 4.53 and Table 4.46, we can see that AUCs of FSR-AIRS2 and one another classifier are above 0.7, which indicate that these classifiers perform fair on this data set. Here, the AUC of FSR-AIRS2 is the highest of all.

The complete interpretation is summarized in Table 4.56. The complete explanation is presented at the end of this section, just after Figure 4.62 and before Table 4.56.

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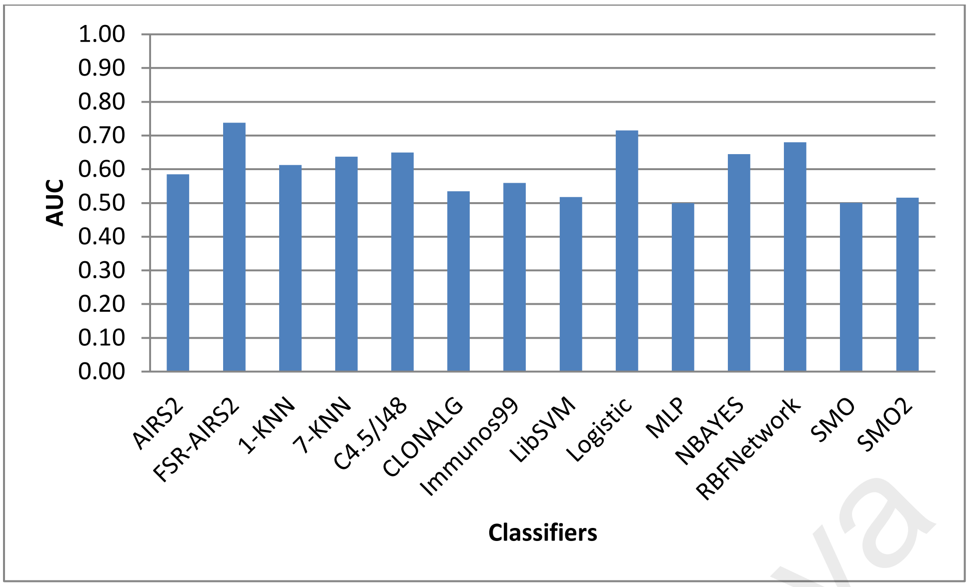

**Figure 4.53: Comparison of FSR-AIRS2 and Other Classifiers' Area under ROC on Liver Disorders Data Set**

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Table 4.47 presents the best average test set of the area under ROC, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: AIRS2, 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Lung Cancer data sets.

All experiments utilized 10 fold cross validation and were averaged over 10 runs.

**Table 4.47: Comparison of FSR-AIRS2 and Other Classifiers' Area under ROC on Lung Cancer Data Set**

| **FSR-AIRS2** | **AIRS2** | **1KNN** | **7KNN** | **C4.5/J48** | **CLONALG** |
|---|---|---|---|---|---|
| 0.929<br>(0.176) | 0.658<br>(0.284) | 0.777<br>(0.252) | 0.826<br>(0.224) | 0.714<br>(0.256) | 0.761<br>(0.260) |
| **Immunos99** | **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** |
| 0.623<br>(0.272) | 0.500<br>(0.0) | 0.604<br>(0.428) | 0.599<br>(0.295) | 0.818<br>(0.254) | 0.744<br>(0.312) |
| **SMO** | **SMO2** | | | | |
| 0.744<br>(0.271) | 0.756<br>(0.281) | | | | |

Figure 4.54 illustrate a comparative graph of various classifiers’ AUC on the Lung Cancer data sets. For interpretation of the values of area under the curve, this thesis uses

the grading point system that was discussed in section 3.4.6. By looking at Figure 4.54 and Table 4.47, we can see that only FSR-AIRS2 has achieved a value above 0.9 for AUC, and this indicates that the proposed method performed excellent on this data set. The difference with majority of well-known classifiers seems to be significant on this data set. The complete interpretation is summarized in Table 4.56. The complete explanation is presented at the end of this section, just after Figure 4.62 and before Table 4.56.

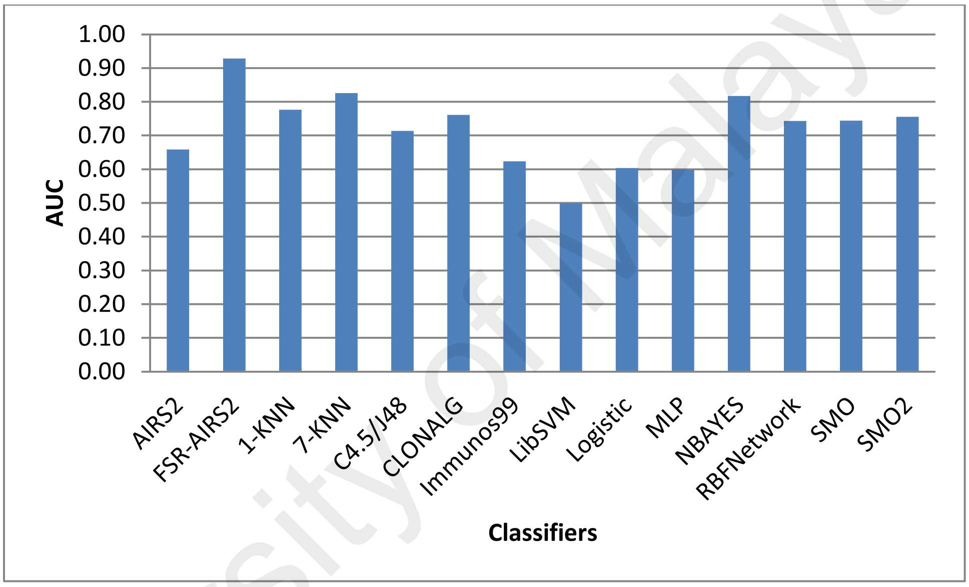

**Figure 4.54: Comparison of FSR-AIRS2 and Other Classifiers' Area under ROC on Lung Cancer Data Set**

Table 4.48 presents the best average test set of the area under ROC, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: AIRS2, 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Pima Indians data sets. All experiments utilized 10 fold cross validation and were averaged over 10 runs.

