ANFIS Interpolation and Its Application for Image Super Resolution

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Declaration and Statement

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STATEMENT 1

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Fuzzy inference systems work through manipulating fuzzy if-then rules. Amongst the various existing fuzzy inference systems, the adaptive network based fuzzy inference system (ANFIS) has become one of the most powerful and popular tools for finding solutions to highly non-linear problems. Whilst promising for practical applications, most existing research related to ANFIS focuses on how to learn such an inference system with sufficient training data. However, in some real situations it is very hard or even impossible to get sufficient data for the required learning process. The shortage of training data significantly degrades the performance of such learned ANFIS models.

In light of this, the concept of ANFIS interpolation is proposed in the thesis, to deal with the problem of ANFIS construction with insufficient training data. It works by interpolating two well trained ANFISs in neighbouring domains where sufficient training data is available, in an effort to improve the performance of the constructed ANFIS in the current problem domain where there is only limited (or sparse) training data. Two types of ANFIS interpolation method are developed, including: 1) An initial method via group based rule interpolation, working through interpolating a group of fuzzy rules with the help of a rule dictionary; 2) An improved method via evolutionary process, in which the interpolated rules act as an initial population and are updated subsequently through the use of a genetic algorithm. Experimental results demonstrate the significantly improved performance of the proposed methods over the original non-interpolation ANFIS model, with the averaged root mean squared error (RMSE) reduced to $1.63 \pm 0.39$ from the original $3.71 \pm 0.98$.

Having recognised the capability of ANFIS in producing effective non-linear mappings, it is applied to address the problem of image super resolution in this thesis, in an effort to learn the non-linear mapping between a low resolution image and a high resolution one. Firstly, a natural image super resolution method with full training data is developed by learning multiple ANFIS mappings, showing the effectiveness of ANFIS model when sufficient training data is provided. A hyperspectral image super resolution method with sparse training data through the use of the proposed ANFIS interpolation methods is then developed, validating the efficacy of the interpolated ANFIS model when only sparse training data is available.
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Chapter 1

Introduction

With the rapid development of computer hardware and software technologies, machine learning has become one of the most attractive topics in the field of computer science in recent years. There is no doubt that the world we live in today is full of all types of data (such as text data, image data, video data and so on), the fast growth of available data makes the management and analysis of data at hand ever more important and also ever more difficult. The machine learning theory is proposed aiming at extracting useful knowledge from those raw data instead of the human brain with higher speed and larger scale, which brings extreme convenience to human life. Different machine learning techniques, representative algorithms including the evolutionary computation, the neural networks, deep learning and fuzzy inference systems etc., are developed with different mechanisms and have different characteristics.

Evolutionary computation [9, 10] is one of the most popular machine learning methods, which offers a set of optimisation algorithms by analogy to natural evolution processes (e.g. crossover, mutation, and survival of the fitness evaluation for genetic algorithms). It provides an effective and efficient way for searching optimal solution in poorly understood and irregular problem spaces. Typically, evolutionary algorithms work with a population of individuals, in which each individual may be one or a set of potential solutions in the solution space. Whilst implemented in a stochastic manner, such algorithms perform a highly effective search in the problem hyperspace, iteratively directing the solution to promising regions. Typical evolutionary algorithms such as genetic algorithm (GA) [121], genetic programming
(GP) [1] and particle swarm optimizer (PSO) [175], have been widely employed for a variety of theoretical and practical applications [87, 143, 148, 161].

Another branch of the machine learning methods is the artificial neural network [54, 117]. The first neurocomputer, Dr. Robert Hecht-Nielsen, defined it as a computing system made up of a number of simple, highly interconnected processing elements, which process information by their dynamic state response to external inputs. Although neural networks are an old topic, they have achieved significant breakthrough in recent decades. With the increase of storage capacity and calculation speed of computers, deep learning [40] technique has been developed as an extension of traditional artificial neural networks, with much more network layers and much more complex network structures. It can better extract and represent the features from data, especially for those multi-dimensional complex data (e.g. image data and voice data). Deep learning algorithms have been applied to various real world applications since proposed (such as classification, tracking, recognition, just to name a few), generating the state of the art results [53, 86, 127]. Different from traditional neural network methods, the layers of network in deep learning methods are much deeper with much more parameters. This gives the network more learning capacity, but increases the required storage space at the mean time.

Apart from the high accuracy of the deep learning algorithms, they suffer from having a huge amount of parameters in a network, which requires a large storage space and long running time in the network training process. Another argued issue in deep learning methods is the interpretability and transparency. Deep neural networks work as a black box, making the physical meaning of the resulting network structures not easy to explain. Different from deep learning, fuzzy inference systems provide an interpretable way for solving machine learning problems [115, 139]. They work by the use of a rule-base containing a set of fuzzy ‘if-then’ rules, in which each fuzzy set is described by a membership function. The interpretability and transparency of fuzzy inference systems is reflected in two aspects: 1) The fuzzy ‘if-then’ rules record the logical representation of the intuitive expert knowledge. 2) The fuzzy sets as well as the underlying membership functions preserve the linguistic meaning of the given label. Fuzzy inference systems have achieved significant successes in performing many real world tasks, such as classification, regression and prediction [4, 23, 48, 72, 114].
1.1 Fuzzy Inference Systems (FIS)

Fuzzy inference systems transform human knowledge to mathematical models (represented by a set of fuzzy rules), and conduct inference in a systematic manner. They are developed based on the fuzzy set theory [168, 177] and the fuzzy logic theory [167]. Based on the fact that the crisp description of the real world information is always imprecise and is easily affected by the subjective factors, fuzzy inference systems handle imprecision, a form of uncertainty to better describe the observations in the real world. The general framework of a fuzzy inference system is shown in Figure 1.1. There are four key components in such an FIS, including the fuzzification interface, the inference engine, the defuzzification interface and the knowledge base. These key components are introduced respectively as follows.

- The *fuzzification interface* transforms crisp values obtained from the real world measurements into fuzzy representations through the use of fuzzy sets. The definition of fuzzy set makes it possible to represent an input value with linguistic meaning, which is implemented by the use of a membership function related to the fuzzy set. Take the representation of a person's height (say, 6 feet) as an example, if using the crisp representation, it is only a fixed value, while in terms of fuzzy representation, it can be interpreted as "This person is high with a high degree of truth". Theoretically any continuous or piecewise differentiable, convex and normal functions can be utilized as Membership Function (MF), commonly used MFs include triangular, trapezoidal, Gaussian and bell-shaped ones.
1.1. Fuzzy Inference Systems (FIS)

- The *inference engine* processes the incoming fuzzy values from the fuzzification interface and then makes the decision together with the knowledge base. The most commonly used inference engine is the compositional rule of inference [166]. It works by firing or matching rules in the rule-base, and the final decision is made by composing the consequences of all the fired rules.

- The *defuzzification interface* performs the inverse operation to the fuzzification interface. Usually in real world tasks, the output of a fuzzy inference system should be real values, keeping the same as its input, so the defuzzification interface is designed to map the fuzzy values obtained from the inference engine into crisp values. Generally, the choice of the defuzzification method depends on what kind of decision the fuzzy inference system is going to make. One of the most commonly used defuzzification methods is using the centre of the area, e.g. the centre of gravity (COG) of a triangular fuzzy set.

- The *knowledge base* contains two components, the rule-base, containing the collection of fuzzy ‘if-then’ rules, and the data base, containing the parameters in rules (e.g. membership functions of the fuzzy partitions associated to the linguistic variables).

Fuzzy ‘if-then’ rules are the most important components in a fuzzy inference system. Different types of fuzzy rule have been developed in the literature. According to whether the consequence of a fuzzy rule is associated with its rule antecedent or not, the fuzzy rules can be classified into two categories, the mamdani-type rules and the Takagi-Sugeno-Kang (TSK)-type rules. In the mamdani-type rules [108], the input variables only appear in the antecedent parts, while in the TSK-type rules [131] those variables also appear in the consequent parts as a linear function of the input.

Based on the two types of fuzzy rule, there are accordingly two forms of knowledge representation in fuzzy inference systems: Mandani-type models and TSK-type models. Mandani models are classical fuzzy systems which have been popular in many real world applications [19], while TSK representatives have also played an increasingly important role in such applications, including for example, stock market prediction [23] and EGG signals recognition [72]. The success of TSK-type fuzzy inference systems is largely owing to their capability of approximating complex non-linear functions [36].
1.2. Training Data Shortage Issues

Generally, there exist two ways to construct the knowledge base of a fuzzy inference system. One way is to translate expert knowledge into fuzzy rules directly, and the corresponding fuzzy inference systems are also called fuzzy expert systems [18, 103, 107]. It offers very good fuzzy representation of expert knowledge. But for large real-world problems, it may be very hard to ensure the efficiency and accuracy of the resulted knowledge base when such strategy is utilised. The other way for building an effective knowledge base is to use data-driven methods. In such FISs, the fuzzy rules are obtained from data by using machine learning techniques rather than obtained from expert knowledge directly [19, 30, 33, 34, 78].

1.2 Training Data Shortage Issues

Owing to the simplicity and explainability in representing human knowledge, fuzzy inference systems have become one of the most popular tools for finding solutions to various real world problems (e.g., [4, 30, 124]). They have been studied for many years, in both the design of the inference engine [136, 159, 166] and the induction of the rule-base [2, 163]. Amongst such research, how to construct an effective FIS from data is becoming a more and more attractive topic. For such data-driven based fuzzy inference systems, it is necessary to get sufficient training data for the required learning process in order to train a useful model. Most existing studies on fuzzy inference system construction assume that sufficient training data is available [116]. This assumption can hold for many cases in this age with sufficient well-distributed data, however, in some special situations, it is really hard or even impossible to obtain enough data for the required training procedure (such as some remote sensing tasks, or medical problems). In such cases, the shortage of data will severely restrict the potential of the learned fuzzy inference systems.

In the relevant literature, a typical way to solve this practical issue (of training data shortage) is to conduct the learning process through a so-called transfer learning procedure [41, 116, 128, 178, 179]. Such techniques exploit the knowledge accumulated from data in an auxiliary domain (termed source domain) to support predictive modelling in the problem domain at hand (termed target domain). Particularly, transfer learning usually works, by constructing non-linear mappings between the target and the source domain and transferring the data or the model parameters.
between a certain source domain and a target domain via learned mappings. In so doing, it is feasible to utilise the knowledge regarding a given source model to approximately perform fuzzy inference in the target domain.

An alternative solution to this challenging problem is through the use of Fuzzy Rule Interpolation (FRI) technique [12, 84, 133]. Conventional fuzzy inference methods [136, 159, 166] must work with dense rule-base, in which the input region is completely covered. However, under the data shortage situations the resulting rule-base will be a sparse rule-base with ‘gaps’, therefore the conventional fuzzy inference methods cannot drive a conclusion. The FRI technique is developed to enable fuzzy inference to be performed on sparse rule-bases. In general, for a given observation that does not match any rule of a sparse rule-base, FRI techniques work by interpolating new rules from the existing ones. Typically, FRI interpolates a fuzzy rule by selecting and averaging given rules that are the closest to an unfired observation, thereby enabling fuzzy systems to perform inference even if no rules can be fired by pattern matching. Based on the general FRI idea, transformation based FRI (T-FRI) [58, 59] has been proposed for improved performance through scale and move transformations. This greatly increases the accuracy of the interpolated rules and has led to a number of advanced theoretical and applicational developments over the past decade (e.g., [24, 26, 27, 73, 93, 113, 155, 156]). However, the existing literature of FRI is mainly focussed on Mandani-type models, apart from limited initial attempt as reported in [95, 152, 172, 173], the research on FRI with TSK-type models is still rather rare.

1.3 Research Objectives and Contributions

Considering the data shortage problem mentioned above, the main goal of this thesis will focus on how to construct an effective fuzzy inference system with insufficient training data (termed as sparse data in this thesis). Among the various fuzzy inference systems, the ANFIS (Adaptive Network-based Fuzzy Inference System) which is implemented within the framework of a network structure, has become one of the most popular FISs due to its simplicity and effectiveness. Therefore, how to construct an ANFIS with insufficient training data (or sparse training data) is chosen as a key research objective in this thesis, although other fuzzy inference systems can also be studied in the same way.
In particular, the main research objective in the thesis can be achieved from the following three perspectives:

1. Inspired by the observation in transfer learning theory that knowledge accumulated from neighbouring domains (with sufficient data) may help the inference of the current problem domain of interest (with sparse data), in this thesis, the concept ‘ANFIS interpolation’ is proposed, which is defined as the construction of a new ANFIS in the target domain, by the assistance of two source ANFISs in the source domains. Reflecting the fact that an ANFIS is a set of fuzzy rules, an initial ANFIS interpolation method is proposed by interpolating a group of fuzzy rules, which is an extension of the popular fuzzy rule interpolation (FRI) technique.

2. The initial ANFIS interpolation method will terminate when a group of rules have been interpolated. How to further optimise these interpolated rules presents the second challenge that is addressed in the thesis. Evolutionary computation is introduced to iteratively update the interpolated rules by encoding those rules into specific chromosomes, in an effort to obtain improved performance.

3. Apart from the theoretical studies, another important goal of the thesis is to investigate how the proposed techniques may perform in dealing with real word problems. Particularly, the proposed methods are applied to the problem of image super resolution. Both full training data and sparse training data are used to evaluate the performance of the learned and the interpolated ANFIS models respectively.

Following these initial objectives, the main contributions of this thesis include ANFIS interpolation and its application to image super resolution problems, are listed as follows:

- An initial ANFIS interpolation technique via group rule interpolation is proposed, which is implemented by interpolating a group of fuzzy rules. Experimental results on benchmark data sets indicate that the proposed approach significantly improves the performance of ANFIS in data shortage situations. The proposed approach has been published in the Proceedings of the 18th annual UK workshop on Computational Intelligence and the journal of IEEE Transactions on Cybernetics.
1.4. Structure of Thesis

- An improved ANFIS interpolation technique via evolutionary computation is proposed, which is implemented by using the interpolated rules as an initial population and updating the system via a genetic algorithm. This work is validated against a number of benchmark data sets, the results indicate that it further improves the performance of the initial ANFIS interpolation method. The work has been published in the journal of *IEEE transactions on Fuzzy Systems*.

- An image super resolution method via ANFIS is proposed, with full training data. It works by learning non-linear mappings from the low resolution image space to the high resolution image space using learned ANFIS models. Experiments indicate that ANFIS works very well for this practical image super resolution problem when sufficient training data is provided. This proposed approach has been published in the *Proceedings of the 2017 IEEE International Conference on Fuzzy Systems*.

- A hyperspectral image super resolution method via the proposed ANFIS interpolation technique is proposed, with sparse training data. Different from the natural RGB images, the hyperspectral images are special images which are much harder to obtain, so in such cases, the training data could be sparse. The experimental results of this real world application suggest that the proposed ANFIS interpolation techniques can not only significantly improve the poor performance caused by training data shortage on benchmark data sets, but also have promising application prospect. This work is currently being prepared for journal submission.

1.4 Structure of Thesis

This section outlines the structure of the remainder of this thesis. The relationship among the main chapters of this thesis is illustrated in Figure 1.2. In summary, Chapter 2 provides the background knowledge of ANFIS, image super resolution together with the review of typical fuzzy rule interpolation methods. Based on this, Chapters 3 and 4 present the theoretical part of this thesis and Chapters 5 and 6 give the application part of the thesis on image super resolution problems. Particularly, Chapter 3 presents an initial ANFIS interpolation method via group rule interpolation; Chapter 4 presents an improved ANFIS interpolation scheme via an evolutionary process; Chapter 5 provides the application of ANFIS on the image super resolution problem with full training data; Finally, Chapter 6 extends this application problem
using a special type of image (hyperspectral image), and applies the techniques developed in Chapters 3 and 4 for hyperspectral image super resolution with sparse training data.

![Diagram of thesis structure](image.png)

Figure 1.2: Relationship among main thesis chapters

**Chapter 2: Background**

This chapter provides the background knowledge that is relevant to the proposed work in this thesis. Primarily, a formal introduction of ANFIS including its network structure and the parameter learning strategy is presented, which forms a key basis upon which to develop the main research of the thesis. A brief introduction to the fuzzy rule interpolation technique is then followed in this chapter, which provides the fundamental knowledge for the proposed ANFIS interpolation. Finally, this chapter also introduces the basic knowledge of the image super resolution problem, forming the basis of the application part of the proposed work. The image super resolution (ISR) is a classical task in the field of image processing, and various classes of algorithms have been proposed in the literature, among which the most popular one in the recent decades is the learning based super resolution (SR) approaches, giving the state of the art results, on which the establishment of the proposed SR method in Chapter 5 is based.
Chapter 3: ANFIS Interpolation - A Group Rule Interpolation Based Approach

To deal with the data shortage situations in the construction of an ANFIS, this chapter proposes an initial ANFIS interpolation approach to improve the performance of the original ANFIS model trained with sparse training data using group based rule interpolation. In particular, it works by interpolating a group of fuzzy rules in a certain given problem domain with the assistance of existing ANFISs in its neighbouring domains. The construction process involves a number of computational mechanisms, including a rule dictionary which is created by extracting the rules from the existing ANFISs; a group of rules which are interpolated by exploiting the local linear embedding algorithm to build an intermediate ANFIS; and a fine-tuning method which refines the resulting intermediate ANFIS. The experimental evaluation on both synthetic and real world data sets is reported, demonstrating that when facing the data shortage situations, the proposed approach helps significantly improve the performance of the original ANFIS modeling mechanism.

Chapter 4: ANFIS Interpolation - An Evolutionary Approach

This chapter presents an extension of the method in Chapter 3, improving the interpolated ANFIS model through the use of evolutionary computation. The proposed approach takes the interpolated rules as an initial population, and updates these candidate rules via a genetic process. The crossover and mutation operations over these candidate rules are then executed in an effort to attain candidates of improved performance. When this genetic learning process terminates the chromosomes in the final population either collectively form or each individually represent a learned ANFIS, depending on whether a single fuzzy rule or a set of fuzzy rules representing an entire ANFIS is implemented with a chromosome within the evolving population. Comparative experimental evaluations on both synthetic and real world data sets are carried out, demonstrating that in spite of data shortage, the proposed interpolation approach is able to produce ANFIS models that significantly outperform those trained using existing learning mechanisms.
Chapter 5: Image Super Resolution with Full Training Data via Multiple Learned ANFIS Mappings

This chapter provides an application of ANFIS on the image super resolution problem. The proposed approach aims to generate a high resolution image using a low resolution one, using multiple learned ANFIS mappings. It presents an implemented learning system that captures the relationship between a high resolution image space and a low resolution one using an external image database. In particular, a collected large number of low resolution and high resolution image patch pairs are divided into different groups with a clustering method. For each clustered group of the training samples, an ANFIS mapping is learned for super resolution. The post processing techniques (including a non-local means filter and an iterative back projection operator) are subsequently employed to suppress the displeasing artefacts of the resulting reconstructed high resolution image. The proposed approach is evaluated using a range of natural images and compared with a number of existing popular ISR algorithms, demonstrating its effectiveness.

Chapter 6: Hyperspectral Image Super Resolution with Sparse Training Data via ANFIS Interpolation

Given the promising results achieved with ANFIS interpolation generated from Chapters 3 and 4 on benchmark data sets, in this chapter, the proposed ANFIS interpolation techniques are applied to a real-world hyperspectral image super resolution problem. Hyperspectral images are a special image type, in which there are dozens or hundreds of image bands while some of the image bands are very hard to obtain. This characteristic means that the training data in some image bands are sparse. The proposed super resolution approach uses the learned ANFIS models over the image bands with sufficient training data as source ANFISs, to assist the construction of the target ANFIS models over the image bands with sparse training data. Experimental results show that compared with the original ANFIS model, the interpolated ANFIS model gives remarkable improvements over the data shortage bands.
Chapter 7: Conclusion

This chapter summarises this thesis and lists the key contributions, together with a discussion of topics which set up the basis for future research.

Appendices

Appendix A lists the publications arising from the work presented in this thesis, including the published journal papers and conference papers. Appendix B summarises the abbreviations employed throughout the thesis.
Chapter 2

Background

FUZZY inference system enables the tolerance of imprecision when dealing with real life inference problems, which is closer to human reasoning. Among the various types of existing fuzzy inference systems, those implemented in an adaptive network structure (ANFIS) have gained more and more attention in the recent decades, owing to their simplicity and effectiveness.

This chapter reviews the background knowledge relevant to the work to be presented in the later part of this thesis, the remainder of this chapter is structured as follows. ANFIS, which is the main research topic of the thesis, is firstly introduced in Section 2.1, with its network structure and associated parameter learning method. Section 2.2 introduces the basic idea and the typical algorithms of the fuzzy rule interpolation method, which will form the base of the interpolation of ANFISs. A brief introduction to image super resolution and the most popular representative method (the learning based image super resolution) is presented in Section 2.3. Finally Section 2.4 summarizes this chapter.

2.1 Adaptive Network based Fuzzy Inference System (ANFIS)

ANFIS [66] is a fuzzy inference system that implements approximate reasoning within the general framework of an adaptive network. It works by equivalently extracting
2.1. Adaptive Network based Fuzzy Inference System (ANFIS)

useful (interpretable) knowledge in terms of a set of fuzzy rules directly from training
data, and has proven to be very suitable for highly non-linear problems. Thanks to
its simplicity and effectiveness, it has been widely applied to various kinds of real
world problems (e.g., [11, 47, 135, 144]). The following gives a formal introduction
to the basic concepts of ANFIS, including an illustrative network structure and the
associated data-driven process for learning the parameters of such networks.