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**Table 4.48: Comparison of FSR-AIRS2 and Other Classifiers' Area under ROC on Pima Indians Data Set**

| FSR-AIRS2 | AIRS2 | 1KNN | 7KNN | C4.5/J48 | CLONALG |
|---|---|---|---|---|---|
| 0.996<br>(0.015) | 0.694<br>(0.062) | 0.668<br>(0.051) | 0.787<br>(0.053) | 0.751<br>(0.069) | 0.595<br>(0.073) |
| **Immunos99** | **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** |
| 0.563<br>(0.056) | 0.500<br>(0.0) | 0.831<br>(0.049) | 0.800<br>(0.054) | 0.815<br>(0.051) | 0.789<br>(0.056) |
| **SMO** | **SMO2** | | | | |
| 0.713<br>(0.055) | 0.716<br>(0.055) | | | | |

Figure 4.55 illustrate a comparative graph of various classifiers' AUC on the Pima Indians data sets. For interpretation of the values of area under the curve, this thesis uses the grading point system that was discussed in section 3.4.6. By looking at Figure 4.55 and Table 4.48, we can see that only FSR-AIRS2 has achieved a value above 0.9 for AUC, and this indicates that the proposed method performed excellent on this data set. The difference with majority of well-known classifiers seems to be significant on this data set.

The complete interpretation is summarized in Table 4.56. The complete explanation is presented at the end of this section, just after Figure 4.62 and before Table 4.56.

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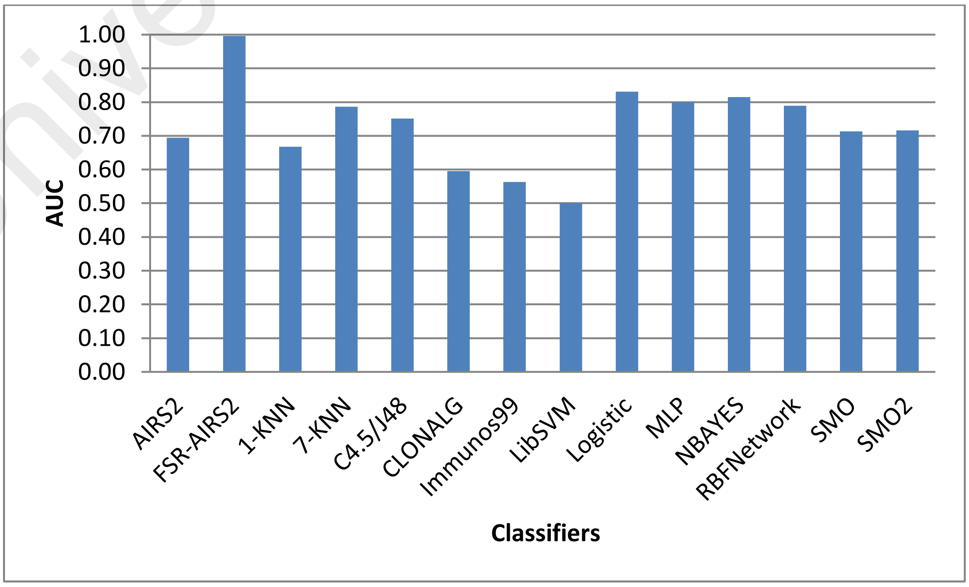

**Figure 4.55: Comparison of FSR-AIRS2 and Other Classifiers' Area under ROC on Pima Indians Data Set**

Table 4.49 presents the best average test set of the area under ROC, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: AIRS2, 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Statlog (Heart) data sets. All experiments utilized 10 fold cross validation and were averaged over 10 runs.

**Table 4.49: Comparison of FSR-AIRS2 and Other Classifiers' Area under ROC on Statlog (Heart) Data Set**

| **FSR-AIRS2** | **AIRS2** | **1KNN** | **7KNN** | **C4.5/J48** | **CLONALG** |
|---|---|---|---|---|---|
| 0.846<br>(0.096) | 0.770<br>(0.084) | 0.760<br>(0.085) | 0.873<br>(0.066) | 0.786<br>(0.094) | 0.623<br>(0.077) |
| **Immunos99** | **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** |
| 0.653<br>(0.085) | 0.504<br>(0.013) | 0.905<br>(0.054) | 0.500<br>(0.0) | 0.902<br>(0.054) | 0.891<br>(0.058) |
| **SMO** | **SMO2** | | | | |
| 0.834<br>(0.064) | 0.808<br>(0.068) | | | | |

Figure 4.56 illustrate a comparative graph of various classifiers' AUC on the Statlog (Heart) data sets. For interpretation of the values of area under the curve, this thesis uses the grading point system that was discussed in section 3.4.6. By looking at Figure 4.56 and Table 4.49, we can see that Logistic and NBayes have achieved a value of 0.9 for AUC, and this indicates that they performed excellent on this data set. FSR-AIRS2 ranked 5th and has got a grade of B (Good).

The complete interpretation is summarized in Table 4.56. The complete explanation is presented at the end of this section, just after Figure 4.62 and before Table 4.56.

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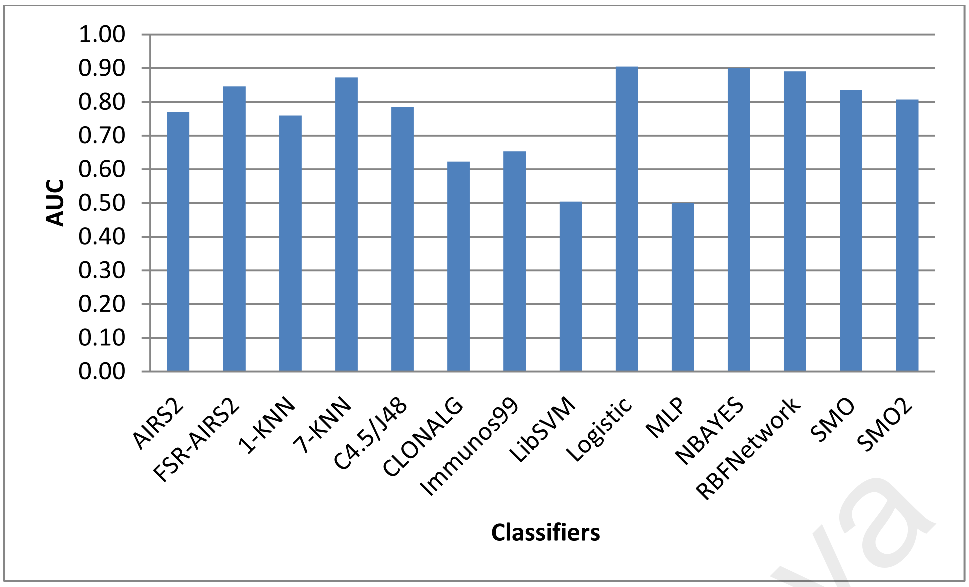

**Figure 4.56: Comparison of FSR-AIRS2 and Other Classifiers' Area under ROC on Statlog (Heart) Data Set**

Table 4.50 presents the best average test set of the area under ROC, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: AIRS2, 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Statlog (Image Segmentation) data sets.

All experiments utilized 10 fold cross validation and were averaged over 10 runs.

**Table 4.50: Comparison of FSR-AIRS2 and Other Classifiers' Area under ROC on Statlog (Image Segmentation) Data Set**

| **FSR-AIRS2** | **AIRS2** | **1KNN** | **7KNN** | **C4.5/J48** | **CLONALG** |
|---|---|---|---|---|---|
| 0.943<br>(0.158) | 0.981<br>(0.011) | 0.995<br>(0.008) | 1.000<br>(0.0) | 0.994<br>(0.009) | 0.586<br>(0.123) |
| **Immunos99** | **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** |
| 0.540<br>(0.31) | 0.852<br>(0.040) | 0.999<br>(0.001) | 0.999<br>(0.003) | 0.992<br>(0.004) | 0.996<br>(0.005) |
| **SMO** | **SMO2** | | | | |
| 0.995<br>(0.006) | 0.993<br>(0.010) | | | | |

Figure 4.57 illustrate a comparative graph of various classifiers’ AUC on the Statlog (Image Segmentation) data sets. For interpretation of the values of area under the curve,

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this thesis uses the grading point system that was discussed in section 3.4.6. By looking at Figure 4.57 and Table 4.50, we can see that 7KNN, Logistic, and MLP, and RBF Network have achieved a value very close to 1 for AUC. However, FSR-AIRS2 and ten other well-known classifiers ranked excellent on this data set. The complete interpretation is summarized in Table 4.56. The complete explanation is presented at the end of this section, just after Figure 4.62 and before Table 4.56.

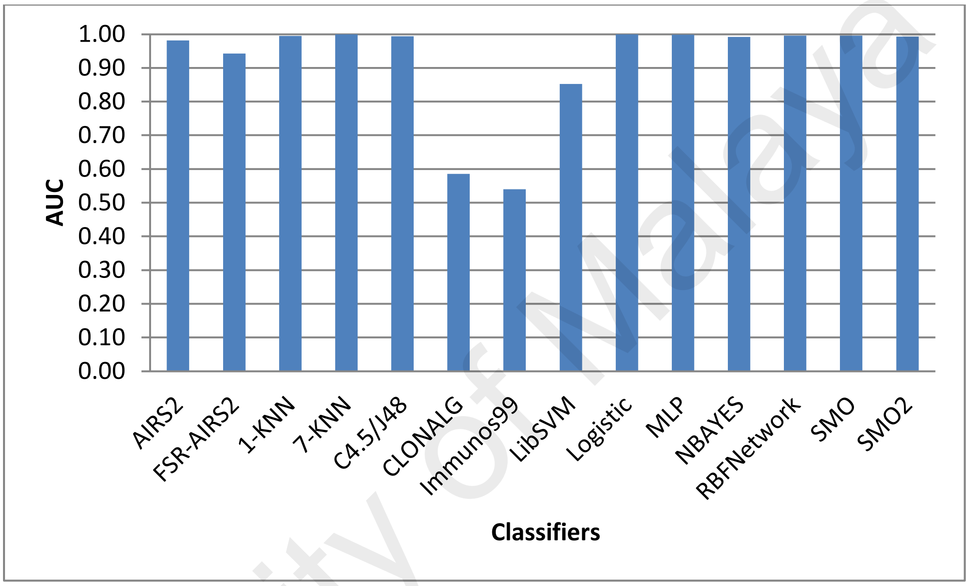

**Figure 4.57: Comparison of FSR-AIRS2 and Other Classifiers' Area under ROC on Statlog (Image Segmentation) Data Set**

Table 4.51 presents the best average test set of the area under ROC, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: AIRS2, 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Statlog (Vehicle Silhouettes) data sets.