2.1.1 Network architecture

For easy understanding, a simple ANFIS with two input variables \( (x_1 \text{ and } x_2) \) and
one output variable \( (y) \) is used here for illustration (whilst more complex structures
can be readily expanded from this basic form). In particular, suppose that there are
two fuzzy if-then rules of Takagi-Sugeno-Kang’s type [130] in the rule base of this
example ANFIS, as follows:

Rule 1: If \( x_1 \) is \( A_1 \) and \( x_2 \) is \( B_1 \), then \( y_1 = p_1 x_1 + q_1 x_2 + r_1 \)

Rule 2: If \( x_1 \) is \( A_2 \) and \( x_2 \) is \( B_2 \), then \( y_2 = p_2 x_1 + q_2 x_2 + r_2 \)

Figure 2.1 shows the corresponding TSK-type fuzzy reasoning process (a) and the
equivalent ANFIS structure (b). As shown in Figure 2.1(a), in the TSK-type fuzzy
reasoning, the output of each rule is a linear combination of all the input variables,
and the overall output is the weighted average \( (\bar{w}_1 y_1 + \bar{w}_2 y_2) \) of each rule’s output.
The network structure of a general ANFIS contains five layers of computing elements,
as shown in Figure 2.1(b). In this figure, the square nodes stand for adaptive com-
puting units with modifiable parameters, and the circle nodes represent those fixed
units without parameters. Further details of the individual layers within this ANFIS
are outlined below.

Layer 1: Each node \( i \) in this layer is a square unit defined by a fuzzy set \( O_{ij} \) of the
membership function: \( \mu_{O_{ij}}(x_i), i, j \in \{1, 2\} \), where \( x_i \) denotes the input variable to
node \( i \), and \( O_{11} \in \{A_i|i = 1, 2\} \) and \( O_{12} \in \{B_i|i = 1, 2\} \) denote the fuzzy sets defined
on the domains of \( x_1 \) and \( x_2 \), respectively. Such a membership function can be
specified as any continuous or piecewise differentiable, convex and normal functions
such as trapezoidal, triangular, bell-shaped ones. For example, a triangular fuzzy set
is defined as follows in general terms,
2.1. Adaptive Network based Fuzzy Inference System (ANFIS)

\[ \mu_0(x) = \begin{cases} 
  k_1 x + b_1 & a_0 \leq x \leq a_1 \\
  k_2 x + b_2 & a_1 \leq x \leq a_2 \\
  0 & \text{otherwise} 
\end{cases} \quad (2.1) \]

where \( a_0 \) and \( a_2 \) are the two extreme points delimiting the fuzzy set with a membership value of 0, and \( a_1 \) stands for the normal point of the set whose membership value is 1. \( k_1 = 1/(a_1 - a_0) \), \( b_1 = -a_0/(a_1 - a_0) \), \( k_2 = 1/(a_1 - a_2) \), and \( b_2 = -a_2/(a_1 - a_2) \). In ANFIS terms, \( k_1, k_2, b_1, b_2 \) are called premise parameters as they are associated

Figure 2.1: (a) TSK-type fuzzy reasoning. (b) Equivalent ANFIS structure representing two TSK rules
with the underlying input variable (which appears in the antecedent part of a rule). Incidentally, the notion of representative value that is often used in FRI for such a triangular-shaped fuzzy set $O(a_0, a_1, a_2)$ can be simply defined as:

$$Rep(O) = \frac{a_0 + a_1 + a_2}{3} \quad (2.2)$$

The Gaussian-shaped and bell-shaped functions are also commonly used membership functions, which are defined in Equation (2.3) and (2.4) respectively:

$$\mu_O(x) = \exp\left[-\frac{(x - m)^2}{\sigma}\right] \quad (2.3)$$

$$\mu_O(x) = \frac{1}{1 + \left[\left(\frac{x - c}{a}\right)^2\right]^b} \quad (2.4)$$

where $m, \sigma, a, b, c$ are the corresponding premise parameters.

Layer 2: Each node in this layer is a circle unit which multiplies the incoming membership of each attribute and gives the product as its (local) output, denoted by $w_i$. $w_i$ is also the firing strength of the $i$th rule ($i = 1, 2$):

$$w_i = \mu_{A_i}(x_1) \times \mu_{B_i}(x_2) \quad (2.5)$$

Layer 3: Each node in this layer is also a circle unit, calculating the relative proportion of the $i$th rule’s firing strength to the total of both rules’ firing strengths:

$$\tilde{w}_i = \frac{w_i}{w_1 + w_2} \quad (2.6)$$

where again, $i = 1, 2$. To reflect the underlying semantics, the outputs of this layer are termed as normalised firing strengths.

Layer 4: Each node $i$ in this layer is a square unit implementing the following linear function:

$$\tilde{w}_i(p_i x_1 + q_i x_2 + r_i) = \tilde{w}_i y_i \quad (2.7)$$

where $\tilde{w}_i$ is the output of the previous layer, and $p_i, q_i, r_i$ are the parameters associated with the rule consequents and hence, are termed consequent parameters hereafter.
2.1. Adaptive Network based Fuzzy Inference System (ANFIS)

Layer 5: This layer is the (global network) output layer, which consists of a single circle unit, computing the overall output in response to the current input to the network, defined as the summation of all its incoming values from the previous layer, namely,

$$y = \sum_i \tilde{w}_i y_i = \tilde{w}_1 y_1 + \tilde{w}_2 y_2$$  \hspace{1cm} (2.8)

Each layer within a general ANFIS is summarised in Table 2.1.

<table>
<thead>
<tr>
<th>Layer</th>
<th>Activity</th>
<th>Parameter</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Fuzzifying crisp value</td>
<td>Premise parameter</td>
</tr>
<tr>
<td>2</td>
<td>Computing firing strength of each rule</td>
<td>No</td>
</tr>
<tr>
<td>3</td>
<td>Normalising firing strength</td>
<td>No</td>
</tr>
<tr>
<td>4</td>
<td>Computing local output</td>
<td>Consequent parameter</td>
</tr>
<tr>
<td>5</td>
<td>Computing global output</td>
<td>No</td>
</tr>
</tbody>
</table>

Table 2.1: Functionality of individual layers in ANFIS

2.1.2 Hybrid learning algorithm

Given the network structure, the only uncertain part of an ANFIS concerns the parameters in the first layer (premise parameters describing the fuzzy sets) and the fourth layer (consequent parameters specifying the linear functions). In the original work reported in [66], these parameters are trained using a hybrid learning method [67] combining gradient descent and Least Square Estimation (LSE).

Considering a simple adaptive network structure in which there is only one output variable:

$$output = F(\vec{I}, S)$$ \hspace{1cm} (2.9)

where $F(\cdot, \cdot)$ denotes the function of the fuzzy inference system, $\vec{I}$ denotes the set of the input variables, and $S$ denotes the set of parameters. If there exists a function $H$ such that the composite function $H \circ F$ is linear in a part of the parameters of $S$, then these parameters can be identified by the LSE. Suppose that $S$ can be decomposed into two sets $S_1$ and $S_2$:

$$S = S_1 \oplus S_2$$ \hspace{1cm} (2.10)
2.1. Adaptive Network based Fuzzy Inference System (ANFIS)

where $\oplus$ denotes direct sum, and $H \circ F$ is linear in the elements of $S_2$. Applying $H$ to Equation (2.9), it can be written as:

$$H(output) = H \circ F(I, S) = H \circ F(I, S_1 \oplus S_2)$$  \hspace{1cm} (2.11)

Since $H \circ F$ is linear for $S_2$, when giving the values of parameters in $S_1$, and specifying the training data into Equation (2.11), a linear matrix equation $AX = B$ can be obtained, where $X$ denotes the unknown vector whose elements are the parameters in $S_2$. By minimizing the squared error $||AX - B||^2$ using LSE, the solution of $AX = B$ (denoted by $X^*$) can be expressed as:

$$X^* = (A^T A)^{-1} A^T B$$  \hspace{1cm} (2.12)

where $(A^T A)^{-1} A^T$ is the pseudo-inverse of $A$. Since Equation (2.12) is a concise solution, it is computational expensive for doing the matrix inverse. So instead of solving Equation (2.12) directly, a sequential formula [8] is employed to iteratively compute the LSE of $X$:

$$\begin{align*}
X_{i+1} &= X_i + S_{i+1} a_{i+1} (b_{i+1}^T - a_{i+1}^T X_i) \\
S_{i+1} &= S_i - \frac{S_i a_{i+1} a_{i+1}^T S_i}{1 + a_{i+1}^T S_i a_{i+1}}
\end{align*}$$  \hspace{1cm} (2.13)

where $i = 0, 1, \ldots, P - 1$, $P$ denotes the number of training data pairs, $a_{i}^T$ is the $i$ th row vector of $A$, $b_{i}^T$ is the $i$ th element of $B$, $S_i$ is called the covariance matrix with $S_0 = \gamma I$ ($\gamma$ is a positive large number and $I$ is the identity matrix), $X_0$ is set to be $X_0 = 0$, and the least square estimate $X^*$ is equal to $X_P$.

Based on the above analysis, the parameters in $S_2$ can be calculated by Equation (2.13), then the gradient descent and LSE can be combined to update the parameters. Each loop of the hybrid learning algorithm is composed of a forward pass and a backward pass. In the forward pass, the input training data go through each node of the network until matrices $A$ and $B$ are obtained, then the parameters in $S_2$ can be identified using the sequential least square formulas in Equation (2.13). After that, the function signals keep going forward to get the estimated output of the current loop, which will be used to calculate the output error together with the desired output. Then, in the backward pass, with the identified parameters in $S_2$, the parameters in $S_1$ is computed by the gradient descent algorithm.

From the above ANFIS architecture (see Figure 2.1(b)), it is observed that given the values of premise parameters, the overall output can be expressed as a linear
2.2. Fuzzy Rule Interpolation (FRI)

combinations of the consequent parameters. More precisely, the output $y$ in Figure 2.1(b) can be rewritten as:

$$
y = \frac{w_1}{w_1 + w_2} y_1 + \frac{w_2}{w_1 + w_2} y_2$$

$$= \bar{w}_1 y_1 + \bar{w}_2 y_2$$

$$= (\bar{w}_1 x_1) p_1 + (\bar{w}_1 x_2) q_1 + (\bar{w}_1) r_1$$

$$+ (\bar{w}_2 x_1) p_2 + (\bar{w}_2 x_2) q_2 + (\bar{w}_2) r_2$$

(2.14)

which is linear in the consequent parameters ($p_1, q_1, r_1, p_2, q_2, r_2$). Define $S, S_1, S_2$ in Equation (2.10) as follows:

$$\begin{cases}
S \rightarrow \text{set of total parameters} \\
S_1 \rightarrow \text{set of premise parameters} \\
S_2 \rightarrow \text{set of consequent parameters}
\end{cases}$$

(2.15)

and define $H(\cdot)$ in Equation (2.11) as the identify function, then the composite function $H \circ F$ satisfies the condition that $H \circ F$ is linear in a part of parameters in $S$ (i.e. the parameters in $S_2$), therefore the hybrid learning algorithm (the combination use of LSE method and gradient descent method) can be applied directly. More specifically, in the forward pass, the input values of the training samples are fed forward to compute the output with the premise parameters being fixed, and the consequent parameters are optimised by LSE. Then, in the backward pass, the consequent parameters are set to be fixed, while the error rates between the computed output and the expected ones (as part of the given training samples) are propagated backward, with the premise parameters updated using the gradient descent method. Table 2.2 summarizes the activities in each pass.

Table 2.2: Two passes in the hybrid learning procedure for ANFIS

<table>
<thead>
<tr>
<th></th>
<th>Forward pass</th>
<th>Backward pass</th>
</tr>
</thead>
<tbody>
<tr>
<td>Premise parameters</td>
<td>Fixed</td>
<td>Gradient descent</td>
</tr>
<tr>
<td>Consequent parameters</td>
<td>LSE</td>
<td>Fixed</td>
</tr>
<tr>
<td>Signals</td>
<td>Node Outputs</td>
<td>Error Rates</td>
</tr>
</tbody>
</table>

2.2 Fuzzy Rule Interpolation (FRI)

Fuzzy systems utilise a fuzzy rule-base to perform the inference. For most fuzzy inference systems, it is assumed that the rule-bases are complete. The complete
rule-base (or dense rule-base) ensures that for any possible input, there exists at least one fired fuzzy rule whose antecedent part overlaps the input data. Therefore, the conclusion can be drawn by combining the consequences of all the fired rules. However, in certain problems, the rule-base can be incomplete (or sparse) in which some rules are missed. For a sparse rule-base, the input space is not fully covered, there may exist an empty space between the membership functions of two rule antecedents. In this case, for the observations that fall into the ‘empty space’, the conventional fuzzy reasoning methods are highly likely to conclude nothing. Figure 2.2 shows the difference between a dense rule-base and a sparse rule-base. Note that there is a subtle nuance between the concepts of ‘sparse data’ and ‘sparse rule-base’. A sparse rule-base is generated from sparse data, but sparse data does not necessarily lead to a sparse rule-base. Even sparse data can result in a dense rule-base with badly generated rules.

![Figure 2.2: Dense and sparse rule-base](image)

Fuzzy rule interpolation (FRI) techniques are proposed to overcome this challenging issue, which enable a fuzzy inference system with a sparse rule-base to perform
2.2. Fuzzy Rule Interpolation (FRI)

The basic idea of FRI is to interpolate a rule at the place where no rule can be fired with the given observation, by combining the information of the neighbouring rules. A number of FRI methods have been developed in the literature [75, 76, 120], which can be approximately classified into two categories, the single step rule-based interpolation and the intermediate rule based interpolation. The most representative approaches for these two categories are the KH (Kóczy and Hirota) method and the T-FRI (transformation based FRI) method respectively, which will be reviewed in the following sections. Most existing FRI techniques in the literatures are with Mamdani-type rules, while the development of TSK-type FRI is still rather rare. Some initial work has been reported most recently [31, 95, 173], which will be reviewed later.

2.2.1 The KH approach

The KH (Koczy and Hirota) method [83, 84] is the very first and classic FRI technique, which is based on the $\alpha$-cuts theory. The $\alpha$-cut $A_\alpha$ of a fuzzy set $A$ is defined as:

$$A_\alpha = \{ x | A(x) \geq \alpha, \alpha \in [0, 1] \}$$  \hspace{1cm} (2.16)

where $A(x)$ is the membership function of fuzzy set $A$. Theoretically, every fuzzy set can be approximated by the use of the family of its $\alpha$-cuts.

For a given observation $A^*$ that does not match with any rule in the rule-base, the KH method selects a few (usually two) neighbouring rules and then conducts the linear combination to obtain the inference result. For simplicity, suppose that both of the two selected flanking rules ($R_1$ and $R_2$) are with only one input variable, formatted as follows:

$$R_1 : \text{If } x \text{ is } A_1, \text{ then } y \text{ is } B_1$$

$$R_2 : \text{If } x \text{ is } A_2, \text{ then } y \text{ is } B_2$$

The KH method produces the conclusion using the assumption that the ratio of distances between the conclusion and the rule consequents should be identical with that of distances between the observation and the rule antecedents. The required conclusion $B^*$ is determined by the following equation:
2.2. Fuzzy Rule Interpolation (FRI)

\[
d(A^*, A_1) \frac{d(A^*, A_2)}{d(B^*, B_1)} = \frac{d(B^*, B_1)}{d(B^*, B_2)}
\]

(2.17)

where \(d(., .)\) denotes the fuzzy distance between the two fuzzy sets. According to the resolution principle [125, 165], every fuzzy set can be represented as a family of its \(\alpha\)-cuts. Therefore the Equation (2.17) can be written as:

\[
\frac{d(A^*_{a}, A_{1a})}{d(A^*_{a}, A_{2a})} = \frac{d(B^*_{a}, B_{1a})}{d(B^*_{a}, B_{2a})}
\]

(2.18)

where \(\alpha \in [0, 1]\). Define the lower and upper distances between \(\alpha\)-cuts \(A^*_{a}\) and \(A_{1a}\) as follows:

\[
d_L(A^*_{a}, A_{1a}) = d(\inf \{A^*_{a}\}, \inf \{A_{1a}\})
\]

(2.19)

\[
d_U(A^*_{a}, A_{1a}) = d(\sup \{A^*_{a}\}, \sup \{A_{1a}\})
\]

(2.20)

Figure 2.3: Lower and upper distances between two \(\alpha\)-cuts.

The lower and upper distances are illustrated in Figure 2.3. Using the lower and upper distances, Equation (2.18) is transformed into:

\[
\frac{d_L(A^*_{a}, A_{1a})}{d_L(A^*_{a}, A_{2a})} = \frac{d_L(B^*_{a}, B_{1a})}{d_L(B^*_{a}, B_{2a})}
\]

(2.21)

\[
\frac{d_U(A^*_{a}, A_{1a})}{d_U(A^*_{a}, A_{2a})} = \frac{d_U(B^*_{a}, B_{1a})}{d_U(B^*_{a}, B_{2a})}
\]

(2.22)

From Equation (2.19), Equation (2.21) can be written as:
2.2. Fuzzy Rule Interpolation (FRI)

\[
\begin{align*}
d_L(A^*_a, A_{1a}) &= d_L(B^*_a, B_{1a}) \\
&= \frac{d_l(A^*_a, A_{2a})}{d_l(B^*_a, B_{2a})} \\
&= \frac{d(\inf\{B^*_a\}, \inf\{B_{1a}\})}{d(\inf\{B^*_a\}, \inf\{B_{2a}\})} \\
&= \inf\{B^*_a\} - \inf\{B_{1a}\} \\
&= \inf\{B_{2a}\} - \inf\{B^*_a\}
\end{align*}
\]

(2.23)

Then it can be solved as follows:

\[
\begin{align*}
\inf\{B^*_a\} &= \frac{\inf\{B_{1a}\} d_l(A^*_a, A_{2a}) + \inf\{B_{2a}\} d_l(A^*_a, A_{1a})}{d_l(A^*_a, A_{1a}) + d_l(A^*_a, A_{2a})} \\
&= \frac{\inf\{B_{1a}\} + \inf\{B_{2a}\}}{1 + 1} \frac{1}{d_l(A^*_a, A_{1a}) + d_l(A^*_a, A_{2a})}
\end{align*}
\]

(2.24)

\[
\sup\{B^*_a\} = \frac{\sup\{B_{1a}\} d_u(A^*_a, A_{1a}) + \sup\{B_{2a}\} d_u(A^*_a, A_{2a})}{d_u(A^*_a, A_{1a}) + d_u(A^*_a, A_{2a})}
\]

(2.25)

(2.26)

Where

\[
\begin{align*}
w_{1L} &= \frac{1}{d_l(A^*_a, A_{1a})}, & w_{2L} &= \frac{1}{d_l(A^*_a, A_{2a})} \\
w_{1U} &= \frac{1}{d_u(A^*_a, A_{1a})}, & w_{2U} &= \frac{1}{d_u(A^*_a, A_{2a})}
\end{align*}
\]

(2.27)

(2.28)

From this, \(B^*_a\) can be obtained by \(B^*_a = [\inf\{B^*_a\}, \sup\{B^*_a\}]\). Then the conclusion fuzzy set \(B^*\) can be constructed by the resolution principle of fuzzy set, as follows:

\[
B^* = \bigcup_{\alpha \in [0, 1]} B^*_a
\]

(2.29)

Theoretically, all possible \(\alpha\)-cuts (which is an infinite number) should be considered to interpolate an approximate conclusion. However, in order to reduce the
complexity in practice, only a finite number (usually 2, 3 or 4) of \( \alpha \)-cuts are taken into consideration. The KH approach forms the base of the FRI theory, based on this fundamental KH method, many extended versions have been proposed [132, 137, 146]. For instance, the modified \( \alpha \)-cut based interpolation method [132] solves the ‘abnormal fuzzy set problem’ in the original KH approach through coordinate modification, and reference [146] extends the classical KH approach to more complex version involving multiple rules with multiple antecedent variables.

### 2.2.2 The T-FRI approach

Apart from the earliest linear FRI method (KH method), a number of FRI methods have been proposed to improve the performance of interpolative reasoning. The most popular group will be the transformation-based approaches, termed as scale and move transformation-based fuzzy rule interpolation (T-FRI) [58, 59]. It can handle both interpolation and extrapolation, and guarantees the normality as well as convexity of the interpolated fuzzy sets. The T-FRI is valid for multiple variables involved in multiple fuzzy rules with various types of membership functions (e.g. triangular, trapezoidal, Gaussian and bell-shaped MFs). Due to the simplicity and popularity of the triangular-shaped membership function, here only the T-FRI approach with triangular-shaped MF is introduced as a representative.

#### 2.2.2.1 Representative value

An important concept in the T-FRI is the representative value (Rep) of a fuzzy set that must be defined first. This value captures the important information (such as the overall location) of a fuzzy set, and will guide the scale and move transformations later. For an arbitrary polynomial fuzzy set with \( n \) odd points \( A = (a_0, \ldots, a_{n-1}) \), its general Rep is defined as below:

\[
Rep(A) = \sum_{i=0}^{n-1} w_i a_i
\]  

(2.30)

with \( w_i \) is the weight assigned to point \( a_i \). Different calculation methods of these weights can result in different representative value. The simplest way to specify the
2.2. Fuzzy Rule Interpolation (FRI)

weights is called the ‘average Rep’ method, where all points take the same weight value:

\[
Rep(A) = \frac{1}{n} \sum_{i=0}^{n-1} a_i \tag{2.31}
\]

For example, if \( A \) denotes a triangular-shaped fuzzy set with three points \( a_0, a_1 \) and \( a_2 \), the average Rep is computed as: \( Rep(A) = \frac{(a_0 + a_1 + a_2)}{3} \).