All experiments utilized 10 fold cross validation and were averaged over 10 runs.

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**Table 4.51: Comparison of FSR-AIRS2 and Other Classifiers' Area under ROC on Statlog (Vehicle Silhouettes) Data Set**

| **FSR-AIRS2** | **AIRS2** | **1KNN** | **7KNN** | **C4.5/J48** | **CLONALG** |
|---|---|---|---|---|---|
| 0.847<br>(0.094) | 0.670<br>(0.057) | 0.657<br>(0.050) | 0.812<br>(0.036) | 0.762<br>(0.056) | 0.573<br>(0.083) |
| **Immunos99** | **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** |
| 0.574<br>(0.065) | 0.499<br>(0.003) | 0.901<br>(0.028) | 0.894<br>(0.033) | 0.704<br>(0.050) | 0.789<br>(0.042) |
| **SMO** | **SMO2** | | | | |
| 0.762<br>(0.041) | 0.822<br>(0.043) | | | | |

Figure 4.58 illustrate a comparative graph of various classifiers' AUC on the Statlog (Vehicle Silhouettes) data sets. For interpretation of the values of area under the curve, this thesis uses the grading point system that was discussed in section 3.4.6. By looking at Figure 4.58 and Table 4.51, we can see that only Logistic has achieved a value over 0.9 for AUC, which indicates an excellent performance with this data set. FSR-AIRS2 ranked 3rd, and with three other well-known classifiers achieved grade B (Good) on this data set. The complete interpretation is summarized in Table 4.56. The complete explanation is presented at the end of this section, just after Figure 4.62 and before Table 4.56.

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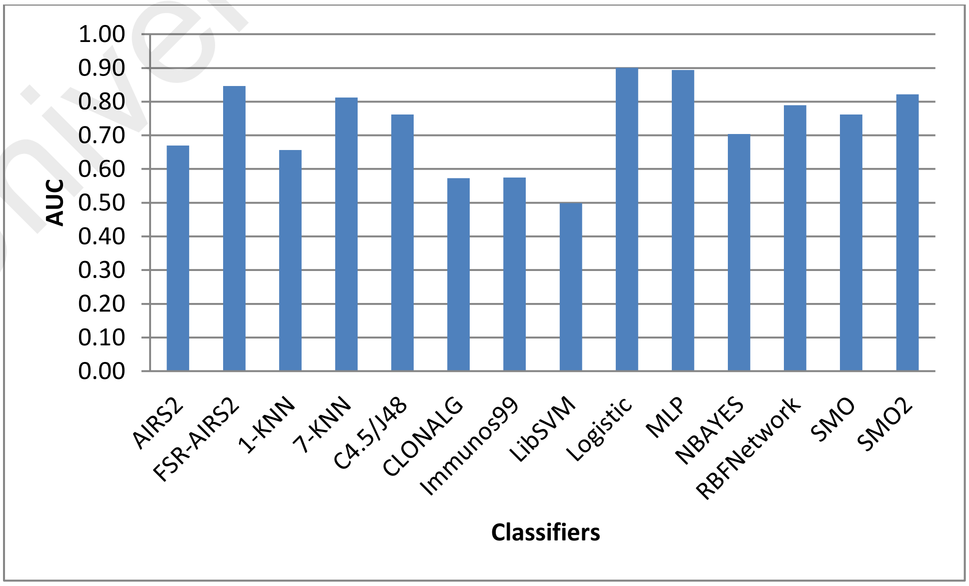

**Figure 4.58: Comparison of FSR-AIRS2 and Other Classifiers' Area under ROC on Statlog (Vehicle Silhouettes) Data Set**

Table 4.52 presents the best average test set of the area under ROC, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: AIRS2, 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Sonar, Mines vs. Rocks data sets. All experiments utilized 10 fold cross validation and were averaged over 10 runs.

**Table 4.52: Comparison of FSR-AIRS2 and Other Classifiers' Area under ROC on Sonar, Mines vs. Rocks Data Set**

| **FSR-AIRS2** | **AIRS2** | **1KNN** | **7KNN** | **C4.5/J48** | **CLONALG** |
|---|---|---|---|---|---|
| 0.979<br>(0.050) | 0.662<br>(0.104) | 0.859<br>(0.086) | 0.890<br>(0.075) | 0.753<br>(0.113) | 0.632<br>(0.101) |
| **Immunos99** | **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** |
| 0.603<br>(0.096) | 0.629<br>(0.077) | 0.762<br>(0.101) | 0.887<br>(0.072) | 0.800<br>(0.095) | 0.812<br>(0.092) |
| **SMO** | **SMO2** | | | | |
| 0.764<br>(0.083) | 0.835<br>(0.078) | | | | |

Figure 4.59 illustrate a comparative graph of various classifiers' AUC on the Sonar, Mines vs. Rocks data sets. For interpretation of the values of area under the curve, this thesis uses the grading point system that was discussed in section 3.4.6.

By looking at Figure 4.59 and Table 4.52, we can see that only FSR-AIRS2 has achieved a value over 0.9 for AUC, which indicates an excellent performance with this data set. Six of well-known classifiers achieved grade B (Good) on this data set.