2.2.2.2 Main steps in T-FRI

Based on the definition of Rep value, the T-FRI approach can be implemented as three key steps. For a given unfired observation, firstly, \( K \) closest rules is selected from the sparse rule-base. Then an intermediate rule is generated by weighted averaging the chosen closest rules. Finally, the scale and move transformation is applied on the intermediate rule to obtain the final result. These three steps will be described in detail as follows.

A. K closest rules selection

Without losing generality, a fuzzy rule \( R_i \) in the sparse rule-base and an unfired observation \( O^* \) is represented as follows:

\[
Rule \ R_i : \text{if } X_1 \text{ is } A_{i1} \text{ and } \ldots \text{ and } X_m \text{ is } A_{im}, \text{ then } Y \text{ is } B_i \tag{2.32}
\]

\[
O^* : X_1 \text{ is } A^*_1 \text{ and } \ldots \text{ and } X_m \text{ is } A^*_m \tag{2.33}
\]

where \( A_{ij} \) denotes the \( j \)th antecedent fuzzy set in rule \( R_i \), \( B_i \) is the consequent fuzzy set of rule \( R_i \), \( A^*_j \) denotes the \( j \)th fuzzy set in observation \( O^* \), and \( m \) is the number of input variables.

The fuzzy distance \( d_{ij} \) between two fuzzy sets is defined as the distance of their corresponding representative values:

\[
d_{ij} = d(A_{ij}, A^*_j) = d(Rep(A_{ij}), Rep(A^*_j)) \tag{2.34}
\]

Since different variables may have different ranges, each distance measure related to one variable is normalised to \([0, 1]\), as follows:
2.2. Fuzzy Rule Interpolation (FRI)

\[ d'_j = d(A_{ij}, A'_j) / (\max_j - \min_j) = d(\text{Rep}(A_{ij}), \text{Rep}(A'_j)) / (\max_j - \min_j) \]  

(2.35)

where \( \max_j \) and \( \min_j \) denote the maximal and minimal values of variable \( X_j \) respectively. Then the distance \( d_i \) between rule \( R_i \) and observation \( O^* \) is computed as:

\[ d_i = \sqrt{\sum_{j=1}^{m} (d'_j)^2} \]  

(2.36)

After calculating the distances \( \{d_i\} \) between a given observation and all the fuzzy rules in the sparse rule-base, the \( K \) rules that have the minimal distances will be chosen as the \( K \) closest rules, and will be used for constructing the intermediate rule subsequently.

B. Intermediate rule construction

By combining the \( K \) closest rules selected from the sparse rule-base, the intermediate rule will result, which has the following format:

\[ \text{if } X_1 \text{ is } A'_1 \text{ and } \ldots \text{ and } X_m \text{ is } A'_m, \text{ then } Y \text{ is } B' \]  

(2.37)

where \( A'_j, j = 1, 2, \ldots, m \) is calculated as:

\[ A'_j = A''_j + \delta_j (\max_j - \min_j) \]  

(2.38)

\( A''_j \) is the weighted average of the \( K \) selected rules:

\[ A''_j = \sum_{k=1}^{K} w'_{kj} A_{kj} \]  

(2.39)

where each \( w'_{kj} = w_{kj} / \sum_{k=1}^{K} w_{kj} \) denotes the normalized weight, so that the sum of all the weights will equal to one. The weight \( w_{kj} \) is computed according to the fuzzy distance between \( O_j^* \) and \( A_{kj} \), generally, a larger distance will result in a smaller weight. Usually \( w_{kj} \) can be simply defined as (2.40), although alternative non-increasing functions (such as \( w_{kj} = \exp^{-d(O_j^*, A_{kj})} \)) can also be adopted to assign the weights.

\[ w_{kj} = \frac{1}{d(O_j^*, A_{kj})} \]  

(2.40)
2.2. Fuzzy Rule Interpolation (FRI)

In (2.38), \( \delta_j \) is a constant defined by:

\[
\delta_j = \frac{\text{Rep}(A'^*_j) - \text{Rep}(A''_j)}{\max_j - \min_j}
\]  

(2.41)

In doing so, the Rep value of \( A'_j \) will keep the same with that value of \( A'^*_j \). By analogy to the antecedent part, the consequent part \( B' \) of the intermediate rule is obtained by:

\[
B' = B'' + \delta_a (\max - \min)
\]

(2.42)

where \( \max, \min \) are the maximal and minimal value of the output variable \( Y \) respectively, and \( B'' \) and \( \delta_a \) are computed as:

\[
B'' = \sum_{k=1}^{K} w'_k B_k
\]

(2.43)

\[
\delta_a = \frac{1}{m} \sum_{j=1}^{m} \delta_j
\]

(2.44)

where \( K \) denotes the number of closest rules selected from the sparse rule-base, \( w'_{k_j} = (1/m) \sum_{j=1,...,m} w'_j \) is the mean value of \( w'_{k_j} \), \( j = 1, \ldots, m \). The subscript \( a \) in \( \delta_a \) and \( w'_{k_a} \) means ‘average’.

C. Scale and move transformation

The construction method of the intermediate rule can only insure that the Rep value of \( A'_j \) and \( O'^*_j \) as close as possible, but the shapes of these two fuzzy sets can be rather different, so the scale and move transformation is then introduced to solve this problem. This process is implemented in two stages: scale transformation and move transformation.

- Scale transformation: For a given fuzzy set \( A'_j = (a'_{j0}, a'_{j1}, a'_{j2}) \) of the intermediate rule, the scale factor \( s_{A_j} \) is defined by:

\[
s_{A_j} = \frac{a'^*_{j2} - a'^*_{j0}}{a'_{j2} - a'_{j0}}
\]

(2.45)

where \( a'^*_{j0} \) and \( a'^*_{j2} \) are the two extreme points of fuzzy set \( A'^*_j = (a'^*_{j0}, a'^*_{j1}, a'^*_{j2}) \). Then, the scaled fuzzy set \( \tilde{A}'_j = (\tilde{a}'_{j0}, \tilde{a}'_{j1}, \tilde{a}'_{j2}) \) can be calculated as follows:

\[
\begin{align*}
\tilde{a}'_{j0} &= \frac{(1 + 2s_{A_j})a'_{j0} + (1 - s_{A_j})a'_{j1} + (1 - s_{A_j})a'_{j2}}{3} \\
\tilde{a}'_{j1} &= \frac{(1 - s_{A_j})a'_{j0} + (1 + 2s_{A_j})a'_{j1} + (1 - s_{A_j})a'_{j2}}{3} \\
\tilde{a}'_{j2} &= \frac{(1 - s_{A_j})a'_{j0} + (1 - s_{A_j})a'_{j1} + (1 + 2s_{A_j})a'_{j2}}{3}
\end{align*}
\]

(2.46)
According to the intuition that a similar rule antecedent will lead to a similar rule consequent, the scaled consequent fuzzy set $\tilde{B}' = (\tilde{b}_0', \tilde{b}_1', \tilde{b}_2')$ can be obtained by using the same scale factor:

$$
\begin{align*}
\tilde{b}_0' &= \frac{(1 + 2s_B)b_0' + (1 - s_B)b_1' + (1 - s_B)b_2'}{3} \\
\tilde{b}_1' &= \frac{(1 - s_B)b_0' + (1 + 3s_B)b_1' + (1 - s_B)b_2'}{3} \\
\tilde{b}_2' &= \frac{(1 - s_B)b_0' + (1 - s_B)b_1' + (1 + 2s_B)b_2'}{3}
\end{align*}
$$

(2.47)

where $s_B = (1/m)\sum_{j=1,\ldots,m} s_{A_j}$ is the average value of all $s_{A_j}$.

- Move transformation: The move factor is defined as:

$$
m_{A_j} = \begin{cases} 
3(a^*_j - \bar{a}'_j) & a^*_j \geq \bar{a}'_j \\
\frac{\bar{a}'_j - \bar{a}'_j}{3} & a^*_j \leq \bar{a}'_j
\end{cases}
$$

(2.48)

Given $m_{A_j}$, the conclusion $B^*$ can be estimated as:

$$
\begin{align*}
\begin{cases} 
\tilde{b}_0^* &= \tilde{b}_0' + m_B \frac{\tilde{b}_1' - \tilde{b}_0'}{3} \\
\tilde{b}_1^* &= \tilde{b}_1' - 2m_B \frac{\tilde{b}_1' - \tilde{b}_0'}{3} & \text{if } m_B \geq 0 \\
\tilde{b}_2^* &= \tilde{b}_2' + m_B \frac{\tilde{b}_1' - \tilde{b}_0'}{3} \\
\tilde{b}_0^* &= \tilde{b}_0' + m_B \frac{\tilde{b}_2' - \tilde{b}_1'}{3} \\
\tilde{b}_1^* &= \tilde{b}_1' - 2m_B \frac{\tilde{b}_2' - \tilde{b}_1'}{3} & \text{otherwise} \\
\tilde{b}_2^* &= \tilde{b}_2' + m_B \frac{\tilde{b}_2' - \tilde{b}_1'}{3}
\end{cases}
\end{align*}
$$

(2.49)

where $m_B = (1/m)\sum_{j=1,\ldots,m} m_{A_j}$.

Based on this fundamental T-FRI approach, a series of advanced improvements have been developed over the past decades [24, 73, 74, 112, 155, 156], including the backward fuzzy rule interpolation [73], the rough fuzzy rule interpolation [24], the dynamic fuzzy rule interpolation [112] and the adaptive fuzzy rule interpolation [155, 156], just to name a few.
2.2. Fuzzy Rule Interpolation (FRI)

2.2.3 The TSK-type rule interpolation

Most existing FRI techniques in the literatures are the Mamdani-type rule interpolation, while the development of TSK-type FRI is still rather rare, although some initial work has most recently been reported in [31, 95, 173]. As mentioned previously, different from the Mamdani-type rules in which the consequent part is a fuzzy set, in the TSK-type rules the consequent is usually a crisp polynomial function. A typical TSK-type rule \( R_i \) can be represented as follows:

\[
R_i : \text{if } x_1 \text{ is } A_{i1} \text{ and } \ldots \text{ and } x_m \text{ is } A_{im} \text{, then } y_i = \sum_{j=0}^{m} p_{ij} x_j
\]  

(2.50)

where \( x_0 = 1 \) is the constant term of the polynomial function. Therefore, the TSK-type fuzzy rule interpolation methods are also slightly different as compared with the classical Mamdani-type fuzzy rule interpolation methods. This section summarizes the main steps of the existing representative TSK-type FRI methods reported in [31, 95, 173].

For a given observation \( O^* (i f \ x_1 \text{ is } A^*_1 \text{ and } \ldots \text{ and } x_m \text{ is } A^*_m) \) and the rule \( R_i \) in the sparse rule-base represented as Equation (2.50), the TSK-type rule interpolation approaches (with triangular-shaped membership functions) are implemented as the following steps:

**Step 1:** Compute the similarity measure between the observation \( O^* \) and each rule \( R_i \) in the sparse rule-base;

The similarity measure can be defined using various ways. The simplest and also the most popular method to define the similarity measure is using the fuzzy distance between two fuzzy sets, which is wildly adopted in the literature (such as reference [31], and the T-FRI approaches [58, 59]). Alternatively in the TSK+ approach [95], a new similarity measurement between two triangular fuzzy sets is developed, taking both the similarity and the distance between the two fuzzy sets into consideration. Suppose that \( A = (a_0, a_1, a_2) \) and \( A' = (a'_0, a'_1, a'_2) \) are two fuzzy sets in a normalized variable domain, their similarity degree \( S(A, A') \) is defined as follows:

\[
S(A, A') = (1 - \frac{\sum_{i=0}^{2} |a_i - a'_i|}{3}) \cdot d
\]  

(2.51)
where $d$ is called the ‘distance factor’ that is calculated by:

$$
d = \begin{cases} 
1 & a_0 = a_1 = a_2 \text{ & } a_0' = a_1' = a_2' \\
1 - \frac{1}{1 + e^{-s||A,A'|| + 5}} & \text{otherwise}
\end{cases}
$$

(2.52)

where $||A,A'||$ denotes the fuzzy distance between $A$ and $A'$ (which is defined as the distance between their representative values), $s(s > 0)$ is a sensitive factor, where smaller $s$ will result in the similarity degree $S(A,A')$ more sensitive to the distance between the two fuzzy sets. The constant 5 in the equation ensures that the distance factor $d$ is close to one when the fuzzy distance between $A$ and $A'$ is zero.

The proposed similarity measure has the following properties:

1) A larger $S(A,A')$ indicates higher similarity degree between $A$ and $A'$;

2) $A$ and $A'$ are identical if and only if $S(A,A') = 1$;

3) $S(A,A') > 0$ unless $(a_0 = a_1 = a_2 = 0 \text{ and } a_0' = a_1' = a_2' = 1)$ or $(a_0 = a_1 = a_2 = 1 \text{ and } a_0' = a_1' = a_2' = 0)$.

**Step 2:** Choose $K$ closest rules according to the similarity measure;

Similar with the Mamdani-type rule interpolation, the TSK-based approaches also choose a portion of closest rules to contribute to the interpolation result according to the calculated similarity measures. The choice of $K$ can be various in different approaches: In the TSK+ method [95], all the rules in the sparse rule-base are utilized without selection; in reference [173], $K$ is set to be a fixed small value to avoid the bad influence of the rules with low similarity; while in the weighted T-FRI approach [93], it has been proven that only two chosen rules can achieve the best performance.

**Step 3:** Construct an intermediate rule;

The intermediate rule is constructed by weighted averaging all the selected $K$ closest rules. Suppose that the constructed intermediated rule has the following format:

$$R': \text{if } x_1 \text{ is } A_1' \text{ and } \ldots \text{ and } x_m \text{ is } A_m', \text{ then } y' = \sum_{j=0}^{m} p'_j x_j$$

(2.53)

where

$$A'_j = \sum_{k=1}^{K} w_k A_{kj}, \text{ } j = 1, \ldots, m.$$

(2.54)
2.2. Fuzzy Rule Interpolation (FRI)

\[ p'_j = \sum_{k=1}^{K} w_k p_{kj}, \quad j = 0, \ldots, m. \tag{2.55} \]

The weights \( w_k \) are calculated according to the similarity between the observation \( O^* \) and the \( K \) closest rules \( R_k \). Generally, a higher similarity between \( O^* \) and \( R_k \) will result in larger weight \( w_k \), although different methods can be designed to calculate the weights. For instance, in TSK+ \cite{95} the weights are computed using the proposed similarity measure:

\[ S(O^*_1, A_{k1}) \land S(O^*_2, A_{k2}) \land \cdots \land S(O^*_m, A_{km}) \tag{2.56} \]

where \( S(O^*_j, A_{kj}), j = 1, \ldots, m \) is defined by Equation (2.51), \( \land \) is a t-norm that is usually implemented by minimum operator. An alternative way to obtain the weights proposed in \cite{31} is through solving a linear equation group with the constraint that \( \text{Rep}(O^*_j) = \text{Rep}(A_{kj}) \):

\[
\begin{aligned}
    \text{Rep}(A^*_1) &= \sum_{k=1}^{K} w_k \text{Rep}(A_{k1}) \\
    &\vdots \\
    \text{Rep}(A^*_j) &= \sum_{k=1}^{K} w_k \text{Rep}(A_{kj}) \\
    &\vdots \\
    \text{Rep}(A^*_m) &= \sum_{k=1}^{K} w_k \text{Rep}(A_{km})
\end{aligned}
\tag{2.57}
\]

In comparison with the possible alternatives that typically use the Euclidean norm and usually rely on an extra move operator when constructing the intermediate rule \cite{58, 59}, such constraints directly assess how much contribution of each selected rule may make to the resulting intermediate rule, avoiding more complicated computation.

**Step 4:** Inference using the intermediate rule.

Finally, the inference result will be obtained by using the constructed intermediate rule. In summary, the overall process of several existing TSK-type fuzzy rule interpolation is very similar with the intermediate rule based Mamdani-type FRI approaches, they all have the \( K \) closest rule selection and the intermediate rule construction steps. However, there are also some new techniques introduced to the TSK-type interpolation methods (e.g. the computation methods of the similarity measure, and different ways of identifying weights). Of course, the TSK-based FRI methods are still at their infancy with rare existing approaches, more promising methods will be developed in the future.
2.3 Image Super Resolution

High resolution (HR) images are desired in many real world applications, such as medical diagnosis, remote sensing problems and so on [164] (shown as Figure 2.4). However, due to hardware and communication channel limitations as well as budget constraints, images are sometimes obtained with low resolution (LR). To increase the spatial resolution of an image can be accomplished by either reducing the pixel size by sensor manufacturing techniques or increasing the chip size of the sensors, both of which are severely constrained by the physical limitation of imaging systems and also lead to huge budget burden. Therefore, image super resolution (SR) reconstruction algorithms [118] have been developed in order to efficiently improve the spatial resolution of a given image using computer software, and also to provide clear images for the subsequent image processing tasks (such as recognition, classification and detection).

![Medical diagnosis](image1.png) ![Remote Sensing](image2.png)

Figure 2.4: Application examples of image super resolution reconstruction. Source images are obtained from [134, 147].

Image super resolution techniques aim to generate an HR image from one or more given LR images. This section firstly gives a general description of the image super resolution problem, then the most popular super resolution algorithm (the learning based SR) is introduced in detail.

2.3.1 Problem description

Image resolution reflects how much detail is contained in an image, an image with higher resolution means that more details are captured. An illustration of HR image and LR image of the same scene is shown in Figure 2.5.
2.3. Image Super Resolution

Image super resolution techniques, also termed as image zooming or image enlargement, aim to generate an HR image using one or multiple input LR images. According to the number of the input LR images used, the existing SR approaches can be broadly categorized into two classes: 1) single-frame approaches using only one LR input image, and 2) multi-frame approaches using multiple LR input images of the same scene (shown as Figure 2.6).

Muti-frame images SR approaches [97, 99, 170] usually need geometrical registration of sub-pixel level over the multiple input LR images, and then the registered images are fused to obtain an HR image. The accurate sub-pixel level registration can be very time consuming, and inaccurate registration will seriously effect the super resolution results. Also, images of the same scene are sometimes very hard to obtain due to the weather changes, light limitation or the noise affect. Therefore, the single-frame SR algorithms are getting more and more popular as they do not
2.3. Image Super Resolution

need to collect various LR images of the same scene as input. In single-frame SR problems, the observed LR image $X$ is assumed to be the down sampled version of the desired HR image $Y$:

$$X = H Y$$  \hspace{1cm} (2.58)

Here, $H$ represents the down sampling operator. Single-frame SR is therefore, the inverse problem of the above image degradation equation. For a given LR input $X$, infinitely many HR images $Y$ satisfy Equation (2.58), thus super resolution is an extremely ill-posed inverse problem. In order to handle such a problem, extra information is needed.

Existing single-frame SR methods [13, 14, 50, 150] typically adopt three different types of techniques: the interpolation based methods, the reconstruction based methods and the learning based methods. The interpolation based methods [56, 96] are the oldest image SR algorithms which are implemented by simply interpolating the image pixels. For example, as shown in Figure 2.7, images are seen as matrices of pixels in computer (the A, B, C denote image pixels). When an image is enlarged, the number of pixels will increase, so the task of image SR is to estimate the missing pixels. Interpolation based approaches aim to interpolate the existing pixels to fill in the blanks. The most commonly used interpolation methods include the nearest interpolation, bilinear interpolation and the bicubic interpolation, which are already proven techniques and have been wildly used in computer software or web pages for zooming pictures.

![Figure 2.7: Interpolation based image SR. Source images are obtained from [141].](image)

However, researchers have pointed out that large size is not the only meaning of high resolution, the term 'high resolution' also means more information and clearer details. Also, the interpolation based approaches usually utilise a base function that only considers the correlations of neighbouring pixels to approximate the missing pixels in HR images, therefore tending to cause blurred edges and generating overly
smoothed images. So the resulting image generated by the interpolation methods is still a low resolution image to some extent, and they are often be used as the initial step during the whole super resolution process in the improved approaches. After that, the interpolated large size image will be sequentially enhanced to get the real high resolution one, and this enhancement process is also what the recent super resolution researches focus on.

To further improve the image resolution, the reconstruction based methods [77, 98] are proposed, in which prior knowledge is introduced in an attempt to restrain the solution. For instance, the sparse representation base image SR [150] uses the image sparsity in the frequency domain as an extra constraint added in the reconstruction process, improving the quality of the enlarged image significantly; the similarity based image SR algorithms [22, 25] add the similarity constraint among image patches in an effort to eliminate the artefacts or noise in the reconstructed HR images; and in [35], the heavy-tail distribution property of image histogram is utilized as an extra prior knowledge to improve the super resolution accuracy. Although such strategies may offer much better performance than interpolation based techniques, important problems such as missing details remain.

More recently, the learning based methods have been proposed to tackle the challenging ISR problem via learning dictionaries [158] or relationships [122, 149, 171] from an external image database. Empirical results have shown that these approaches generally lead to improved visual outcomes, thereby forming the state of the art results in single frame ISR. The following section will give a brief introduction of the learning based ISR and review some typical literatures.

### 2.3.2 Learning based image SR

The learning based super resolution approaches collect a large amount of image pairs of both resolutions as the training data set, which will be subsequently utilised to learn the relationship between the high resolution image and the low resolution image. And once the relationship is learned, it can be applied on new testing images. So when it comes a new low resolution image, the corresponding high resolution image is estimated using the learned relationship ‘R’, with patch-by-patch or pixel-by-pixel strategy. This is illustrated in Figure 2.8. Typical examples of learning based SR are listed in references [43, 122, 171]. In particular, the learning based SR methods
mainly include the learning of linear mappings, the learning of deep convolutional neural networks and the learning of fuzzy rules. These three representative types of learning based approaches are briefly introduced as follows.