The complete interpretation is summarized in Table 4.56. The complete explanation is presented at the end of this section, just after Figure 4.62 and before Table 4.56.

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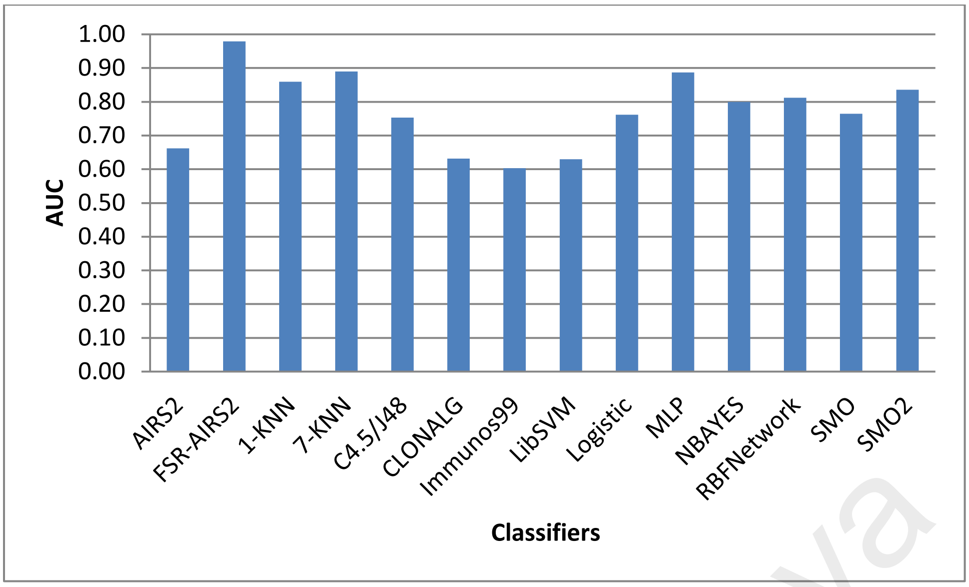

**Figure 4.59: Comparison of FSR-AIRS2 and Other Classifiers' Area under ROC on Sonar, Mines vs. Rocks Data Set**

Table 4.53 presents the best average test set of the area under ROC, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: AIRS2, 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Vertebral Column_2C data sets. All experiments utilized 10 fold cross validation and were averaged over 10 runs.

**Table 4.53: Comparison of FSR-AIRS2 and Other Classifiers' Area under ROC on Vertebral Column_2C Data Set**

| **FSR-AIRS2** | **AIRS2** | **1KNN** | **7KNN** | **C4.5/J48** | **CLONALG** |
|---|---|---|---|---|---|
| 0.842<br>(0.104) | 0.730<br>(0.098) | 0.801<br>(0.070) | 0.851<br>(0.064) | 0.843<br>(0.086) | 0.695<br>(0.124) |
| **Immunos99** | **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** |
| 0.793<br>(0.058) | 0.500<br>(0.0) | 0.936<br>(0.039) | 0.930<br>(0.045) | 0.881<br>(0.056) | 0.881<br>(0.063) |
| **SMO** | **SMO2** | | | | |
| 0.709<br>(0.086) | 0.714<br>(0.089) | | | | |

Figure 4.60 illustrate a comparative graph of various classifiers' AUC on the Vertebral Column_2C data sets. For interpretation of the values of area under the curve, this thesis uses the grading point system that was discussed in section 3.4.6. By looking at

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Figure 4.60 and Table 4.53, we can see that only Logistic and MLP have achieved a value over 0.9 for AUC, which indicates an excellent performance with this data set. FSR-AIRS2 ranked sixth, and together with five of well-known classifiers achieved grade B (Good) on this data set.

The complete interpretation is summarized in Table 4.56. The complete explanation is presented at the end of this section, just after Figure 4.62 and before Table 4.56.

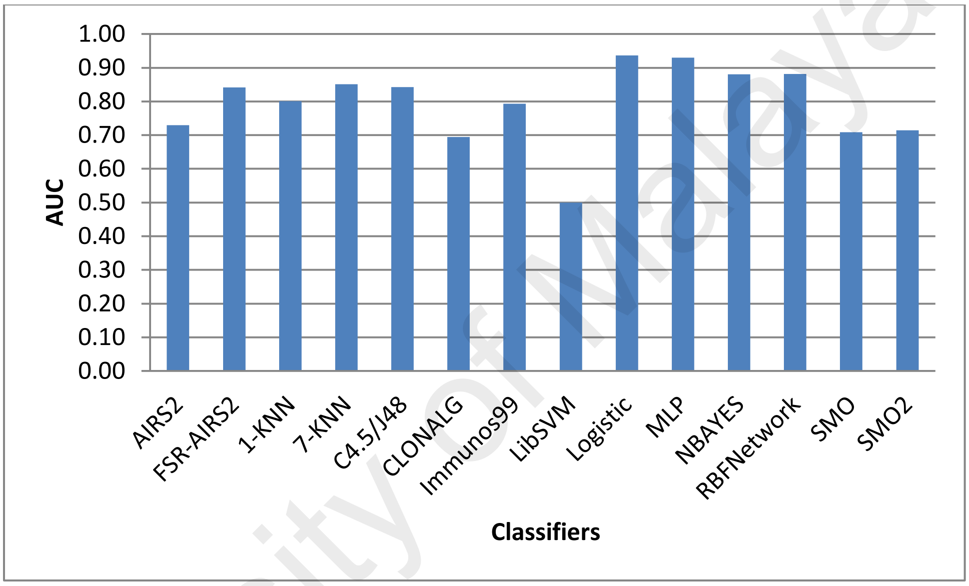

**Figure 4.60: Comparison of FSR-AIRS2 and Other Classifiers' Area under ROC on Vertebral Column_2C Data Set**

Table 4.54 presents the best average test set of the area under ROC, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: AIRS2, 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Vertebral Column_3C data sets.

All experiments utilized 10 fold cross validation and were averaged over 10 runs.

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**Table 4.54: Comparison of FSR-AIRS2 and Other Classifiers' Area under ROC on Vertebral Column_3C Data Set**

| FSR-AIRS2 | AIRS2 | 1KNN | 7KNN | C4.5/J48 | CLONALG |
|---|---|---|---|---|---|
| 0.890<br>(0.107) | 0.739<br>(0.106) | 0.747<br>(0.100) | 0.890<br>(0.054) | 0.839<br>(0.087) | 0.656<br>(0.149) |
| **Immunos99** | **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** |
| 0.752<br>(0.103) | 0.500<br>(0.0) | 0.947<br>(0.038) | 0.940<br>(0.041) | 0.925<br>(0.047) | 0.909<br>(0.055) |
| **SMO** | **SMO2** | | | | |
| 0.833<br>(0.076) | 0.852<br>(0.075) | | | | |

Figure 4.61 illustrate a comparative graph of various classifiers' AUC on the Vertebral Column_3C data sets. For interpretation of the values of area under the curve, this thesis uses the grading point system that was discussed in section 3.4.6. By looking at Figure 4.61 and Table 4.54, we can see that Logistic, MLP, NBayes, and RBF Network have achieved a value over 0.9 for AUC, which indicates an excellent performance with this data set. FSR-AIRS2 ranked fifth, and together with four of well-known classifiers achieved grade B (Good) on this data set.

The complete interpretation is summarized in Table 4.56. The complete explanation is presented at the end of this section, just after Figure 4.62 and before Table 4.56.

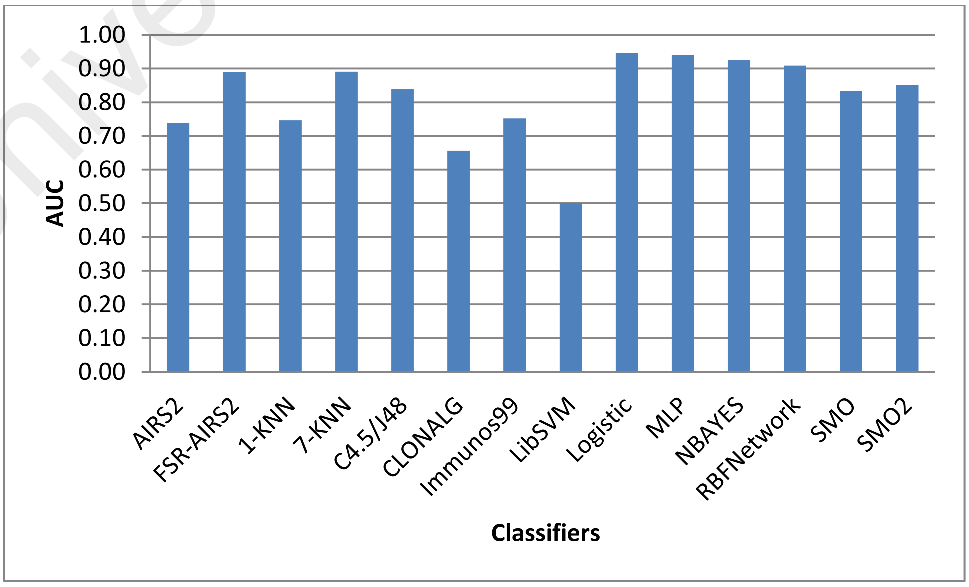

**Figure 4.61: Comparison of FSR-AIRS2 and Other Classifiers' Area under ROC on Vertebral Column_3C Data Set**

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Table 4.55 presents the best average test set of the area under ROC, together with the standard deviations (given in parenthesis) obtained from FSR-AIRS2 and other well-known classifiers: AIRS2, 1-KNN, 7-KNN, C4.5/J48, CLONALG, Immunos99, LibSVM, Logistic, MLP, Naïve Bayes, RBF Network, SMO, and SMO2 on the Wisconsin Breast Cancer Data set (WBCD) (Original). All experiments utilized 10 fold cross validation and were averaged over 10 runs.

**Table 4.55: Comparison of FSR-AIRS2 and Other Classifiers' Area under ROC on Wisconsin Breast Cancer Data Set (WBCD) (Original)**

| **FSR-AIRS2** | **AIRS2** | **1KNN** | **7KNN** | **C4.5/J48** | **CLONALG** |
|---|---|---|---|---|---|
| 1.000<br>(0.0) | 0.963<br>(0.026) | 0.944<br>(0.031) | 0.990<br>(0.011) | 0.947<br>(0.038) | 0.504<br>(0.047) |
| **Immunos99** | **LibSVM** | **Logistic** | **MLP** | **NBayes** | **RBF Netw.** |
| 0.537<br>(0.028) | 0.511<br>(0.014) | 0.994<br>(0.007) | 0.988<br>(0.011) | 0.988<br>(0.011) | 0.989<br>(0.010) |
| **SMO** | **SMO2** | | | | |
| 0.964<br>(0.023) | 0.960<br>(0.026) | | | | |

Figure 4.62 illustrate a comparative graph of various classifiers' AUC on the Wisconsin Breast Cancer Data set (WBCD) (Original). For interpretation of the values of area under the curve, this thesis uses the grading point system that was discussed in section 3.4.6.