A. Learning of linear mappings

The type of relationships or mappings $R$ can be various. Generally, they can be classified into two classes: the linear class, and the non-linear class. Linear mappings are first proposed and commonly used in the literatures due to their simplicity \cite{14, 149, 171}. For example, the method proposed in \cite{171} works by learning multiple linear mappings from the LR feature space onto the HR feature space, in order to perform single-frame image SR. And in \cite{149}, the feature space is split into numerous subspaces, and exemplars for each subspace are collected to learn the effective linear mapping functions.

But in more cases, linear mappings are too simple to describe the complex relationship between the low resolution image and the high resolution image, so the non-linear mappings are proposed to achieve better performances. Existing literatures mentioned two types of non-linear mappings: the deep convolutional neural network, and the fuzzy rule.

B. Learning of deep CNNs

As the rapid increasement of the computer storage capacity and the calculation speed, the traditional neural network can be designed much deeper than ever before,
which greatly improves the network ability in capturing accurate features and has been wildly utilized in a range of image processing tasks [53, 86, 101, 142]. The deep convolutional neural network (CNN) is one of the most powerful network structures in deep learning. For deep CNN based image super resolution problems, different CNNs are designed and utilised to extract image features and construct an end-to-end non-linear mapping between LR and HR images [43, 52, 88]. Owing to the powerful capacity in capture deep level image features, these approaches represent the state of the art techniques in image SR.

However, such a strategy usually requires a large amount of network parameters to work successfully, and may consume a lot of time for training despite their accuracy. A possible alternative is to explore fuzzy rule based approaches [122] which can produce non-linear mappings through the use of a set of fuzzy rules, resulting in lightweight models and making the training process faster.

C. Learning of fuzzy rules

As an LR image patch can be generated from any of the many possible HR image patches, this uncertainty of the image SR problem makes it natural to introduce fuzzy technique into the learning based approaches, which is well demonstrated in reference [122]. The image SR methods based on learning of fuzzy rules work by transferring the image pixels (or image features) of a given image into corresponding fuzzy representations and using fuzzy ‘if-then’ rules to describe the non-linear relationship between the LR and the HR images. Given a pixel (or an extracted image feature) in the low resolution image as an input, the corresponding pixel in the high resolution image will be the output of the fuzzy rule inference.

The work of [122] addresses the ISR problem through fuzzy clustering and fuzzy rule learning, updating the desired HR pixels as a linear combination of the input LR pixels and the relevant cluster centroid. In particular, the fuzzy clustering technique approximately classifies the given image pixels into different types firstly, assuming there exist a set of fuzzy rules concluding each type. Then, for each type of image pixels, a non-linear mapping consisting of a set of fuzzy rules is learned. A number of learning methods can be adopted for learning the relevant parameters in the fuzzy rules, such as the LSE, evolutionary algorithms. Amongst the various learning methods, the ANFIS has been proven to be a popular tool for generate a set of effective fuzzy rules through an adaptive neural network structure, this ANFIS based ISR approach is developed in this thesis and will be detailed described later in Chapter 5.
2.4 Summary

In this chapter, a number of background techniques have been introduced, forming the fundamental knowledge required to develop the work of this thesis. In particular, the basic concepts of ANFIS are reviewed in the first place. The typical fuzzy rule interpolation techniques are systemically outlined. These FRI techniques include the original KH approach and the popular T-FRI approach with Mamdani-type rules, and several existing TSK based rule interpolation approaches. Finally, the background knowledge of image super resolution is briefly introduced, and some recent popular image super resolution methods are reviewed.

Based on the background material presented in this chapter, Chapter 3 studies the problem of how to extend the traditional fuzzy rule interpolation to ANFIS interpolation, resulting in a group rule based interpolation approach.
Chapter 3

ANFIS Interpolation - A Group Rule Interpolation Based Approach

ALTHOUGH ANFIS models have been widely used in various real world problems, the way to drive an effective ANFIS model with sparse training data still remains a challenging problem, similarly to many other algorithms. As reviewed previously in Section 1.2, the transfer learning and the FRI techniques may provide potential solutions to this important practical issue. Inspired by the basic ideas of transfer learning (that the knowledge obtained from the source domain can be transferred and used in the target domain) and fuzzy rule interpolation (that a new fuzzy rule can be constructed by interpolating two neighbouring rules), this chapter focusses on the introduction of a transfer-learning based approach to fuzzy rule interpolation for ANFIS construction. It combines the aforementioned ideas underlying the two distinct approaches to learn ANFISs for situations where there is only limited training data available in the given target domain. Particularly, to construct a new ANFIS in a target domain, the proposed approach seeks the assistance of two neighbouring ANFISs that have been generated from two source domains (where sufficient training data is available).

Because the proposed approach is ANFIS based, it has the following features:

1. Traditional FRI methods are concerned with individual rule interpolation within one fixed problem area, and are designed to interpolate a rule for an unmatched
3.1 The Framework for the Proposed Approach

In this section, the main idea underlying the proposed approach and the overall procedures implementing the idea are presented. At the highest level, this approach can be stated as follows. Without losing generality, suppose that sparse training data (not sufficient for learning an effective ANFIS) in the target domain $T$ is given, expressed in a collection of input-output pairs $\{(x, y)\}$, and that two ANFISs (denoted
3.1. The Framework for the Proposed Approach

as \( \mathcal{A}_1 \) and \( \mathcal{A}_2 \) respectively) are already trained over the source domains \( S_1 \) and \( S_2 \). Then, the goal of this work is to generate a new ANFIS \( \mathcal{A}_{\text{int}} \) over \( T \), through an innovative way of group-based rule interpolation. Note that here, \( x \) stands for the vector of all input variables.

**Algorithm 3.1:** ANFIS Interpolation - A group rule interpolation based approach.

**Input:**
- Two source ANFISs in source domains: \( \mathcal{A}_1, \mathcal{A}_2 \);
- Sparse training data in target domain: \( \{(x, y)\} \);
- Number of closest atoms: \( K \)

// Stage 1: Rule Dictionary Generation
1. Extract fuzzy rules \( \{R_i\} \) from \( \mathcal{A}_1 \) and \( \mathcal{A}_2 \);
2. Construct antecedent part of rule dictionary \( D_a \) via Equation (3.3);
3. Construct consequent part of rule dictionary \( D_c \) via Equation (3.4);

// Stage 2: Intermediate ANFIS Construction
4. Divide \( \{(x, y)\} \) into \( C \) clusters, \( C \) is decided by Equation (3.5);
5. for each cluster centre \( c^{(k)} \) do
   6. Select \( K \) closest atoms in \( D_a \);
   7. Compute weights \( w^{(k)} \) for chosen atoms using Equation (3.8) and (3.9);
   8. Create rule antecedent using chosen atoms with index set \( \mathcal{K} \) in \( D_a \) by Equation (3.11);
   9. Create rule consequent using atoms in \( D_c \) with the same index set \( \mathcal{K} \) by Equation (3.12);
6. end
7. Integrate all interpolated rules to form the intermediate ANFIS \( \mathcal{A}' \);

// Stage 3: ANFIS Fine-tuning
8. Use sparse training data \( \{(x, y)\} \) to fine tune \( \mathcal{A}' \).

**Output:**
- Interpolated ANFIS in target domain: \( \mathcal{A}_{\text{int}} \).

To be concise, the overall algorithm implementing the proposed approach is shown in Figure 3.1, with detailed steps summarised in Algorithm 3.1. The entire process of constructing an effective ANFIS with sparse data over target domain involves three stages:

1. Rule dictionary generation,
2. Intermediate ANFIS construction,
3. ANFIS fine-tuning.
3.1. The Framework for the Proposed Approach
3.2 Implementation of Proposed Approach

In stage 1, a rule dictionary is firstly generated by separating and reorganising rules extracted from source ANFISs \( \mathcal{A}_1 \) and \( \mathcal{A}_2 \). After that, in stage 2, an intermediate ANFIS is interpolated by the following procedure: a) clustering the sparse data of target domain into \( C \) clusters; b) interpolating a new rule for each cluster using LLE; and c) integrating all the newly generated rules in a network (to form the intermediate ANFIS). Finally in stage 3, the sparse training data is reused to refine the resulting intermediate ANFIS through retraining. The specifications for these three stages are further described in the following section.

3.2 Implementation of Proposed Approach

This section details the three stages that have been outlined in the framework of the proposed approach, including the rule dictionary generation stage, the intermediate ANFIS construction stage and the ANFIS fine-tuning stage.

3.2.1 Rule dictionary generation

To support interpolation of (groups of) fuzzy rules that are to be subsequently used for building an intermediate ANFIS, a rule dictionary (RD) is firstly constructed. Such a dictionary consists of an antecedent unit \( D_a \) and a consequent unit \( D_c \), which are designed as two separate memories devised to respectively store collected rule antecedent parts and consequent parts that are extracted from given ANFISs. In general, it can be assumed that \( \mathcal{A}_1 \) and \( \mathcal{A}_2 \) consist of \( n_1 \) and \( n_2 \) rules respectively. Thus, the extracted rules can be expressed in the following format:

\[
R_{i_1}^{\mathcal{A}_1} : \text{if } x_1 \text{ is } A_1^{\mathcal{A}_1} \text{ and } \ldots \text{ and } x_m \text{ is } A_m^{\mathcal{A}_1}, \text{ then } y_i = \sum_{j=0}^{m} p_{ij}^{\mathcal{A}_1} x_j \quad (3.1)
\]

\[
R_{i_2}^{\mathcal{A}_2} : \text{if } x_1 \text{ is } A_1^{\mathcal{A}_2} \text{ and } \ldots \text{ and } x_m \text{ is } A_m^{\mathcal{A}_2}, \text{ then } y_i = \sum_{j=0}^{m} p_{ij}^{\mathcal{A}_2} x_j \quad (3.2)
\]

where \( m \) denotes the number of input variables, and \( p_{i0}^{\mathcal{A}_t}, t \in \{1, 2\} \) is a coefficient within the linear combination in a consequent part (with a set value of \( x_0 = 1 \) for the representation to meet the eye).
3.2. Implementation of Proposed Approach

The rule dictionary \( D = \{ D_a, D_c \} \) is generated by separating and reorganising the rule antecedents and rule consequents of the aforementioned rules. In particular, \( D_a \in \mathbb{R}^{m \times n} \), consisting of all the rule antecedent parts:

\[
D_a = \begin{bmatrix}
A_{1,1}^{a} & A_{1,2}^{a} & \cdots & A_{1,n}^{a} \\
A_{2,1}^{a} & A_{2,2}^{a} & \cdots & A_{2,n}^{a} \\
\vdots & \vdots & \ddots & \vdots \\
A_{m,1}^{a} & A_{m,2}^{a} & \cdots & A_{m,n}^{a}
\end{bmatrix}
\]

where each column \( d_i^a = [A_{1,i} \ A_{2,i} \ \cdots \ A_{m,i}]^T \), \( i \in \{1, 2\} \), (each \( A_{j,i} \), \( j = 1, 2, \ldots, m \), contains a fuzzy set value for a given input variable within a certain rule) forming an atom of the dictionary unit \( D_a \). \( n_1 \) is the number of rules in \( \mathcal{A}_1 \), \( n_2 \) is the number of rules in \( \mathcal{A}_2 \), and \( n = n_1 + n_2 \) denotes the number of atoms in the rule dictionary. Similarly, the consequent unit \( D_c \in \mathbb{R}^{(m+1) \times n} \), consisting of the consequent parts of each and every rule (of the source domains), which can be expressed by

\[
D_c = \begin{bmatrix}
p_{1,0}^c & p_{1,1}^c & p_{1,2}^c & \cdots & p_{1,n}^c \\
p_{2,0}^c & p_{2,1}^c & p_{2,2}^c & \cdots & p_{2,n}^c \\
\vdots & \vdots & \vdots & \ddots & \vdots \\
p_{m,0}^c & p_{m,1}^c & p_{m,2}^c & \cdots & p_{m,n}^c
\end{bmatrix}
\]

with each atom \( d_i^c = [p_{i,0}^c \ p_{i,1}^c \ p_{i,2}^c \ \cdots \ p_{i,m}^c]^T \), \( i \in \{1, 2\} \).

### 3.2.2 Intermediate ANFIS construction

An intermediate ANFIS is a set of new rules interpolated with the assistance of the rule dictionary created as above. The construction of an intermediate ANFIS is completed by three sub-steps: clustering sparse training data; interpolating rules; and integrating interpolated rules.

#### 3.2.2.1 Clustering sparse training data

The sparse training data given in the form of \( \{(x, y)\} \) within the target domain are firstly partitioned into \( C \) clusters on a variable by variable basis by using K-means algorithm.
3.2. Implementation of Proposed Approach

clustering algorithm [105]. Clustering is utilised in order to minimise the derivation of any redundant rules, so that similar training data which belong to one cluster will (eventually) only lead to one rule. It is implemented in a ‘variable by variable’ fashion. That is, clustering is iteratively applied to all training data according to the first variable of the domain (with variables ordered in any preferable order), and then, for each resulting cluster, it is applied again to the data within the current cluster according to the second variable, etc. Following this ‘variable by variable’ clustering strategy, the resulting clusters will cover all possible regions of the input variables. The number of clusters \( C \), which is also the expected number of rules in the intermediate ANFIS, is decided by Equation (3.5) below:

\[
C = \prod_{j=1}^{m} \left\lfloor \frac{n_1^{(j)} + n_2^{(j)}}{2} \right\rfloor
\]  

where \( n_1^{(j)} \) is the number of fuzzy sets of the \( j \)th variable in \( \mathcal{A}_1 \), \( n_1 = \prod_{j=1}^{m} n_1^{(j)} \); and similarly, \( n_2^{(j)} \) is that of \( \mathcal{A}_2 \), \( n_2 = \prod_{j=1}^{m} n_2^{(j)} \). Note that here Equation (3.5) is not looking for the smallest \( C \).

### 3.2.2.2 Interpolating rules

With respect to the resulting centroid of each cluster, a single newly interpolated rule is generated by exploiting the locally linear embedding algorithm (LLE) [126]. This is due to the recognition that LLE is one of the most classical and promising manifold learning methods, which is originally developed for tackling dimensionality reduction problems and has now been widely utilised in performing different types of machine learning task (e.g., [22, 70]). LLE generates a neighbourhood preserving mapping between a \( D \)-dimensional data space and a \( d \)-dimensional data space, assuming that the data of these two spaces lie on or near the same manifold. Without losing generality, suppose that each data point \( X_i \) in the \( D \)-dimensional data space is expected to be reconstructed by its \( K \) nearest neighbours \( \{X_j\} \), and that the reconstruction error is measured by the following cost function:

\[
\varepsilon(w) = |X_i - \sum_j w_j X_j|^2
\]  

where the weight \( w_j \) modifies the contribution of the \( j \)th neighbour to the current data point \( X_i \).
3.2. Implementation of Proposed Approach

For each data point $X_i$ in the $D$-dimensional data space, LLE involves the following implementation steps in an effort to construct the corresponding data point $Y_i$ in the $d$-dimensional data space (thereby reducing the data dimensionality). Firstly, find the $K$ nearest neighbours $\{X_j\}$ to $X_i$ in $D$-dimensional data space. Secondly, compute the weights $\{w_j\}$ of the selected neighbours by minimising the cost function Equation (3.6) subject to: 1) that $X_i$ is reconstructed only from its neighbours, while setting $w_j = 0$ if $X_j$ does not belong to the set of neighbours; 2) that $\sum_j w_j = 1$. Finally, compute the corresponding data point $Y_i$ regarding $X_i$ in $d$-dimensional data space using weights $\{w_j\}$ and corresponding neighbours $\{Y_j\}$ regarding $X_j$ such that $Y_i = \sum_j w_j Y_j$. Further details regarding this algorithm can be found in [126].

Similar to the LLE algorithm, the rule antecedent space and the rule consequent space are seen as the two spaces lying on the same manifold, and a new rule is interpolated for each cluster following the three steps, as outlined in Figure 3.2. Here, the first two steps are conducted in the antecedent RD space, while the third step is conducted in the consequent RD space. These three steps are described as follows.

![Figure 3.2](image.png)

Figure 3.2: Illustrative implementation of single rule interpolation: (a) Choosing K closest neighbours. (b) Calculating weights of chosen neighbours. (c) Generating new rule.

A. Choosing the K closest atoms

To interpolate a new rule for a given cluster, the first step is choosing $K$ closest atoms in $D_a$. For each cluster $C_k$, its centroid regarding the $m$ antecedent attributes is denoted by $c^{(k)} = (c_1, c_2, \cdots, c_m)^T$. With the previously obtained antecedent rule dictionary $D_a$, the $K$ closest atoms (a column in $D_a$ denotes an atom) to $c^{(k)}$ are selected using the Euclidean distance metric (though any other distance metrics can be utilised as an alternative if preferred):
3.2. Implementation of Proposed Approach

\[d_i = d(d_i, c^{(k)}) = \sum_{j=1}^{m} d(A_{ij}^{d_i}, c_j)^2\] (3.7)

where \(d_i\) is the distance between \(d_i\) and \(c^{(k)}\), \(d(A_{ij}^{d_i}, c_j) = |\Rep(A_{ij}^{d_i}) - c_j|, t \in \{1, 2\}\). \(\Rep(A_{ij}^{d_i})\) stands for the representative value of the fuzzy set \(A_{ij}^{d_i}\). \(m\) is the number of input variables. The \(K\) atoms \(\{d_i\}\) in \(D_a\) which have the smallest distances are chosen as the closest neighbours, whose index set is denoted by \(\mathcal{K}\). That is, \(\forall i \in \mathcal{K}, \max \{d(d_i, c^{(k)})\} < d(d_j, c^{(k)}), j \notin \mathcal{K}\) and \(|\mathcal{K}| = K\).

B. Calculating the construction weights

Based on the obtained closest atoms \(\{d_i| i \in \mathcal{K}\}\), the aim of step 2 is to find the best construction weights that indicate the relative significance of each selected atom. This process can be seen as the reconstruction of \(c^{(k)}\) using \(\{d_i\}\). Thus, the weights required for rule interpolation can be obtained by minimising the following reconstruction error:

\[w^{(k)} = \min \|c^{(k)} - \sum_{i \in \mathcal{K}} \Rep(d_i) w_i^{(k)} \|^2, \text{ s.t. } \sum_{i \in \mathcal{K}} w_i^{(k)} = 1\] (3.8)

where \(w_i^{(k)}\) is the relative weighting of \(d_i\) as compared to the rest, \(\Rep(d_i) = [\Rep(A_{i,1}^{d_i}) \Rep(A_{i,2}^{d_i}) \cdots \Rep(A_{i,m}^{d_i})]^T, t \in \{1, 2\}\). Essentially it is a constrained least square optimisation problem which has the following solution:

\[w^{(k)} = G^{-1}1^T (c^{(k)}1^T - X)^T\] (3.9)

where \(G = (c^{(k)}1^T - X)^T (c^{(k)}1^T - X)\) is a Gram matrix, 1 denotes a column vector of ones, and \(X\) denotes an \(m \times K\) matrix whose columns are the chosen atoms \(\{d_i| i \in \mathcal{K}\}\).

C. Generating the new rule

Fundamentally speaking, FRI techniques are developed by performing similarity-based analytic reasoning, assuming that if the rule conditions are similar, then the consequents should also be similar. Reflecting this intuitive presumption in the view of LLE is that the underlying assumption for generating a new rule is: its antecedent part and consequent part lie on the same manifold. That is, if the centroid \(c^{(k)}\) can be represented as a linear combination of the \(K\) selected atoms indexed by \(\mathcal{K}\) in the antecedent rule dictionary \(D_a\), then the corresponding consequent can be expressed
as the linear combination of the atoms (whose locations are also indexed by $\mathcal{X}$) in the rule consequent dictionary $D_c$. Based on this (practically working) presumption, a newly interpolated rule $R_k^{\alpha'}$ in response to cluster $C_k$ is generated by applying the weight $w^{(k)}$ on both the antecedent and the consequent part, with the following format:

$$R_k^{\alpha'}: \text{if } x_1 \text{ is } A_1^{\alpha'} \text{ and } \ldots \text{ and } x_m \text{ is } A_m^{\alpha'}, \text{ then } y_k = \sum_{j=0}^{m} p_{kj} x_j$$ (3.10)

where the antecedent part is obtained by

$$A_{kj}^{\alpha'} = \sum_{i \in \mathcal{X}} w^{(k)}_{i} A_{ij}^{\alpha'}, \quad j = 1, 2, \ldots, m, \quad k = 1, 2, \ldots, C.$$ (3.11)

$t \in \{1, 2\}$, and similarly the consequent part is obtained by

$$p_{kj}^{\alpha'} = \sum_{i \in \mathcal{X}} w^{(k)}_{i} p_{ij}^{\alpha'}, \quad j = 0, 1, 2, \ldots, m, \quad k = 1, 2, \ldots, C.$$ (3.12)

### 3.2.2.3 Integrating the rules

The above completes the process of producing a newly interpolated rule. By integrating all such interpolated rules, the intermediate ANFIS $\mathcal{A}'$ results. This is implemented by putting all the newly generated rules into an ANFIS network, which is an inverse operation of extracting rules from a given network. A simple and generic example is given here to show this procedure.