By looking at Figure 4.62 and Table 4.55, we can see that the proposed method, the FSR-AIRS2 and ten of well-known classifiers have achieved a value over 0.9 for AUC, which indicates an excellent performance with this data set. The complete interpretation is summarized in Table 4.56.

The complete explanation is presented at the end of this section, just after Figure 4.62 and before Table 4.56.

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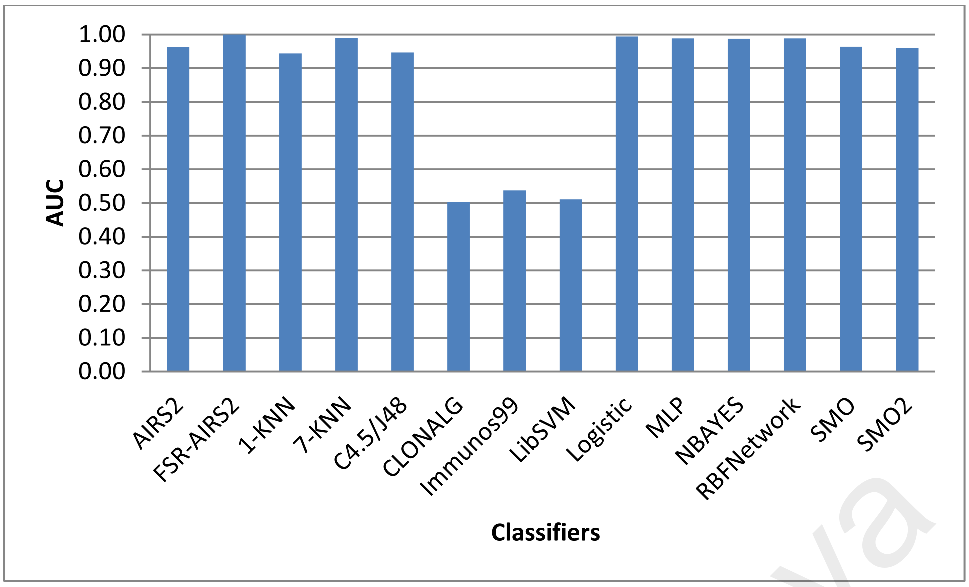

**Figure 4.62: Comparison of FSR-AIRS2 and Other Classifiers' Area under ROC on Wisconsin Breast Cancer Data Set (WBCD) (Original)**

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Table 4.56 shows the ranking of classifiers based on their achieved grades for area under ROC. To evaluate the performance of classifiers based on their AUC, we looked at each classifier individually and determined the frequency of their AUCs rankings. **FSR-AIRS2** was ranked excellent (A) 10 times, good (B) 4 times and Fair (C) 1 time. **Naïve Bayes** classifier obtained 9 times A, 4 times B, 1 time C, and 1 time D. Followed by **Logistic** which obtained 9 times A, 3 times B, 2 times C, and 1 time D. **MLP** ranked 4th with 8 times A, 4 times B, and 3 times F. **RBF Network** achieved 8 times A, 3 times B, 3 times C, and 1 time D. **7KNN** ranked 6th with 7 times A, 6 times B, 1 time C, and 1 time D. **SMO** ranked 7th with 6 times A, 3 times B, 5 time C, and 1 time F. **1KNN** obtained 6 times A, 6 times B, 6 times C, and 3 times D. **SMO2** ranked next with 5 times A, 6 times B, 3 times C, and 1 time F. **C4.5/J48** ranked 10th with 5 times A, 4 times B, 5 times C, 4 times D, and 1 time F. It was followed by **AIRS2** with 5 times A, 2 times B, 3 times C, and 1 time F. **LibSVM** ranked 12th with 3 times A, 1 time B, 1 time D, and 10 times F. **CLONALG** obtained 1 time A, 2 times B, 3 times C, 4 times D, and 5 times F. Immunos99 was ranked 14th with 1 times A, 2 times B, 2 times C, 4 times D, and 6 times F.

**Table 4.56:** Evaluation of Classifiers on Area under ROC

| Rank | Classifier | A | B | C | D | F |
|---|---|---|---|---|---|---|
| 1 | FSR-AIRS2 | 10 | 4 | 1 | - | - |
| 2 | Naïve Bayes | 9 | 4 | 1 | 1 | - |
| 3 | Logistic | 9 | 3 | 2 | 1 | - |
| 4 | MLP | 8 | 4 | - | - | 3 |
| 5 | RBF Network | 8 | 3 | 3 | 1 | - |
| 6 | 7KNN | 7 | 6 | 1 | 1 | - |
| 7 | SMO | 6 | 3 | 5 | - | 1 |
| 8 | 1KNN | 6 | 3 | 3 | 3 | - |
| 9 | SMO2 | 5 | 6 | 3 | - | 1 |
| 10 | C4.5/J48 | 5 | 4 | 5 | 1 | - |
| 11 | AIRS2 | 5 | 2 | 3 | 4 | 1 |
| 12 | LibSVM | 3 | 1 | - | 1 | 10 |
| 13 | CLONALG | 1 | 2 | 3 | 4 | 5 |
| 14 | Immunos99 | 1 | 2 | 2 | 4 | 6 |

The above mentioned results and the classification results that were presented in section 4.6.3.2 suggest that the development of FSR-AIRS2 has improved the performance, and in comparison with other classifiers, FSR-AIRS2 seems to perform better.