Suppose that there are two input variables $x_1$ and $x_2$, and that a small number of training data associated with each variable is divided into two clusters. Thus, the sparse training data can be divided into $2 \times 2 = 4$ clusters as follows:

- **Cluster 1**: $\{(x_1)_1, (x_2)_1\}$
- **Cluster 2**: $\{(x_1)_1, (x_2)_2\}$
- **Cluster 3**: $\{(x_1)_2, (x_2)_1\}$
- **Cluster 4**: $\{(x_1)_2, (x_2)_2\}$

where $\{(x_1)_u, (x_2)_v\}$ represents the cluster including the $u$-th portion of $x_1$ and the $v$-th portion of $x_2$, with $u, v \in \{1st, 2nd\}$, e.g., $\{(x_1)_1, (x_2)_1\}$ represents the cluster
including the first portion of $x_1$ and the first portion of $x_2$. From these clusters, the following four rules are newly generated according to the above three steps:

Rule 1: If $x_1$ is $A_1$, $x_2$ is $B_1$, then $y = p_{11}x_1 + p_{12}x_2 + p_{10}$

Rule 2: If $x_1$ is $A_1$, $x_2$ is $B_2$, then $y = p_{21}x_1 + p_{22}x_2 + p_{20}$

Rule 3: If $x_1$ is $A_2$, $x_2$ is $B_1$, then $y = p_{31}x_1 + p_{32}x_2 + p_{30}$

Rule 4: If $x_1$ is $A_2$, $x_2$ is $B_2$, then $y = p_{41}x_1 + p_{42}x_2 + p_{40}$

These rules form the specification for a new (intermediate) ANFIS network to be constructed, by assigning the premise parameters $\{A_q, B_r\}, q, r \in \{1, 2\}$ in Layer 1, and the consequent parameters $\{p_{ij}\}$ in Layer 4, as shown in Figure 3.3.

Figure 3.3: Integrating newly generated rules as an (intermediate) ANIFS

### 3.2.3 ANFIS fine-tuning

In the final stage, the intermediate ANFIS $\mathcal{A}'$ is employed as an initial network here to train the final interpolated ANFIS $\mathcal{A}_{int}$, using the sparse training data provided. The training procedure is basically the same as the traditional ANFIS training algorithm summarised in Section 2.1, with just one exception as described below.

The traditional procedure for ANFIS learning takes ‘zeros’ or ‘random values’ as the initial parameters of the network. This is practically acceptable for problems where
a large amount of training data is available. However, this is a rather inefficient strategy under the data shortage situations as for the present consideration. In general, a good initial setting is very important to the performance of a learning algorithm. Thus, instead of using random initials, the parameters embedded in the interpolated intermediate ANFIS are herein utilised to populate the initial network setting. In so doing, the final interpolated ANFIS in the target domain is one that is obtained through a fine-tuning procedure over the intermediate ANFIS that is derived from source domains. As such, the entire ANFIS construction can be performed with little training data.

3.3 Complexity Analysis

The time complexity of Algorithm 3.1 is estimated here. There are totally three stages listed in Algorithm 3.1. As Stage 3 is the same as that for conducting traditional ANFIS training, only the complexity of the procedures regarding rule interpolation (i.e., that of Stages 1 and 2) is addressed. As indicated before, for computational simplicity, triangular fuzzy sets with three characteristic points each are used for implementation. Note that the following notations are employed for the complexity analysis:

\[ m \] : number of antecedent attributes

\[ n \] : number of fuzzy rules in rule dictionary

\[ K \] : number of chosen closest rules

\[ C \] : number of clusters in training data

\[ N \] : number of sparse training data points

In Stage 1 (rule dictionary generation, lines 1-3), the main task is to extract all the parameters from the given ANFIS networks (in the source domains). All the parameters of an ANFIS appear in either the first layer or the forth layer, with the premise parameters in layer one and the consequent parameters in layer four. Premise parameters are fuzzy sets, each of which contains three sub-parameters (say, \( a_0 \), \( a_1 \), and \( a_2 \)), so the number of premise parameters is \( 3m \). Similarly, the
number of consequent parameters is \( m + 1 \). Thus, the time complexity for extracting one rule is \( O(4m + 1) \), and the time complexity for computing the entire Stage 1 is \( n \times O(4m + 1) = O(4mn + n) \).

In Stage 2 (intermediate ANFIS construction, lines 4-11), line 4 for clustering using K-means algorithm takes \( O(NCm) \). The sequence of lines 6-9 repeats \( C \) times. Particularly, line 6 involves two operations: 1) computing the Euclidean distances, of a complexity \( O(n) \); and 2) sorting the distances, of a complexity \( O(n^2) \). Then, in line 7, the weight is calculated once for each chosen rule, thereby being of a complexity \( O(K) \). Finally, lines 8-9 take a complexity of \( O(4m + 1) \), in which the weighted average is calculated once for each parameter. Thus, the time complexity for Stage 2 is estimated to be \( O(NCm) + C \times [O(n) + O(n^2) + O(K) + O(4m + 1)] = O(NCm) + O(Cn^2) \).

Together, the overall time complexity for group rule interpolation bar that required by Stage 3 (for running the standard procedure to perform ANFIS fine-tuning with a small number of training data) is estimated to be \( O(4mn + n) + O(NCm) + O(Cn^2) = O(NCm) + O(Cn^2) \). Compared with the standard ANFIS learning method, the complexity of ANFIS interpolation is slightly larger, but it is practically doable, since usually \( m \) and \( C \) are fixed in advance and both \( n \) and \( N \) are not a very large number.

### 3.4 Experimentation

Both synthetic and real world data are considered in the experiments to qualitatively and quantitatively evaluate the proposed ANFIS interpolation approach. Section 3.4.2 validates the approach by looking into two synthetic function modelling cases, and in Section 3.4.3, the effectiveness of the proposed approach in dealing with real world situations is shown. Section 3.4.4 discusses the model parameters, and examines the robustness of the proposed approach in response to the use of different amounts of training data.

#### 3.4.1 Experimental setup

For all experiments carried out, triangular membership functions are employed due to their popularity and simplicity. The number of selected closest atoms is
3.4. Experimentation

empirically set to 3 unless otherwise stated (and a further investigation into the potential impact of different settings for this value will be reported towards the end of this section). To reflect the capability of the proposed approach in handling different data, both normalised and unnormalised data are investigated. In particular, for the experiments on synthetic data, the original data without normalisation is used despite that the data involves significantly skewed distributions over different magnitudes. In the experiments on the problem involving real world data, the input variables are normalised to $[0, 1]$.

The RMSE (Root-Mean-Squared Error) index is chosen to evaluate the performance of different ANFISs on both the source and the target data. Particularly, the RMSE measured from the source ANFIS $\mathcal{A}_1$ on the source domain data $S_1$ is denoted by $E_{\mathcal{A}_1(S_1)}$; that from $\mathcal{A}_2$ on $S_2$ by $E_{\mathcal{A}_2(S_2)}$; and that from $\mathcal{A}_1$ and $\mathcal{A}_2$ on the target domain data $T$ by $E_{\mathcal{A}_1(T)}$ and $E_{\mathcal{A}_2(T)}$ respectively. These RMSEs are computed as below:

$$E_{\mathcal{A}_t(x)} = \sqrt{\frac{1}{N_s} \sum_{k=1}^{N_s} (g^*_k - \mathcal{A}_t(x^*_k))^2}$$

(3.13)

where $N_s$ is the number of the testing data points $\{x^*_k\}$ in the domain $S_1, S_2$ or $T$; $g^*_k$ is the relevant ground truth of the $k$th data point; $\mathcal{A}_t(x^*_k), t \in \{1, 2, ori, int\}$ stands for the output value of an ANFIS on the data point $x^*_k$. Obviously, smaller RMSEs indicate better performance.

An original ANFIS developed using only the sparse training data in target domain [66] is also generated here for comparison, denoted by $\mathcal{A}_{ori}$. The RMSE of $\mathcal{A}_{ori}$ on the testing data $T$ is denoted as $E_{\mathcal{A}_{ori}(T)}$, and the RMSE of the interpolated ANFIS $\mathcal{A}_{int}$ using the proposed approach on $T$ is denoted by $E_{\mathcal{A}_{int}(T)}$.

3.4.2 Experiments on synthetic data

Two numerical functions are utilised here to test the proposed approach for working on highly non-linear one and two dimensional data. Further experiments are also included to show the case where absolutely no training samples are available for the target domain.
3.4.2.1 One dimensional input

As the first illustrative experimentation, a one-dimensional input function is used, which is generated by sampling the non-linear function as given below:

\[ y = \frac{\sin(2x)}{e^x} \]  

(3.14)

where \( x \in [0, 9] \), the shape of this function is plotted in Figure 3.4(a).

![Figure 3.4: Illustration of data and source ANFISs. (a) Source data and target data used. (b) Membership functions in each source ANFIS.](image)

A. Illustrative example

In this experimentation, to illustrate the proposed approach, the input domain \( x \in [0, 9] \) is divided into three parts, representing two source domains and one target domain. As indicated previously, samples read off the underlying non-linear function are treated as the data as depicted in Figure 3.4(a). In particular, the left
3.4. Experimentation

Part $x \in [0, 3]$ is used as the first source domain for training the first source (or given) ANFIS $\mathcal{A}_1$, and the right part $x \in [6, 9]$ is used as the second source domain for training the second source ANFIS $\mathcal{A}_2$. The middle part data $x \in [3, 6]$ forms the target domain, which is divided into two sub-parts, with a small portion (20% randomly taken from the target domain, one fold training data is shown in triangles as an example for illustration) as the sparse training data (which is to artificially simulate the situation where little target domain data is available), with the rest used as testing data (80%, shown in pentagrams).

The two source ANFISs are trained using the standard method for ANFIS model learning as outlined in Section 2.1. The membership functions involved are illustrated in Figure 3.4(b). Here, the numbers of membership functions are set to 5 and 6 for $\mathcal{A}_1$ and $\mathcal{A}_2$, respectively. This is to demonstrate a case that is more complex than the usual (where quantity spaces tend to be defined with an equal number of fuzzy sets), making the experiments more challenging.

**Rule dictionary generation**: The rules embedded within the trained source ANFISs $\mathcal{A}_1$ and $\mathcal{A}_2$, form the atoms of the rule dictionary. Table 3.1 lists the rule dictionary constructed by extracting rules from trained ANFISs $\mathcal{A}_1$ and $\mathcal{A}_2$. There are totally 11 rules in the rule dictionary, with 5 from $\mathcal{A}_1$ and 6 from $\mathcal{A}_2$.

<table>
<thead>
<tr>
<th>Rule</th>
<th>Source ANFIS</th>
<th>Antecedent ($a_0, a_1, a_2$)</th>
<th>Consequent</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>$\mathcal{A}_1$</td>
<td>($-0.725, 0.045, 0.684$)</td>
<td>$1.263x - 0.044$</td>
</tr>
<tr>
<td>2</td>
<td>$\mathcal{A}_1$</td>
<td>($-0.040, 0.733, 1.446$)</td>
<td>$0.141x + 0.760$</td>
</tr>
<tr>
<td>3</td>
<td>$\mathcal{A}_1$</td>
<td>(0.768, 1.440, 2.157)</td>
<td>$-0.609x + 1.057$</td>
</tr>
<tr>
<td>4</td>
<td>$\mathcal{A}_1$</td>
<td>(1.465, 2.166, 2.924)</td>
<td>$-0.075x - 0.451$</td>
</tr>
<tr>
<td>5</td>
<td>$\mathcal{A}_1$</td>
<td>(2.201, 2.874, 3.625)</td>
<td>$0.658x - 2.151$</td>
</tr>
<tr>
<td>6</td>
<td>$\mathcal{A}_2$</td>
<td>(5.400, 6.002, 6.570)</td>
<td>$0.250x - 1.665$</td>
</tr>
<tr>
<td>7</td>
<td>$\mathcal{A}_2$</td>
<td>(5.999, 6.599, 7.194)</td>
<td>$0.195x - 1.127$</td>
</tr>
<tr>
<td>8</td>
<td>$\mathcal{A}_2$</td>
<td>(6.605, 7.196, 7.782)</td>
<td>$-0.098x + 0.936$</td>
</tr>
<tr>
<td>9</td>
<td>$\mathcal{A}_2$</td>
<td>(7.234, 7.801, 8.375)</td>
<td>$-0.223x + 1.765$</td>
</tr>
<tr>
<td>10</td>
<td>$\mathcal{A}_2$</td>
<td>(7.815, 8.389, 9.012)</td>
<td>$-0.083x + 0.531$</td>
</tr>
<tr>
<td>11</td>
<td>$\mathcal{A}_2$</td>
<td>(8.401, 8.983, 9.600)</td>
<td>$0.120x - 1.205$</td>
</tr>
</tbody>
</table>
Intermediate ANFIS construction: A group of new rules are interpolated in the target domain to form the intermediate ANFIS. The sparse training data in target domain is firstly clustered into $C$ clusters. The number of clusters $C$ (also the number of rules in the new ANFIS) is decided by Equation (3.5). In this illustrative example, $m = 1, n_1^{(1)} = 5, n_2^{(1)} = 6$, so $C = \lfloor (5 + 6)/2 \rfloor = 5$. The first column of Table 3.2 shows the 5 resulting centroids. Take the first centroid $(c = 3.90)$ for example, a new rule is generated following the three steps (shown in the first row of Table 3.2): 1) choosing $K$ closest neighbours with $K = 3$, the 5th, 4th and 6th atoms of the rule dictionary are chosen as shown in Table 3.2; 2) calculating the relevant weights for chosen atoms, resulting in weights $w_1 = 0.313, w_2 = 0.295, w_3 = 0.392$; 3) generating a new rule by averaging the chosen closest rules, $R' = w_1 R_5 + w_2 R_4 + w_3 R_6$, the antecedent and the consequent parts of the newly generated rule are shown in the last two columns of Table 3.2. Repeating this process for all the 5 centroids, the intermediate ANFIS results.

Table 3.2: Generated new rules for all cluster centroids

<table>
<thead>
<tr>
<th>Centroids</th>
<th>Chosen atoms</th>
<th>weights</th>
<th>new rules</th>
<th>Ant</th>
<th>Con</th>
</tr>
</thead>
<tbody>
<tr>
<td>3.90</td>
<td>(5,4,6)</td>
<td>0.313,0.295,0.392</td>
<td>(3.237,3.891,4.572)</td>
<td>0.282x−1.459</td>
<td></td>
</tr>
<tr>
<td>4.50</td>
<td>(6,5,7)</td>
<td>0.264,0.524,0.212</td>
<td>(3.851,4.489,5.159)</td>
<td>0.452x−1.805</td>
<td></td>
</tr>
<tr>
<td>5.55</td>
<td>(6,7,5)</td>
<td>0.374,0.404,0.222</td>
<td>(4.932,5.549,6.169)</td>
<td>0.318x−1.555</td>
<td></td>
</tr>
<tr>
<td>5.70</td>
<td>(6,7,5)</td>
<td>0.389,0.431,0.179</td>
<td>(5.086,5.700,6.312)</td>
<td>0.299x−1.519</td>
<td></td>
</tr>
<tr>
<td>5.90</td>
<td>(6,7,5)</td>
<td>0.411,0.468,0.121</td>
<td>(5.293,5.902,6.505)</td>
<td>0.273x−1.472</td>
<td></td>
</tr>
</tbody>
</table>

ANFIS fine-tuning: By combining all the new rules, an intermediate ANFIS is constructed with 5 fuzzy rules. From this, the final output ANFIS is obtained by retraining it using the given data. The resultant interpolated ANFIS is shown in Table 3.3.

B. Experimental results

5×5-fold cross validation (5-FCV) is utilised to evaluate the performance of different approaches. Note that conventional 10×10-fold cross validation is not adopted here due to the extremely small number of samples for training, especially for the target domain. Note also that here the 5-FCV takes one piece of data for training while the other four pieces of data for testing, which is slightly different
3.4. Experimentation

Table 3.3: Rules in Interpolated ANFIS $A_{\text{int}}$

<table>
<thead>
<tr>
<th>Rule Number</th>
<th>Antecedent $(a_0, a_1, a_2)$</th>
<th>Consequent</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>$(3.237, 3.891, 4.572)$</td>
<td>$0.117x + 0.029$</td>
</tr>
<tr>
<td>2</td>
<td>$(3.852, 4.490, 5.159)$</td>
<td>$0.027x + 0.006$</td>
</tr>
<tr>
<td>3</td>
<td>$(4.934, 5.579, 6.167)$</td>
<td>$-0.081x - 0.012$</td>
</tr>
<tr>
<td>4</td>
<td>$(5.085, 5.696, 6.313)$</td>
<td>$-0.062x - 0.009$</td>
</tr>
<tr>
<td>5</td>
<td>$(5.288, 5.903, 6.504)$</td>
<td>$-0.0038x - 2.94 \times 10^{-5}$</td>
</tr>
</tbody>
</table>

with the standard 5-FCV where one piece of data is for testing and four pieces of data is for training. The mean and standard deviation values of different methods compared are listed in Table 3.4, and the visual results of 5 folds within the total 5×5 folds are shown in Figure 3.5.

Table 3.4: Experimental results on one-dimensional function

<table>
<thead>
<tr>
<th></th>
<th>Mean ± Standard deviation</th>
</tr>
</thead>
<tbody>
<tr>
<td>$E_{A_1(S_1)}$</td>
<td>$0.003 ± 0.000$</td>
</tr>
<tr>
<td>$E_{A_2(S_2)}$</td>
<td>$0.0006 ± 0.000$</td>
</tr>
<tr>
<td>$E_{A_1(T)}$</td>
<td>$0.287 ± 0.013$</td>
</tr>
<tr>
<td>$E_{A_2(T)}$</td>
<td>$0.255 ± 0.014$</td>
</tr>
<tr>
<td>$E_{A_{ori}(T)}$</td>
<td>$0.121 ± 0.067$</td>
</tr>
<tr>
<td>$E_{A_{int}(T)}$</td>
<td>$0.089 ± 0.039$</td>
</tr>
</tbody>
</table>

By examining the experimental results in both Figure 3.5 and Table 3.4, it can be seen that the two source ANFISs $A_1$ and $A_2$ perform quite well in their corresponding source domains (as $E_{A_1(S_1)}$ and $E_{A_2(S_2)}$ are quite small). However, these two ANFISs do not work in the target domain (as $E_{A_1(T)}$ and $E_{A_2(T)}$ are rather large). This is of course, not surprising since they have been trained using the data for the source domains in the first place. Yet, if the standard training method is used to build an ANFIS for the target domain, it does not work well either, as the performance of the original ANFIS $A_{ori}$ is poor. Again, this may be expected due to data shortage of the target domain. Fortunately, with the assistance of its two neighbouring source ANFISs, the interpolated ANFIS $A_{int}$ improves the results significantly. As shown in the middle part of Figure 3.5(a)-(e), its outcome is much closer to the ground truth.
Figure 3.5: Five folds taken from 5×5-fold cross validation for one-dimensional non-linear function approximation.
3.4. Experimentation

3.4.2.2 Two dimensional input

The two-dimensional synthetic data used in this experimentation is sampled from the following function:

\[ y = \sin\left(\frac{x_1}{\pi}\right)\sin\left(\frac{x_2}{\pi}\right) \]  \hspace{1cm} (3.15)

where \( x_1 \in [-30, 30] \), \( x_2 \in [-10, 10] \). Figure 3.6(a) displays the shape of this function in one period. Similar to the previous experiments on one-dimensional data, the entire underlying domain is divided into 3 parts. Without any particular bias, this is implemented with respect to the first variable \( x_1 \). That is, the region covered by \( x_1 \in [-30, -10] \), \( x_2 \in [-10, 10] \) (with \( step = 1 \) in each dimension, totally 441 data points sampled from the function) forms the first source domain, the region by \( x_1 \in [10, 30] \), \( x_2 \in [-10, 10] \) forms the second source domain, and the region covered by \( x_1 \in [-10, 10] \), \( x_2 \in [-10, 10] \) forms the target domain. There are also 441 data points in the target domain, in which 88 data points (20%) are used for training while 353 points (80%) are used for testing. Experiments on splitting the data with respect to the second variable are also carried out, with similar results achieved as to be reported later.

<table>
<thead>
<tr>
<th></th>
<th>Mean ± Standard deviation</th>
<th>Mean ± Standard deviation</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>splitting ( x_1 )</td>
<td>splitting ( x_2 )</td>
</tr>
<tr>
<td>( E_{sf_1(S_1)} )</td>
<td>0.024 ± 0.000</td>
<td>0.023 ± 0.000</td>
</tr>
<tr>
<td>( E_{sf_2(S_2)} )</td>
<td>0.023 ± 0.000</td>
<td>0.023 ± 0.000</td>
</tr>
<tr>
<td>( E_{sf_1(T)} )</td>
<td>1.176 ± 0.029</td>
<td>1.079 ± 0.030</td>
</tr>
<tr>
<td>( E_{sf_2(T)} )</td>
<td>1.331 ± 0.022</td>
<td>1.586 ± 0.035</td>
</tr>
<tr>
<td>( E_{sf_{ori}(T)} )</td>
<td>0.372 ± 0.063</td>
<td>0.489 ± 0.264</td>
</tr>
<tr>
<td>( E_{sf_{int}(T)} )</td>
<td><strong>0.070</strong> ± 0.016</td>
<td><strong>0.103</strong> ± 0.087</td>
</tr>
</tbody>
</table>

The middle column of Table 3.5 lists the results of 5-FCV for this two dimensional function approximation problem using different ANFISs. As an example, Figure 3.6 shows the visual result of one randomly picked fold, where Figure 3.6(a) displays the ground truth view of this two-dimensional function in target domain; Figure 3.6(b)
3.4. Experimentation

Figure 3.6: One fold of the two-dimensional function-approximation results: (a) Ground truth. (b) Result based on \( \mathcal{A}_{\text{ori}} \). (c) Result based on \( \mathcal{A}_{\text{int}} \).

illustrates the result based on the original ANFIS directly learned from the sparse training data; and Figure 3.6(c) is that of the interpolated ANFIS.

As reflected by these experimental outcomes, the result of the interpolated ANFIS is much more similar to the real view of the underlying highly non-linear two-dimensional function. Without the assistance of group rule interpolation, the outcome from running the ANFIS directly trained by the limited samples is rather different from the ground truth. Again, these results indicate that the ANFIS learned by the proposed interpolation method performs much better than the original ANFIS under the situations where only highly restricted training data is provided.

Note that the above results are obtained using source domains and target domain defined by splitting the domain of the first input variable \( x_1 \). However, similar results can also be obtained via specifying the source domains and target domain with regard to the second variable \( x_2 \) of this function, as listed in the third, i.e., the right-most column of Table 3.5.

Consider a more general situation where both input variables \( x_1 \) and \( x_2 \) are divided into three regions. As such there are totally nine subregions, as shown in Figure 3.7. This gives rise to a general case in which there may be more than two source ANFISs for use to interpolate an ANFIS within a given target domain. For instance, if insufficient training data appears in the central subregion of Figure 3.7, whilst an ANFIS is required to be constructed, then this will be a problem of interpolating multiple ANFISs from given ANFISs within the neighbouring source domains. It is straightforward to extend the proposed work to such a situation as the only difference is regarding rule dictionary generation, where the rules are extracted
from multiple source ANFISs. For this particular example, the result of taking the central subregion as target domain and the other 8 subregions as source domains can be computed, such that the average and standard deviation values of RMSE (over 5-FCV) for the original ANIFS $E_{\text{ori}}(T)$ is $0.215 \pm 0.178$, whilst that for the interpolated ANIFS is $E_{\text{int}}(T) = 0.177 \pm 0.081$, showing a remarkable improvement.

![Figure 3.7: Function approximation with more than two source domains](image)

### 3.4.2.3 Situation with no target training data

Consider a further situation where no target training data is available in the target domain, using the problem of approximating the function as expressed in Equation (3.14). In the area where $x \in [0.5, 2]$, this one dimensional non-linear function may be interpreted approximately as linear, as shown in Figure 3.8. Suppose that the data covered within the left part delimited by $x \in [0.5, 1]$ is used to train the first source ANFIS $\mathcal{A}_1$, and that the data within the right part $x \in [1.5, 2]$ is used to train the second source ANFIS $\mathcal{A}_2$. The data of the middle part $x \in [1, 1.5]$ is fully reserved for testing and hence, no training samples are available over the target domain. Since no target training data is provided, each test data point is seen as a centroid, and the new rule interpolated for this data point forms a special intermediate ANFIS containing just one rule, which is then directly used for inference without retraining. The visual result is also shown in Figure 3.8.

From the results shown, it can be seen that the proposed approach performs very well over this particular problem, even though no target training data is available. However, this should not be overly generalised since for the same underlying function, if the source domains are $[1.5, 2]$ and $[2.5, 3]$, and no information is present in support of the training of the target domain delimited by $[2, 2.5]$, the proposed approach will only produce an approximate model as depicted in Figure 3.9. This does not seem to
perform well, due to the high non-linearity of the function to be approximated within this region. As shown in the target domain of this figure, the interpolated outcome is far away from the ground truth in the bottom area surrounding the minimum point, around which the function shape of target domain and source domains are totally different. Quantitatively, the mean value of RMSE is 0.0948, which is fairly large for this problem. Nevertheless, as previously demonstrated, once there are a small number of training samples provided for the target domain, the approach can result in an accurate ANFIS.

### 3.4.3 Experiments on real world benchmark data

Twelve benchmark datasets taken from the KEEL data repository [5] are used here to evaluate the performance of the proposed ANFIS construction algorithm on real world problems. The datasets used in this experimentation are summarised in Table 3.6.

The generation of the source domains and target domain is similar to the cases where the synthetic data are used, by dividing each dataset into three parts according to one of the input variables. For example, the Quake Dataset has three input variables: ‘Longitude’, ‘Latitude’ and ‘Depth’. This dataset is divided into three sub-datasets using the values of the variable ‘Longitude’. In particular, those instances...
with this variable value being smaller than -40 jointly form the first source domain $S_1$ (of a subtotal of 593 instances), instances with ‘Longitude’ value larger than 92 form the second source domain $S_2$ (1253 instances), and instances with ‘Longitude’ value between $[-40, 92]$ form the target domain $T$ (332 instances). Similar to the experiments on synthetic data reported earlier, 20% (66 instances) of the data in the
target domain are used as the training data, with the remaining 80% (265 instances) used as the testing data. This is very different from the common choice that usually takes a majority of data (often 80% or 90%) for training, and the remaining minority of data for testing. Such a strategy makes the ANFIS construction a challenging problem as only very limited data is available for training. Thus, the proposed interpolation technique is introduced in an effort to generate an effective ANFIS model.

5×5-fold cross validation results of this experimentation are shown in Table 3.7. The average values of all twelve datasets are shown in the bottom row, with the best results shown in bold. As reflected by these results as per Table 3.7, a similar conclusion to what is previously learned from the experiments on synthetic data can be drawn. Both $E_{A_1(T)}$ and $E_{A_2(T)}$ are very large, indicating that the ANFISs trained in the source domains are not suitable for the regression problem in the target domain. Again, this is not surprising. However, those target domain models $A_{ori}$ trained over the limited amounts of data perform significantly better than their counterparts. Since the number of training data is so small for each of the twelve cases, the resultant ANFIS $A_{ori}$ is still not very stable (as indicated by the large standard deviation value in Table 3.7), though its mean RMSE is significantly better. Despite this limitation, the interpolated ANFISs following the proposed approach remarkably minimise the inference error caused by data shortage, as the mean values and the standard deviation values of $E_{A_{int}(T)}$ are much smaller than those of $E_{A_{ori}(T)}$.

Apart from the RMSE values, it is also important and necessary to test the statistic significance of the interpolated ANFIS over the original ANFIS. The pairwise t-test ($p = 0.05$) is employed here for such statistic analysis. The $p$-values of t-test of the interpolated ANFIS ($A_{int}$) over the original ANFIS ($A_{ori}$) are listed in Table 3.8, with $p < 0.05$ representing that $A_{int}$ performs significantly better than $A_{ori}$. In this table, signs (v) and (*) denote statistically better or not respectively. As can be seen from the table, the $p$ values are smaller than 0.05 for almost all datasets, indicating the statistical improvements made by the interpolated ANFIS. In t-test, smaller $p$ value means better result. It can be noticed that the $p$ value of the ‘AutoMPG6’ dataset is quite small, demonstrating the superior performance of the interpolated model.
### Table 3.7: Experimental results on real world datasets

<table>
<thead>
<tr>
<th>Datasets</th>
<th>$E_{a(t)}$</th>
<th>$E_{a_2(t)}$</th>
<th>$E_{a_{ar}(t)}$</th>
<th>$E_{a_{int}(t)}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diabetes</td>
<td>7.045±0.514</td>
<td>10.166±2.045</td>
<td>1.527±0.829</td>
<td>1.058±0.497</td>
</tr>
<tr>
<td>Plastic</td>
<td>5.824±0.128</td>
<td>8.654±0.173</td>
<td>2.003±0.246</td>
<td>1.843±0.105</td>
</tr>
<tr>
<td>Quake</td>
<td>0.563±0.014</td>
<td>1.624±0.063</td>
<td>1.264±0.641</td>
<td>0.542±0.248</td>
</tr>
<tr>
<td>Laser</td>
<td>71.142±0.687</td>
<td>18.514±0.438</td>
<td>12.087±4.739</td>
<td>3.757±2.726</td>
</tr>
<tr>
<td>AutoMPG6</td>
<td>17.672±1.082</td>
<td>18.781±0.886</td>
<td>12.770±1.431</td>
<td>5.120±1.038</td>
</tr>
<tr>
<td>Delta-ail</td>
<td>2.36×10$^{-4}$±1.41×10$^{-5}$</td>
<td>4.76×10$^{-4}$±5.52×10$^{-4}$</td>
<td>3.53×10$^{-4}$±1.09×10$^{-4}$</td>
<td>1.78×10$^{-4}$±1.06×10$^{-5}$</td>
</tr>
<tr>
<td>Friedman</td>
<td>5.583±0.120</td>
<td>4.571±0.091</td>
<td>5.177±0.633</td>
<td>3.004±0.409</td>
</tr>
<tr>
<td>Dee</td>
<td>3.059±0.080</td>
<td>5.614±0.201</td>
<td>1.017±0.339</td>
<td>0.870±0.225</td>
</tr>
<tr>
<td>Delta-elv</td>
<td>0.0023±3.011×10$^{-5}$</td>
<td>0.0074±7.229×10$^{-5}$</td>
<td>0.0034±6.195×10$^{-4}$</td>
<td>0.0020±1.690×10$^{-4}$</td>
</tr>
<tr>
<td>AutoMPG8</td>
<td>13.175±0.412</td>
<td>20.823±0.726</td>
<td>5.801±1.707</td>
<td>5.695±1.199</td>
</tr>
<tr>
<td>Concrete</td>
<td>85.764±2.633</td>
<td>28.918±0.778</td>
<td>27.228±10.894</td>
<td>14.058±2.813</td>
</tr>
<tr>
<td>Stock</td>
<td>37.357±0.797</td>
<td>26.129±0.484</td>
<td>3.843±2.080</td>
<td>2.314±0.803</td>
</tr>
<tr>
<td>Average</td>
<td>20.598±0.539</td>
<td>11.984±0.490</td>
<td>6.060±1.962</td>
<td>3.189±0.838</td>
</tr>
</tbody>
</table>
3.4. Experimentation

Table 3.8: p values of pairwise t-test results

<table>
<thead>
<tr>
<th>Dataset</th>
<th>$\mathcal{A}<em>\text{int}$ v.s. $\mathcal{A}</em>\text{ori}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diabetes</td>
<td>0.0216 (v)</td>
</tr>
<tr>
<td>Plastic</td>
<td>0.0037 (v)</td>
</tr>
<tr>
<td>Quake</td>
<td>$1.12 \times 10^{-5}$ (v)</td>
</tr>
<tr>
<td>Laser</td>
<td>$1.34 \times 10^{-7}$ (v)</td>
</tr>
<tr>
<td>AutoMPG6</td>
<td>$6.41 \times 10^{-18}$ (v)</td>
</tr>
<tr>
<td>Delta-ail</td>
<td>$1.90 \times 10^{-8}$ (v)</td>
</tr>
<tr>
<td>Friedman</td>
<td>$7.08 \times 10^{-15}$ (v)</td>
</tr>
<tr>
<td>Dee</td>
<td>0.0065 (v)</td>
</tr>
<tr>
<td>Delta-elv</td>
<td>$5.92 \times 10^{-12}$ (v)</td>
</tr>
<tr>
<td>AutoMPG8</td>
<td>0.7832 (*)</td>
</tr>
<tr>
<td>Concrete</td>
<td>$2.53 \times 10^{-6}$ (v)</td>
</tr>
<tr>
<td>Stock</td>
<td>0.0013 (v)</td>
</tr>
</tbody>
</table>

3.4.4 Experiments with different settings

The parameter $K$ controls the number of selected closest neighbours in running the LLE algorithm. In the experimental results reported above, this number is empirically set to be 3. In order to investigate the relationship between the parameter $K$ and the experimental outcome, the performance over different $K$ using the ‘Quake’ dataset is given, as shown in Figure 3.10. The conclusion is that for most cases, a smaller $K$ will lead to better result, this finding is similar to what is established in [92] (though that piece of existing work is concerned with a weighted approach to FRI).

It may be expected that if the number of training data becomes smaller, the performance of the trained ANFINs will generally become worse. To verify this hypothesis with experimental investigation, Figure 3.11 shows the outcomes under the condition where a different percentage of training data is employed over the ‘Quake’ dataset.

It can be induced from examining this figure that: 1) independent of what percentages of training data used, interpolated ANFISs outperform the original ANFISs; 2) the less training data is involved the more improvement the interpolated ANFIS makes over its counterpart which is trained just by the use of the sparse set of
training samples. It can be observed from the figure that when the percentage of training data reaches 90%, the performance of the two algorithms are close. This can be expected, because when sufficient training data is available, the superiority of the interpolated ANFIS is not obvious. An interesting observation is that as reflected by the triangular-marked line (which is the plot for interpolated ANFISs), the performance using 30% data is very close to that using 90% data. This is very different from the trend of the results attained using the ANFISs trained without the aid of interpolation. In summary, through the use of the proposed approach, a much improved inference outcome can be achieved while requiring much less training data.

3.5 Summary

How to construct an effective fuzzy inference system with insufficient training data is a practically important and challenging issue. This chapter has proposed a new ANFIS construction method through the use of group rule interpolation. To the best of our knowledge, this is the first time that the interpolation of ANFIS models is proposed (using two source ANFISs to assist the construction of the target one). It significantly differs from the general transfer learning methods in the literature where only one source domain is involved; in this work there are at least two source
domains. The work effectively resolves the data shortage problem for training ANFISs in the target domain. Experiments on both synthetic data and real world data have been carried out, including variations of the experimental background settings. The results have consistently demonstrated that the proposed approach greatly improves the performance in learning ANFIS models for problems where only sparse training data is available.

In comparison with existing work on FRI involving the use of TSK-type representation, this work exhibits the following distinct innovations:

1. As reflected above, rule interpolation is done at the level of a group of rules, instead of at the individual rule level as per the existing techniques. That is, unlike the existing FRI methods where only one intermediate rule is produced at a time, here by one run of the algorithm a group of rules are interpolated. This is because an ANFIS generally represents a set of TSK rules.

2. Learning is accomplished with the use of a dictionary purposefully introduced to facilitate ANFIS interpolation. In existing FRI techniques, there exists a sparse rule-base from which individual closest rules are directly selected for interpolation, but this does not apply to interpolation of a group of rules in a target domain. The rule dictionary is therefore designed for extracting rules from source ANFISs, acting as a sparse rule-base for the selection of the closest rules in the target domain.
3. Weights required for performing interpolation are computed differently. For instance, the active set algorithm [60] is employed in the existing work [31], which is an iterative method; whilst the LLE algorithm is utilised here, which is a one-step method without involving iterations. Different from traditional techniques that rely on the use of Euclidean distance measures to work, the proposed approach provides a theoretically well-formed and systematic method for calculating the weights that are required to construct an intermediate ANFIS during the interpolation process.

In this initial ANFIS interpolation approach, a group of fuzzy rules is interpolated. Following this, Chapter 4 will further optimise these interpolated rules with an evolutionary algorithm.
Chapter 4

ANFIS Interpolation - An Evolutionary Approach

Based on the aforementioned initial ANFIS interpolation approach, an improved ANFIS learning method is proposed in this chapter to deal with the problem of training data shortage. The proposal is to interpolate a number of candidate fuzzy rules first, forming an initial population which is modified via an evolutionary optimisation process subsequently.

In general, evolutionary computation [9, 10] offers a range of optimisation algorithms by analogy to natural evolution processes. Such algorithms perform optimisation with a set of chromosomes, which are able to search the problem hyperspace efficiently and effectively. Applying an evolutionary computation method to aid in building a fuzzy inference system injects learning capacity into the underlying fuzzy systems, which is commonly referred to as evolutionary fuzzy systems (EFS) in the literature (e.g., [7, 38, 39, 51, 129]). Considering genetic algorithms (GAs) being the most popular technique for use in developing such systems, the present work utilises a GA to implement the evolutionary process.

One of the key points of the proposed work is therefore, to examine how an ANFIS may be encoded using a specific chromosome representation. Without prejudgement, two alternative forms of representing fuzzy rules are considered in this chapter, using either individual rule based representation or group of rules (equivalently an entire
4.1. Genetic Algorithm

ANFIS) based representation to construct an initial population for further evolution. The initial population is iteratively updated through crossover and mutation operations, subject to the use of a fitness function, in order to determine whether a chromosome may enter into the next loop. The chromosomes of the highest fitness, namely rules or ANFISs with the best performance, will then be returned when the iterative process terminates. If the chromosomes represent individual rules, they collectively form the required ANFIS; otherwise, each returned chromosome is a learned ANFIS. Such a resulting ANFIS will be fine tuned to obtain the final improved ANFIS model, appropriate to deal with approximate inference in the target domain concerned. Both of the two chromosome representations are systemically evaluated and compared. Experimental results demonstrate that the evolutionary approach further improves the performance of the interpolated ANFIS while being competitive to those popular machine learning methods.

The remainder of this chapter is organised as follows. Section 4.1 reviews the basic knowledge of GA. Section 4.2 details the proposed evolutionary ANFIS interpolation approach. Section 4.3 discusses the complexity for implementing the proposed approach. Experimental results are discussed in Section 4.4. Finally, Section 4.5 concludes this chapter.

4.1 Genetic Algorithm

Inspired by observing natural evolution processes, evolutionary computation [9, 10] is in general, proposed to provide an effective and efficient way for searching optimal solution in poorly understood and irregular problem spaces. Typically, evolutionary algorithms work with a population of individuals, in which each individual may be one or a set of potential solutions in the solution space. Many evolutionary algorithms have been proposed, including genetic algorithms (GAs) [121, 145], genetic programming [1], and particle swarm optimisers [175]. Among these, GAs may be the most commonly adopted and hence, are utilised in this work also.

Mainly owing to the conceptual simplicity and computational effectiveness, GA becomes one of the most popular evolutionary algorithms. In a GA implementation, each individual of the population is encoded as a chromosome, which may be subsequently modified through crossover and mutation subject to a certain probability.
4.2 GA for ANFIS Interpolation

A fitness function is utilised to evaluate the performance of every chromosome within a population. The general implementation of a GA can be summarised in the following steps:

(1) Initialize the population;
(2) Perform crossover and mutation on the population;
(3) Calculate the fitness of each chromosome;
(4) Select a portion of chromosomes to construct a new population;
(5) Loop to step (2) until a certain stopping criterion is met.

Applying GAs for fuzzy systems modelling leads to techniques for building a form of genetic fuzzy learning systems. Typical approaches involve the development of procedures for: 1) Parameter tuning – By assuming that the structure of a fuzzy inference system is pre-defined, this procedure adapts the system’s parameters [55] (such as those defining membership functions or the coefficients specifying the consequent functions in a TSK model) with respect to changes in the model input. 2) Rule selection – By encoding a rule-base as a fixed-length chromosome, this procedure aims to control the complexity of a fuzzy inference system, leaving less room for redundant, incorrect or badly defined rules to exist [64]. 3) Rule-base construction – By encoding both the parameters and the structure of a fuzzy system within each chromosome, this procedure performs parameter estimation and structure identification at the same time [37, 106] (although often at the cost of significantly increasing the problem complexity).

4.2 GA for ANFIS Interpolation

This section presents the proposed novel ANFIS interpolation approach, which is supported by a GA. The problem addressed in this chapter is the same with that in chapter 3, which can be outlined as follows: With only a small number of training data in the target domain $T$, expressed in the form of input-output pairs \{(x, y)\}, ANFIS interpolation is to construct an effective ANFIS $\mathcal{A}_{int}$ over $T$, by interpolating two neighbouring ANFISs, $\mathcal{A}_1$ and $\mathcal{A}_2$, defined on two source domains $S_1$ and $S_2$, respectively. Figure 4.1 summarises the entire interpolation process, consisting of
4.2. GA for ANFIS Interpolation

three main stages: i) population initialisation via observation-guided interpolation of rules embedded in the source ANFISs, based on the method in Chapter 3; ii) interpolation via a GA over the initial population; and iii) ANFIS fine-tuning via the standard ANFIS learning method as described in Section 2.1 (using the given small number of training data in the target domain). The entire evolutionary process will of course depend upon how individuals are to be encoded in a population of chromosomes and how each chromosome may be evaluated. Details of this process are described below.

4.2.1 Chromosome representation: two strategies

How to encode a potential solution with a chromosome is a critical point in GAs. To reflect the fact that an ANFIS is essentially a set of fuzzy rules, there are two strategies that may be taken to represent an ANFIS model within a GA: 1) Encode each underlying rule of the ANFIS as a chromosome, and 2) Encode the entire ANFIS as a chromosome. Both types of chromosomes are introduced here.

4.2.1.1 Rule-based chromosome representation

This representation strategy encodes each rule of an ANFIS as a vector of rule parameters, in the form of (antecedent parameters, consequent parameters). For example, suppose that a rule involving \( m \) antecedent variables that take triangular fuzzy sets as values is expressed by:

\[
\text{If } x_1 \text{ is } A_1 \text{ and } x_2 \text{ is } A_2 \ldots \text{ and } x_m \text{ is } A_m, \\
\text{then } y = p_0 + p_1 x_1 + p_2 x_2 + \cdots + p_m x_m
\]  

(4.1)

where each fuzzy set \( A_i \) \( (i = 1, 2, \ldots, m) \) contains three parameters \( (a_{i0}, a_{i1}, a_{i2}) \) that respectively denote the three vertices of the triangle. Then, the rule based chromosome can be expressed such that

\[
((a_{10}, a_{11}, a_{12}), (a_{20}, a_{21}, a_{22}), \ldots, (a_{m0}, a_{m1}, a_{m2}), p_0, p_1, \ldots, p_m) 
\]  

(4.2)

In general, using triangular fuzzy sets, if a rule contains \( m \) antecedent variables, there will be \( 3m \) premise parameters and \( m + 1 \) consequent parameters. Thus, the length of the corresponding chromosome will be \( 3m + m + 1 = 4m + 1 \).
4.2. GA for ANFIS Interpolation

4.2.1.2 ANFIS-based chromosome representation

In this representation, an entire ANFIS containing $C$ rules is encoded as one chromosome. Suppose that a certain ANFIS contains $m$ input variables $x_1, x_2, \cdots, x_m$, and that the $i$th variable may take one of the $c_i$ triangular fuzzy sets $A_{i1}, A_{i2}, \cdots, A_{ic_i}$ as its value. Then, totally there will be $C = c_1 \times c_2 \times \cdots \times c_m$ rules captured in this ANFIS, and all these rules are collectively encoded as one vector like the following:

$$(\text{rule } 1, \text{rule } 2, \cdots, \text{rule } C) \quad (4.3)$$

where each single rule is coded exactly the same as Equation (4.2). In so doing, the length of an ANFIS based chromosome will be $C \times (4m + 1) = \prod_{i=1}^{m} c_i(4m + 1)$, which is much longer than that of a rule based one.