## 4.7 Summary

This chapter presented three new models: FRA-AIRS, RRC-AIRS2, and FSR-AIRS2. In this chapter we have described these algorithms in detail and explained changes that were made to the regular AIRS2. The areas that were changed are: resource allocation, resource competition, and in addition the classifier KNN was replaced with SVM. The performance of the proposed algorithms on some publicly available standard machine learning data sets were examined. Statistical evidence showed that proposed changes improved the classification accuracy of the algorithm, which signifies the importance of proposed modifications.

The results also suggested that there were signs of improvement in data reduction capabilities. Evaluations of the area under the curve and comparison with other classifiers have shown that our main model, the FSR-AIRS2, has performed well.

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As mentioned earlier, some classifiers were faster than FSR-AIRS2 and some slower in running time. The running times of the FSR-AIRS2 algorithm on benchmark data sets ranked somewhere among well-known classifiers.

This chapter presented details of FRA-AIRS2 and RRC-AIRS2 algorithms and compared their results with that of the AIRS2. Results showed that both algorithms performed well in comparison with the AIRS2.

The "no free lunch theorem" introduced by (Wolpert & Macready, 1997) is still valid, according to this theorem no classifier can significantly outperform all other classifiers across all problem domains. It is simply impossible to have a general purpose classifier that can work on all datasets with highest accuracy, and in least amount of time.

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# CHAPTER 5: CONCLUSIONS AND FUTURE WORK

## 5.1 Conclusion

There is a huge request for new generations of tools to extract significant and useful information from rapidly growing data. One of major tasks of data mining is classification and results of Artificial Immune Recognition System (AIRS2) an immune inspired algorithm has shown its potential for classification purposes. AIRS2 is a classifier offering robust and powerful information processing capabilities. It has been shown that AIRS2 has the potentials to perform better and therefore deserves to be investigated.

Performance of each classifier is measured with its classification accuracy and efficiency and improving them was the goal of this thesis, therefore this research studied and analyzed the algorithm of AIRS2. This study has pointed out to some issues that needed to be addressed.

One of the problems occurred in the resource allocation method of AIRS, where a linear function was used to determine the amount of resources that needed to be allocated, and this linearity has increased the running time of AIRS2 and therefore reduced its efficiency. In order to solve this linearity issue, this thesis replaced the linear function with a fuzzy function.

Resource competition part of AIRS posed another problem, here, premature memory cells were generated which were responsible for reduced accuracy. In order to solve this problem, a new competition mechanism using real world tournament selection strategy was utilized.

Further AIRS2 uses KNN as a classifier and that makes it severely vulnerable to the presence of noise, irrelevant features, and the number of attributes. KNN also uses majority voting and a drawback of this is that the classes with the more frequent instances

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tend to dominate the prediction of the new instance. The consequence of using KNN was ultimately reduction of classification accuracy. This thesis solved this problem with replacing KNN with SVM, which is known as a robust and more accurate classifier.

The new algorithm was dubbed as FSR-AIRS2, its performance was evaluated and compared with the results obtained with AIRS2 on 15 benchmark data sets obtained from UCI machine learning repository. The comparison with AIRS2 showed that FSR-AIRS2 has statistically significantly increased the classification accuracy on almost all (14 out of 15) benchmark data sets.

Comparing the results of FSR-AIRS2 with other classifiers showed that FSR-AIRS2 has achieved higher classification accuracy on majority of data sets. These results indicated that the FSR-AIRS2 algorithm performs comparatively well in relation to other classifiers.

Comparing the data reduction capability of FSR-AIRS2 with that of AIRS2 has shown that FSR-AIRS2 achieved greater efficiency than AIRS2 without sacrificing accuracy. Data reduction causes less runtime and this way increases the efficiency of the algorithm. Of course data reduction depends on the domain, and there can be no assurance that FSR-AIRS2 would keep the trend for all data sets.

While 3 classifiers performed faster in running time, FSR-AIRS2 was able to be faster in most cases on the same benchmark data sets. This is of course encouraging, because it shows that FSR-AIRS2 did not negatively affect the running time of the classifier so much. The results suggest that FSR-AIRS2 is comparable to other classifiers based on the running time. It is not surprising that when FSRARIRS2 has reduced the data set that we see an increase in running time.

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Comparing the AUCs obtained with FSR-AIRS2 to other classifiers showed that that the FSR-AIRS2 has improved the performance, and in comparison with other classifiers, FSR-AIRS2 seems to perform better.

## 5.2 Future Works

This thesis has introduced an improved version of artificial immune recognition system dubbed as FSRARIS2. The focus of this study was to improve the performance of AIRS2. As such, there is inevitably more to be done. This section discusses some of these thoughts here.

### 5.2.1 Utilizing other Classifiers Instead of SVM

In order to improve the performance of the classifier, this study has utilized Support Vector Machine instead of KNN, which has been used by the AIRS1 and AIRS2. The obtained results were encouraging and promising as it has been shown in chapter CHAPTER 4:. However, the search for a better classifier must continue because it is highly demanded. Utilizing other well-known classifiers such as, but not limited to: C4.5, Naïve Bayes, k-Means, and CART may improve the classification performance.

### 5.2.2 Fuzzy Control of Resources

This study used fuzzy logic to control resource allocation mechanism of the algorithm. This concept could be extended to the resource competition mechanism as well which may improve the quality of evolved memory cells and thus improve the performance of the classifier. This study also recommends exploring other fuzzy methods for controlling resources.

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