4.2.2 Population initialisation

An initial population, composed of a number of interpolated rules in the target domain, needs to be generated first, in order to start the evolutionary process. This is accomplished by adopting the group-based FRI mechanism of Chapter 3, over the given (sparse) training data, with the assistance of a rule dictionary constructed by extracting rules from the two source domain ANFISs $\mathcal{A}_1$ and $\mathcal{A}_2$ (as shown in Figure 4.1(b)). Details are as follows.

A rule dictionary $D = \{D_a, D_c\}$ with an antecedent part $D_a$ and a consequent part $D_c$ is generated firstly, to separately store collected rule antecedents and consequents, by extracting and then storing rules from the given source ANFISs. This process is the same with the rule dictionary generation procedure described in Section 3.2.1, so is omitted here.

4.2.2.1 Interpolating candidate rules

In order to form an initial population, a number of rules in the target domain are required. Traditional means for generating the initial population in a GA usually use randomly set parameters in the rules. Whilst this is practical for situations with sufficient training data it becomes a significant challenge for the current case, where
4.2. GA for ANFIS Interpolation

Figure 4.1: Flowchart of proposed approach. (a) Overall flowchart. (b) Population initialization process. (c) Crossover process. (d) Mutation process.
only highly restricted sparse data is available. To address this challenge, FRI is employed to interpolate rules in target domain, in an effort to set up an improved initial network, so as to be able to produce a more effective model with less training data. Given the above rule dictionary, a number of candidate rules in the target domain can indeed be obtained through interpolation by running the following procedure.

To start with, the given training data \{(x, y)\} in the target domain is divided into \(C\) clusters. \(C\) stands for the number of the rules in the ANFIS to be interpolated and is determined by Equation (3.5).

Having obtained the clusters, for each cluster, a set of candidate rules are interpolated to create the initial population. However, the number of training data in each cluster may be very different, and in certain clusters there may be just one datum. For extreme cases where the number of training samples is smaller than \(C\), certain clusters are simply empty, covering no data at all, though such situations may be rare. Therefore, instead of just utilising the raw training data contained within the clusters, individual instances are also artificially generated in an effort to enrich the original sparse training data. For this, the centre of each cluster is used as the seed to generate more individuals. In particular, for those clusters without any training data, the seeds are set to be the same as their neighbouring clusters (of course, such initially identical settings will become different through the evolutionary process).

For each cluster \(C_k\), the centroid is denoted by \(c^{(k)} = (c_1, c_2, \cdots, c_m)^T\) with regard to the \(m\) attributes. Use \(c^{(k)}\) as a seed, a number of artificial data (denoted by \(O = (o_1, o_2, \cdots, o_m)^T\)) can be generated by adding Gaussian white noise with the seed itself being the mean and a small value (\(\delta\)) being the standard deviation for each attribute. This method borrows practical ideas often adopted in the field of electrical engineering. The number of the individual instances in each cluster is set subject to the constraint in which the sum of cluster sizes will be the size of the required initial population. For implementational simplicity, in this work, all clusters are set to be of an equal size. Such an individual generation process can be illustrated as per Figure 4.2.

From the resulting data enriched clusters, for each individual instance within a given cluster, a candidate rule can be generated through interpolation that involves the same steps with Section 3.2.2.2. Firstly, selecting \(K\) closest rules in rule dictionary
by computing the Euclidian distance as defined by Equation (4.4), between the current individual \( O \) and every column of \( D_a \):

\[
d_i = d(d_i^a, O) = \sqrt{\sum_{j=1}^{m} d(A_{ij}^a, o_j)^2}
\] (4.4)

where \( d(A_{ij}^a, o_j) = |\text{Rep}(A_{ij}^a) - o_j|, t \in \{1, 2\} \). The index set associated with the \( K \) selected columns \( \{d_i^a\} \) in \( D_a \) is denoted by \( \mathcal{X} \).

Next, with the obtained closest columns \( \{d_i^a; i \in \mathcal{X}\} \), the candidate rule for the current individual can be interpolated as the weighted average of the selected rules. The weights required for rule interpolation are obtained by solving the optimization problem described as: \( w = \min_w ||O - \sum_{i \in \mathcal{X}} \text{Rep}(d_i^a)w_i||^2 \), s.t. \( \sum_{i \in \mathcal{X}} w_i = 1 \), where \( \text{Rep}(d_i^a) = [\text{Rep}(A_{ij}^a_1) \text{Rep}(A_{ij}^a_2) \cdots \text{Rep}(A_{ij}^a_m)]^T, t \in \{1, 2\} \), and \( w_i \) denotes the relative weighting of the column \( d_i^a \). As mentioned previously in Section 3.2.2.2, the solution of this constraint optimisation problem is: \( w^{(k)} = (G^{-1}1)/(1^T G^{-1}1) \), where \( G = (O1^T - X)^T(O1^T - X), 1 \) is a column vector of ones, and the columns of \( X \) are the selected \( \{d_i^a\}, i \in \mathcal{X}\}. Following the principles of FRI which performs reasoning by analogy, the weights \( w_i \) derived for the antecedent part are applied to the consequent part to attain similarity. Thus, the newly interpolated rule for the current individual has the following format:

\[
R: \text{If } x_1 \text{ is } A_1 \text{ and } \ldots \text{ and } x_m \text{ is } A_m, \text{ then } y = \sum_{j=0}^{m} p_j x_j
\] (4.5)

where

\[
\begin{align*}
A_j &= \sum_{i \in \mathcal{X}} w_i A_{ij}^a, \quad j = 1, 2, \ldots, m, \quad t \in \{1, 2\} \\
p_j &= \sum_{i \in \mathcal{X}} w_i p_{ij}^a, \quad j = 0, 1, 2, \ldots, m, \quad t \in \{1, 2\}
\end{align*}
\] (4.6)
4.2. GA for ANFIS Interpolation

4.2.2.2 Generating initial population

By collecting all the interpolated candidate rules, the initial population will be set up. Depending on which of the two chromosome representation strategies is used, there are slightly differences when forming the initial population. Using rule based chromosome representation, all the candidate rules within one cluster form an initial sub-population for this cluster. Therefore, there are \( C \) initial sub-populations in total, each of which will initiate an independent evolutionary learning process, as shown in Figure 4.3. While using ANFIS based chromosome representation, all the candidate rules are collected to form a global initial population, as shown in the Figure 4.4. Therefore, there is just one initial population in this case.

4.2.3 Crossover and mutation

For an evolutionary process, from the initial sub-population or the entire population (depending upon which coding style is used for chromosome representation), a subset of chromosomes (of an even cardinality) are randomly selected to perform crossover with a pre-specified crossover probability (denotes by \( p_c \)). The chosen chromosomes are then, randomly paired up. For each (so-called parent) pair \((ch1, ch2)\), the standard ‘two-point’ crossover is applied, in which a start position and an end position are randomly determined and subsequently, the genes between them are exchanged. In so doing, two child chromosomes are generated per pair. This procedure is illustrated in Figure 4.1(c).

After crossover, mutation operation follows. Similar to the crossover operation, a subset of the (sub-)population is selected for mutation with a pre-determined probability (denotes by \( p_m \)). For each chosen chromosome, a mutation position is randomly generated. Then, the mutated chromosome is created by randomly adding or subtracting a small value \( \epsilon \) to the gene at that position. The mutation procedure is illustrated in Figure 4.1(d).

Note that as with common approaches in the literature, a larger crossover probability and a smaller mutation probability are empirically assumed.
4.2. GA for ANFIS Interpolation

Figure 4.3: Rule based chromosome representation used in implementation.
4.2. GA for ANFIS Interpolation

Figure 4.4: ANFIS based chromosome representation used in implementation.
4.2.4 Fitness function

Fitness function is used to evaluate the performance of the chromosomes so that better performers can be maintained to enter the next iteration. Designing an appropriate fitness function is important for any evolutionary algorithm. How to define a fitness function however, depends on the application problem at hand. For prediction and estimation tasks, functions that compute the mean square error or the absolute difference error are the most commonly adopted. In this work, the fitness function is implemented on the basis of the RMSE (Root-Mean-Squared Error), which is defined per chromosome as follows:

\[ E = \frac{\sqrt{\sum_{i=1}^{N} (g_k - \mathcal{A}(x_k))^2}}{N} \]  

(4.7)

where \( N \) is the number of training data, \( g_k \) and \( \mathcal{A}(x_k) \) are the \( k \)th expected and estimated output over the evolutionary process, respectively. Suppose that the maximum error permitted is \( E_{\text{max}} \), then such a fitness function may be specified by

\[ F = E_{\text{max}} - E \]  

(4.8)

For the present application, a meaningful fitness measure should be given for an entire ANFIS instead of a single rule. Thus, further consideration may be due, depending upon which chromosome representation is utilised. For ANFIS based chromosome representation, the fitness of each chromosome can be directly obtained using the fitness function above, as per Equation (4.8). However, if individual rule based chromosome representation is employed, the fitness of such a chromosome is obtained using a score table that evaluates and records the performance of every candidate rule, as per Table 4.1, where \( \text{score}_{ij} \) denotes the evaluated (fitness) value of the \( j \)th candidate rule in the \( i \)th cluster and \( S \) is the size of candidates in each cluster.

Note that to capture and reflect the essence of the fitness of a candidate rule, computationally, \( \text{score}_{ij} \) is calculated as the averaging performance of the \( j \)th candidate rule in the \( i \)th cluster across a certain number of randomly generated possible ANFISs. This is necessary because in dealing with practical problems, the number of possible ANFISs can be rather large. For example, suppose that there are 10 rules in the rule-base of an ANFIS, and that there are 5 candidates per underlying
4.2. GA for ANFIS Interpolation

Table 4.1: Score table

<table>
<thead>
<tr>
<th>Cluster</th>
<th>Candidate</th>
<th>1</th>
<th>2</th>
<th>...</th>
<th>C</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td></td>
<td>score1</td>
<td>score2</td>
<td>...</td>
<td>scoreC1</td>
</tr>
<tr>
<td>2</td>
<td></td>
<td>score1</td>
<td>score2</td>
<td>...</td>
<td>scoreC2</td>
</tr>
<tr>
<td>...</td>
<td></td>
<td>...</td>
<td>...</td>
<td>...</td>
<td>...</td>
</tr>
<tr>
<td>S</td>
<td></td>
<td>score1</td>
<td>score2</td>
<td>...</td>
<td>scoreCS</td>
</tr>
</tbody>
</table>

Then, the number of possible ANFISs will be $5^{10}$, which is a huge figure that requires substantial storage and computation power. Thus, in implementation, just a portion of the possible ANFISs are randomly chosen for evaluation. To balance effectiveness and efficiency, the number of chosen possible ANFISs, denoted by $A_{\text{max}}$, may be set empirically (and in this research, $A_{\text{max}} = 500$). This practice (of only a randomly selected portion of possible ANFIS chromosomes being used for evaluation) is common in the literature of applied evolutionary algorithms.

The evaluated ANFISs are subsequently sorted according to their RMSEs in descending order. For individual rule-based representation, the score table is initialised with each cell set to zero and, for the $k$th sorted ANFIS ($k \in \{1, 2, \ldots, A_{\text{max}}\}$), record the candidate rules used, and the scores of those relevant candidate rules are added by $k$. After doing this for all those created possible ANFISs, the score table results. The procedure for computing the score table is summarised as given in Algorithm 4.1.

4.2.5 Summary of GA-based ANFIS interpolation

The proposed evolutionary ANFIS interpolation algorithms are summarised as Algorithm 4.2.

4.2.6 ANFIS Interpolation: contrasting two algorithms

The two algorithms, implemented depending upon which chromosome representation is employed, have already been illustrated in Figures 4.3 and 4.4 respectively. There exist three major differences between these two implementations: 1) The objects
Algorithm 4.1: Calculation of score table.

**Input:**
- Candidate rules;
- \( C \) – Number of clusters;
- \( S \) – Number of candidate rules in each cluster;
- \( A_{\text{max}} \) – Number of ANFISs for evaluation.

1. Make a zero Score Table of \( S \) rows and \( C \) columns;
2. Make a zero Counting Table of \( S \) rows and \( C \) columns;
3. Make \( A_{\text{max}} \) possible ANFISs randomly and record candidate rules used;
4. Evaluate ANFISs and sort them according to RMSE in descending order;
5. for \( k = 1 \) to \( k = A_{\text{max}} \) do
6.     for \( i = 1 \) to \( i = C \) do
7.         record the candidate rule number \( j \) used;
8.         Score Table: \( \text{score}_{ij} \leftarrow \text{score}_{ij} + k \);
9.         Counting Table: \( \text{count}_{ij} \leftarrow \text{count}_{ij} + 1 \);
10.   end
11. end
12. for \( i = 1 \) to \( i = C \) do
13.     for \( j = 1 \) to \( j = S \) do
14.         Score Table: \( \text{score}_{ij} \leftarrow \frac{\text{score}_{ij} \text{count}_{ij}}{} \);
15.     end
16. end

**Output:**
Score table of all candidate rules.

that are evolved during the evolutionary process are different. One using rule-based chromosome (termed ‘Method 1’ hereafter) conducts one evolutionary process per cluster, whilst the other using ANFIS based chromosome (termed ‘Method 2’) initialises the population directly with ANFISs, conducting the evolutionary process only once. This is of course, the fundamental reason for all the differences between these two algorithms. 2) The population initialisation methods are different, as discussed previously in Section 4.2.2.2. 3) The fitness measurement means are different, as described in Section 4.2.4.

Both algorithms have their own advantages and disadvantages, as summarised below. In particular, the individual rule-based approach requires less storage – Each chromosome only represents one rule, meaning that it is generally much shorter than a chromosome in ANFIS based method. This also leads to less running time, as to be indicated in an illustrative example later. However, the entire ANFIS-based representation offers a more convenient means for evaluation – The process of
4.2. GA for ANFIS Interpolation

Algorithm 4.2: ANFIS Interpolation - An evolutionary approach.

**Input:**
- Source ANFISs in source domains: $\mathcal{A}_1, \mathcal{A}_2$;
- Sparse training data in target domain: \{(x, y)\};
- Population size (ANFIS chromosome): $Q$.

// - Population Initialization
1. Extract fuzzy rules $\{R_i\}$ from $\mathcal{A}_1$ and $\mathcal{A}_2$;
2. Construct rule dictionary $D$ by Equations (3.3) and (3.4);
3. Divide sparse training data into $C$ clusters, with respect to Equation (3.5);

for each cluster do
  1. Use centre of each cluster as seed, generate a set of individuals;
  2. for each individual do
     1. Interpolate one candidate rule;
  end
end

if chromosome is rule type then
  for each cluster do
    1. Collect candidate rules within the current cluster, to form an initial sub-population;
  end
else if chromosome is ANFIS type then
  for $i = 1$ to $i = Q$ do
    for each cluster do
      1. Choose one candidate rules in the current cluster;
    end
    1. Form an ANFIS chromosome by all chosen rules;
    1. Collect all ANFIS chromosomes as initial population;
  end
repeat
  // - Crossover and Mutation
  1. Choose chromosomes for crossover with probability $p_c$;
  1. Do two-point crossover for chosen chromosomes;
  2. Choose chromosomes for mutation with probability $p_m$;
  2. Do mutation for chosen chromosomes;
  // - Evaluation
  if chromosome is rule type then
    1. Evaluate chromosomes using Score Table;
  end
else if chromosome is ANFIS type then
  1. Evaluate chromosomes using Equation (4.8);
end
  1. Update population by roulette selection;
until stop criteria is met;

**Output:**
Interpolated ANFIS $\mathcal{A}_{int}$ in target domain.
4.3 Complexity Analysis

assessing the quality of chromosomes to decide whether any of them will enter the next iteration can be directly evaluated in this approach, whilst the evaluation step of rule based chromosomes involves a much more complex procedure (using a score table and using an additional parameter of $A_{\text{max}}$).

4.2.7 Fine-tuning of GA-learned ANFIS model

A GA-learned network (through the process as described above) is used as an intermediate network for further fine-tuning with the sparse training data in target domain through the standard ANFIS learning algorithm. Compared with the use of the original standard ANFIS training procedure, which initialises the network parameters as ‘zeros’ or ‘random values’, the proposed ANFIS learning mechanism employs both fuzzy rule interpolation and GA-based evolutionary procedure, in an effort to produce higher quality initial network parameters. In so doing, the sparse training data is used more efficiently in the fine-tuning procedure for generating ANFIS of improved performance.

4.3 Complexity Analysis

The time complexity of the proposed methods (for both the rule based and ANFIS based chromosome representation) is analysed here. According to Algorithm 4.2, there are generally three stages in performing evolutionary ANFIS interpolation: population initialisation, crossover and mutation, and chromosome evaluation. As indicated previously, triangular fuzzy sets are utilised in implementing both methods and hence, the complexity analysis only involves the use of such fuzzy sets. The notations used are listed as follows:

\[ m \] : number of antecedent attributes

\[ n \] : number of fuzzy rules in rule dictionary

\[ N \] : number of sparse training data points

\[ C \] : number of clusters in training data
4.3. Complexity Analysis

\( P \): number of individuals in each cluster

\( Q \): population size for ANFIS based chromosomes

\( A_{\text{max}} \): number of ANFISs used in calculating score table

### 4.3.1 Rule-based chromosome representation

In the ‘Population Initialisation’ step, lines 1-2 extract all the rule parameters from sources ANFISs to construct the rule dictionary. There are totally \( n \) rules, with \( 4m + 1 \) parameters in each rule. Thus, running lines 1-2 costs \( O(4mn + n) \). Following this, line 3 for clustering takes \( O(N Cm) \). Lines 4-9 repeat \( C \times P \) times implementing candidate rule interpolation, each of which includes three sub-steps: (1) selecting \( K \) closest rules (at the cost of \( O(n^2) \)), (2) calculating weights (at \( O(K) \)) and (3) generating new rules (at \( O(4m + 1) \)). Therefore, the complexity for computing lines 4-9 is \( C \times P \times [O(n^2) + O(K) + O(4m + 1)] = O(CPn^2) \). Next, lines 10-14 jointly lead to \( C \) initial populations, costing \( O(C) \). Hence, the sub-total complexity for this step is \( O(4mn + n) + O(N Cm) + O(CPn^2) + O(C) = O(N Cm) + O(CPn^2) \).

In the ‘Crossover and Mutation’ step, the crossover and mutation operation repeats \( C \) times. Line 25 selects \( p_c P \) rules for crossover, costing \( O(p_c P) \). In line 26, there are \( [(p_c P)/2] \) pairs of chromosomes. For each pair, in the worst case, all the parameters within the two chromosomes are exchanged, taking \( O(4m + 1) \). Then, in performing the mutation operation, lines 27-28 take \( O(p_m P) \). Thus, the sub-total complexity is \( C \times [O(p_c P) + [(p_c P)/2] \times O(4m + 1) + O(p_m P)] = O(mCP) \).

The rule based chromosome uses a score table to implement the ‘Chromosome Evaluation’ step. In running Algorithm 4.1, lines 1-2 take \( O(SC) \). Line 3 makes \( A_{\text{max}} \) ANFISs with \( C \) rules in each, costing \( O(A_{\text{max}} C) \). Line 4 costs \( O(A_{\text{max}}^2) \) for sorting the \( A_{\text{max}} \) RMSEs. Following this, lines 5-11 repeat \( A_{\text{max}} \) \( C \) times, costing \( O(A_{\text{max}} C) \). Lines 12-16 repeat \( SC \) times with a complexity of \( O(1) \) each time. Thus, the sub-total complexity for the ‘Chromosome Evaluation’ step is \( O(SC) + O(A_{\text{max}} C) + O(A_{\text{max}}^2) = O(A_{\text{max}}^2) \).

In summary, the overall complexity for the proposed approach with rule based chromosome is: \( O(N Cm) + O(CPn^2) + O(mCP) + O(A_{\text{max}}^2) \).
4.3. Complexity Analysis

4.3.2 ANFIS-based chromosome representation

For the method that exploits ANFIS based chromosome representation, the ‘Population Initialisation’ step is almost the same as that for the method using rule based chromosomes, except for its final population construction process as given in lines 15-23, which costs \(O(QC)\). Thus, running this ‘Population Initialisation’ step is at the cost of \(O(4mn+n)+O(NCm)+O(CPn^2)+O(QC) = O(NCm)+O(CPn^2)+O(QC)\). Different from the method with rule based chromosome representation, here, the crossover and mutation operation are only implemented once within the population of the size \(Q\). Line 25 takes \(O(p_cQ)\). In line 26 the crossover operation repeats for \(\lfloor(p_cQ)/2\rfloor\) times, and in the worst case, each crossover incurs exchanges across all the \(C(4m+1)\) parameters in each ANFIS based chromosome, thereby costing \(O(C(4m+1))\). Following this, lines 27-28 take \(O(p_mQ)\). The sub-total complexity for the ‘Crossover and Mutation’ step is therefore, \(O(p_cQ)+\lfloor(p_cQ)/2\rfloor \times O(C(4m+1))+O(p_mQ) = O(mCQ)\). Finally in the ‘Chromosome Evaluation’ step, line 33 evaluates all the \(Q\) chromosomes by sorting the related RMSEs, costing \(O(Q^2)\). Hence, the overall complexity for the method with ANFIS based chromosome representation is: \(O(NCm)+O(CPn^2)+O(mCQ)+O(Q^2)\).

<table>
<thead>
<tr>
<th>Main steps</th>
<th>Rule-based chromosome</th>
<th>ANFIS-based chromosome</th>
</tr>
</thead>
<tbody>
<tr>
<td>Population Initialization</td>
<td>(O(NCm) + O(CPn^2))</td>
<td>(O(NCm)+O(CPn^2)+O(QC))</td>
</tr>
<tr>
<td>Crossover and Mutation</td>
<td>(O(mCP))</td>
<td>(O(mCQ))</td>
</tr>
<tr>
<td>Chromosome Evaluation</td>
<td>(O(A_{\text{max}}^2))</td>
<td>(O(Q^2))</td>
</tr>
<tr>
<td>Overall</td>
<td>(O(NCm) + O(CPn^2) + O(mCP) + O(A_{\text{max}}^2))</td>
<td>(O(NCm)+O(CPn^2)+O(mCQ)+O(Q^2))</td>
</tr>
</tbody>
</table>

For clarity, the outcomes of the above computational complexity analysis are summarised in Table 4.2. Comparing the overall complexity of running the method using rule based chromosome representation and that using ANFIS based chromosome representation, it can be seen that the first two items \((O(NCm) + O(CPn^2))\) in each are the same. Moreover, in implementations, \(A_{\text{max}}\) and \(Q\) are usually set as the same number because both denote the number of ANFISs to be evaluated. Thus, the only difference between the complexities of these two methods lies in their respective
third items: \((O(mCP) \text{ vs. } O(mCQ))\). From this analysis, it can be concluded that the complexities of the two proposed methods do not differ very much. The time complexity of using the ANFIS based chromosome representation is slightly higher than that of using the rule based one, because that the value of \(Q\) is typically larger than that of \(P\). This is verified experimentally later.

4.4 Experimentation and Validation

This section presents a systematic experimental evaluation of the proposed approach. Section 4.4.1 provides the general experimental set-up, including the parameters used, comparative methods employed, and performance index measured. Section 4.4.2 validates the two proposed algorithms by looking into a few synthetic function modelling cases, while Section 4.4.3 shows the effectiveness of the proposed approach in performing TSK regression over ten benchmark datasets.

4.4.1 Experimental setup

In the experimental studies, triangular membership functions are used in implementing the first layer of an ANFIS due to their popularity and simplicity. Both normalised and unnormalised data are used, reflecting the capability of the proposed approach in dealing with different data representations. Particularly, original data is used without normalisation in the synthetic data experiments for the convenience of result illustration. While in the experiments involving benchmark datasets, all input domains of the original data are normalised to \([0, 1]\). The classical roulette algorithm is employed for chromosome selection when updating the population in an evolutionary process. Following the common practice in the literature, the crossover and mutation probabilities are chosen as \(p_c = 0.8\) and \(p_m = 0.2\), respectively, unless otherwise stated. In setting up the initial population, the number of candidate rules of each cluster is set to \(P = 5\). Note that \(P\) is the number of candidate rules per cluster in the very original population before any crossover and mutation, which differs in principle from the figure \(S\) in Table 4.1, that stands for the number of candidate rules in each cluster in the evaluation step.

Regression results using different ANFISs are compared, including: 1) An original ANFIS trained with the classical ANFIS learning method [66], using the sparse data
4.4. Experimentation and Validation

in the target domain only, named as 'Original ANFIS' hereafter; 2) An interpolated ANFIS obtained by the first ANFIS interpolation method described in Chapter 3, named as 'Method 0' (which interpolates one rule with respect to the centre of each cluster without involving evolutionary computation); 3) An interpolated ANFIS obtained by the proposed ‘Method 1’ (via rule based chromosome representation); and 4) An interpolated ANFIS obtained by the proposed ‘Method 2’ (via ANFIS based chromosome representation).

RMSE is taken to evaluate the performance of different ANFISs, as per the definition of Equation (4.7), where \( N \) now represents the number of the testing data points \( \{x_k\} \) in the target domain; \( g_k \) denotes the corresponding ground truth of the \( k \)th data point; and \( \mathcal{A}(x_k) \) stands for the output of different ANFISs on the data point \( x_k \). Obviously, a smaller RMSE indicates a better performance, given otherwise the same conditions while performing statistical analyses.

4.4.2 Experiments on synthetic data

In this experimental study, synthetic data is created by sampling three non-linear functions, including two 1-D functions and one 2-D function, these function relationships used in the experiments are listed in Table 4.3.

<table>
<thead>
<tr>
<th>No.</th>
<th>Function</th>
<th>( x ) range</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>( \cos(x) \cdot x )</td>
<td>( x \in [-10, 10] )</td>
</tr>
<tr>
<td>2</td>
<td>( \frac{\sin(2x)}{e^{x/5}} )</td>
<td>( x \in [-10, 10] )</td>
</tr>
<tr>
<td>3</td>
<td>( \sin(x_1/\pi)\sin(x_2/\pi) )</td>
<td>( x_1 \in [-30, 30], x_2 \in [-10, 10] )</td>
</tr>
</tbody>
</table>

4.4.2.1 Illustrative example

This is presented in order to show the main working procedures of the proposed ANFIS interpolation approach and the differences between the two types of chromosome representation. The first one dimensional non-linear function \( y = \cos(x) \cdot x \) is used for giving the illustrative example, the underlying function is plotted for illustration in Figure 4.5.
As shown in Figure 4.5, the input domain \([-10, 10]\) is divided into three parts to simulate the source data and the target data. In particular, there are totally 201 data points sampled from this continuous function (with a sampling step of 0.1), in which the data in the left part (67 data points, shown in dashed line) forms the first source domain, which is used for training the first source ANFIS \(A_1\), and the data in the right part (67 data points, shown in dotted line) forms the second source domain for training the corresponding second ANFIS \(A_2\). These two source ANFISs \((A_1\) and \(A_2)\) are pre-trained using the standard ANFIS learning algorithm as described in Section 2.1, with 4 and 5 fuzzy rules resulted, respectively. The remaining data of the middle part (also 67 data points, shown in real line) forms the target domain, unlike the two source domains, it will be subsequently divided into two sub-parts with a small portion (20%, 13 data points) for training and the rest 80% (54 data points) for testing.

Following the proposed approach, the fuzzy rules embedded within the two well trained ANFISs \(A_1\) and \(A_2\) are extracted, forming the columns of the rule dictionary, with \(4 + 5 = 9\) rules in total, as shown in Table 4.4. Note that the rule dictionary is the same for either the rule chromosome based method or the ANFIS chromosome based one.

Next, the sparse training data (13 data points) is clustered into \(C\) clusters, \(C = \lfloor (4 + 5)/2 \rfloor = 4\), as determined with respect to Equation (3.5). Details of each cluster are listed in Table 4.5, from which it can be seen that the number of raw data in each
### Table 4.4: Rule dictionary

<table>
<thead>
<tr>
<th>Rule</th>
<th>Source ANFIS</th>
<th>Antecedent ((a_0, a_1, a_2))</th>
<th>Consequent</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>(A_1)</td>
<td>((-12.2, -10.02, -7.83))</td>
<td>14.09(x) + 149.33</td>
</tr>
<tr>
<td>2</td>
<td>(A_1)</td>
<td>((-9.95, -7.82, -5.55))</td>
<td>7.16(x) + 55.41</td>
</tr>
<tr>
<td>3</td>
<td>(A_1)</td>
<td>((-7.79, -5.59, -3.39))</td>
<td>13.83(x) + 72.83</td>
</tr>
<tr>
<td>4</td>
<td>(A_1)</td>
<td>((-5.62, -3.39, -1.2))</td>
<td>10.99(x) + 40.84</td>
</tr>
<tr>
<td>5</td>
<td>(A_2)</td>
<td>((1.75, 3.39, 5.09))</td>
<td>7.16(x) - 27.67</td>
</tr>
<tr>
<td>6</td>
<td>(A_2)</td>
<td>((3.39, 5.05, 6.7))</td>
<td>10.02(x) - 48.99</td>
</tr>
<tr>
<td>7</td>
<td>(A_2)</td>
<td>((5.01, 6.7, 8.33))</td>
<td>6.36(x) - 36.38</td>
</tr>
<tr>
<td>8</td>
<td>(A_2)</td>
<td>((6.71, 8.35, 9.96))</td>
<td>3.30(x) - 31.56</td>
</tr>
<tr>
<td>9</td>
<td>(A_2)</td>
<td>((8.36, 10.01, 11.65))</td>
<td>9.81(x) - 106.53</td>
</tr>
</tbody>
</table>

For each generated individual, a candidate rule is interpolated. As such, there are totally \(4 \times 5 = 20\) interpolated rules (namely, number of clusters times that of individuals in each cluster), which are subsequently used to construct the initial population. For the method using rule based chromosome representation, the initial population contains 4 initial sub-populations, each with 5 chromosomes. For the method with ANFIS based chromosome representation, one candidate rule in each cluster is chosen and used for constructing possible ANFISs. There are 5 different choices in each cluster, so the number of possible ANFISs is \(5^4 = 625\), which is also the size of the initial population. This is a doable number for the current simple illustrative case, however, for more complex problems with tens of clusters, this number will become excessively large and therefore, will require a huge storage space. In order to keep this under control, only a portion of all possible ANFISs are randomly selected as the chromosomes in implementing the initial population.
<table>
<thead>
<tr>
<th>Cluster</th>
<th>Center</th>
<th>Raw data</th>
<th>Number of data points</th>
<th>Generated individuals</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>−2.3</td>
<td>−2.3</td>
<td>1</td>
<td>−2.3, −2.43, −2.18, −2.67, −2.5</td>
</tr>
<tr>
<td>2</td>
<td>−0.62</td>
<td>0.2, −1.1, −0.4, −0.6, −1.2</td>
<td>5</td>
<td>−0.62, −0.75, −0.5, −0.99, −0.82</td>
</tr>
<tr>
<td>3</td>
<td>1.26</td>
<td>1.4, 0.9, 1.5</td>
<td>3</td>
<td>1.26, 1.13, 1.37, 0.89, 1.05</td>
</tr>
<tr>
<td>4</td>
<td>2.52</td>
<td>2.2, 3.2, 2, 2.7</td>
<td>4</td>
<td>2.52, 2.38, 2.63, 2.15, 2.31</td>
</tr>
</tbody>
</table>
Denote the number of possible ANFISs to take as $Q$, then, as stated previously, $Q = 500$ is empirically set in the present experimental studies.

In this illustrative example, the length of the individual rule-based chromosome is $(4m + 1) = 5$ ($m = 1$), while that of the entire ANFIS-based chromosome is $5 \times 4 = 20$ (with 4 rules in each ANFIS). From this setup of the initial population, the crossover and mutation operations are followed. The changes incurred to the number of the chromosome during and after one evolutionary iteration is shown in Table 4.6. Of course, for rule based chromosome representation, this number is counted within one sub-population. Taking the method running on the entire ANFIS-based chromosome representation as an example, the population is initialised as $Q = 500$ chromosomes at the beginning. Then 400 chromosomes are chosen as parents for crossover with a crossover probability $p_c = 0.8$, resulting in 400 children. After crossover, the number of chromosomes becomes $500 + 400 = 900$. Similarly, 100 chromosomes are chosen for mutation with a mutation probability $p_m = 0.2$, resulting in 100 new chromosomes, and the number of chromosomes after mutation becomes $900 + 100 = 1000$. Finally, the evaluation process will select 500 chromosomes out of these 1000 to enter into the next iteration, ensuring that the population size remains the same.

Table 4.6: Number of chromosomes in one (sub-)population during different processes within one evolutionary iteration

<table>
<thead>
<tr>
<th></th>
<th>Initial Population</th>
<th>After Crossover</th>
<th>After Mutation</th>
<th>After Evaluation</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Rule chromosome</strong></td>
<td>5</td>
<td>9</td>
<td>10</td>
<td>5</td>
</tr>
<tr>
<td><strong>ANFIS chromosome</strong></td>
<td>500</td>
<td>900</td>
<td>1000</td>
<td>500</td>
</tr>
</tbody>
</table>

As mentioned previously, the methods for fitness evaluation of the two types of chromosome encoding are different. For the entire ANFIS-based representation, the evaluation is simply done using Equation (4.8) and hence, its illustration is omitted. Only is the evaluation of the individual rule-based chromosomes explained below.

Having produced four sub-populations (each with 10 chromosomes), a score table of size $10 \times 4$ is computed according to Algorithm 4.1. Figure 4.6 presents four instances of computed tables during one iteration. Firstly, the score table is initialised as a zero table of size $10 \times 4$, as illustrated in Table (a) of this figure. Then,
500 ($A_{\text{max}}$) possible ANFISs are randomly generated, with the rules used in these ANFISs recoded. The resulting ANFISs are evaluated using Equation (4.7) and are sorted in descending order according to their RMSEs. In this illustrative example, the first ANFIS (with the largest RMSE) is composed of 4 candidate rules indexed by candidates [3, 10, 6, 4]. That is, the first rule of this ANFIS is the third candidate rule (or chromosome) in cluster 1, the second rule is the tenth candidate in cluster 2, the third rule is the sixth candidate in cluster 3, and the last rule is the forth candidate rule in cluster 4. The value in each of the four corresponding locations (or cells) in the score table is therefore, added by 1, resulting in Table (b) of Figure 4.6. Next, given the ordered indices [1, 7, 6, 10] of the second ANFIS, the values in their corresponding locations are added by 2, leading to Table (c) of Figure 4.6. This process is repeated for all of the 500 ANFISs. Averaging over such 500 tables results in the final score table that consists of the scores or fitness of all candidate rules, as shown in Table (d) of Figure 4.6, where the candidate rule with the largest average score in each cluster is shown in bold. Of course, here, the scores are the averages of how many times a certain candidate rule is utilised by the randomly generated (500) ANFISs.

### 4.4.2.2 Accuracy and runtime performance

The classical 5×5-fold cross validation is applied in the experiments to statistically evaluate the performance of different ANFISs. The mean and standard deviation values of RMSE using different ANFISs are listed in the first half of Table 4.7, while the visual result of one randomly selected fold regarding the first function modelling problem is shown in Figure 4.7.

As can be seen from the results, the ‘Original ANFIS’ gives the worst outcomes (which is not surprising due to data shortage in the target domain). While ‘Method 0’ (proposed in Chapter 3) shows an already significantly improved performance over the ‘Original ANFIS’, the GA-based algorithms produce further enhanced results. Quantitatively, running either ‘Method 1’ or ‘Method 2’ leads to smaller RMSE values with a narrower standard deviation, as shown in Table 4.7. Qualitatively, the shape of the estimated function by either of the proposed methods is much closer to that of the ground truth, as depicted in Figure 4.7.

Comparing the two proposed algorithms themselves, the results demonstrate that ‘Method 1’ (which represents individual rules as chromosomes) performs slightly
4.4. Experimentation and Validation

Figure 4.6: Example for score table computation

better than ‘Method 2’ (which expresses an entire ANFIS as one chromosome), for this function modelling problem. The likely reason for this is that, as the rule based chromosomes are shorter than the ANFIS based ones, there are more opportunities for crossover and mutation operations to take effect under the same probabilistic set up.

Both implementations for the proposed ANFIS interpolation approach are also compared with five conventional machine learning methods: linear regression (LinR), support vector regression (SVR), classification and regression tree (CART), random forest (RF), and an evolutionary ANFIS method (E-ANFIS [111]) in which the genetic algorithm is used to learn the network parameters (without interpolation). The
### Table 4.7: Accuracy (Mean ± Standard deviation) and running time (seconds) of different methods on synthetic data

<table>
<thead>
<tr>
<th>Methods</th>
<th>Function 1</th>
<th>Function 2</th>
<th>Function 3</th>
<th>Run time</th>
</tr>
</thead>
<tbody>
<tr>
<td>Original</td>
<td>0.913 ± 1.184</td>
<td>1.329 ± 1.153</td>
<td>0.468 ± 0.244</td>
<td>0.32 ± 0.21</td>
</tr>
<tr>
<td>ANFIS</td>
<td>0.364 ± 0.406</td>
<td>0.905 ± 0.743</td>
<td>0.351 ± 0.148</td>
<td>0.65 ± 0.26</td>
</tr>
<tr>
<td>Method 0</td>
<td>0.294 ± 0.401</td>
<td>0.691 ± 0.461</td>
<td>0.334 ± 0.147</td>
<td>40.21 ± 27.33</td>
</tr>
<tr>
<td>Method 1</td>
<td>0.317 ± 0.417</td>
<td>0.794 ± 0.552</td>
<td>0.325 ± 0.096</td>
<td>55.42 ± 29.70</td>
</tr>
<tr>
<td>Method 2</td>
<td>0.317 ± 0.441</td>
<td>0.794 ± 0.552</td>
<td>0.325 ± 0.096</td>
<td>55.42 ± 29.70</td>
</tr>
<tr>
<td>LinR</td>
<td>1.243 ± 0.055</td>
<td>0.772 ± 0.022</td>
<td>0.471 ± 0.007</td>
<td>3.04 ± 2.52</td>
</tr>
<tr>
<td>SVR</td>
<td>1.234 ± 0.064</td>
<td>0.789 ± 0.030</td>
<td>0.470 ± 0.007</td>
<td>3.44 ± 2.13</td>
</tr>
<tr>
<td>CART</td>
<td>1.302 ± 0.329</td>
<td>1.394 ± 0.235</td>
<td>0.393 ± 0.037</td>
<td>3.32 ± 1.75</td>
</tr>
<tr>
<td>RF</td>
<td>0.547 ± 0.133</td>
<td>0.805 ± 0.167</td>
<td>0.408 ± 0.024</td>
<td>3.61 ± 0.78</td>
</tr>
<tr>
<td>E-ANFIS</td>
<td>1.552 ± 0.478</td>
<td>0.836 ± 0.048</td>
<td>0.476 ± 0.012</td>
<td>359.21 ± 126.42</td>
</tr>
</tbody>
</table>

evaluation results are listed in the second half of Table 4.7. From the accuracy over the three function modelling case studies, it can be observed that the proposed ANFIS interpolation methods (‘Method 1’ or ‘Method 2’) perform better in terms of mean error values. Although the classical machine learning methods (especially the LinR approach) may give better standard deviation values, their overall accuracy is lower than what is achieved by the proposed methods.

The average running time (also showing in the ‘Mean ± Standard deviation’ form) of different methods over the three function modelling cases is shown in the last column of Table 4.7. Comparing the two proposed methods with other approaches, as can be expected, they run faster than ‘E-ANFIS’ but incur more computation than the rest. However, the considerably improved accuracy they gain over the other approaches justifies this increase in computational cost. Comparing the two proposed methods themselves, it can be seen that the method employing individual rule-based
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Figure 4.7: Visual illustration of one-fold result by different ANFISs

chromosome representation consumes less time, this conforms to the theoretical analysis presented in Section 4.3.

4.4.3 Experiments on real data

A number of investigations are carried out here, looking into the issues regarding accuracy, amount of training data and key GA parameters (namely, crossover and mutation rates).

4.4.3.1 Datasets and experimental environment

Table 4.8 lists the ten popular benchmark real-world regression datasets, taken from the KEEL data repository [5], which are used here to further evaluate the
4.4. Experimentation and Validation

performance of both GA-based ANFIS interpolation algorithms.

Table 4.8: Datasets used in experimental study

<table>
<thead>
<tr>
<th>Dataset</th>
<th>Attribute No.</th>
<th>Instance No.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diabetes</td>
<td>2</td>
<td>43</td>
</tr>
<tr>
<td>Plastic</td>
<td>2</td>
<td>1650</td>
</tr>
<tr>
<td>Quake</td>
<td>3</td>
<td>2178</td>
</tr>
<tr>
<td>Laser</td>
<td>4</td>
<td>993</td>
</tr>
<tr>
<td>AutoMPG6</td>
<td>5</td>
<td>392</td>
</tr>
<tr>
<td>Delta-ail</td>
<td>5</td>
<td>7129</td>
</tr>
<tr>
<td>Friedman</td>
<td>5</td>
<td>1200</td>
</tr>
<tr>
<td>Dee</td>
<td>6</td>
<td>365</td>
</tr>
<tr>
<td>Delta-elv</td>
<td>6</td>
<td>9517</td>
</tr>
<tr>
<td>ANACALT</td>
<td>7</td>
<td>4052</td>
</tr>
</tbody>
</table>

To conduct this set of experimental investigations, the source domains and target domain are created in a similar manner to the synthetic data experiments, by splitting each entire dataset into three parts according to one of the input variables.

4.4.3.2 Accuracy analysis

The 5×5-fold cross validation results over the ten datasets are shown in Table 4.9, with the average RMSE values listed in the last row and the best results indicated in bold. Similar observation can be made from Table 4.9 to those results obtained from the synthetic data experiments. The ‘Original ANFIS’ gives the poorest performance as expected, and the other three interpolated ANFISs improve the inference results obviously. Amongst the three interpolation-based methods, both GA-based implementations outperform ‘Method 0’ for most cases, though there is no clear winner between the two themselves.

The p-values of the pairwise t-test (p = 0.05) over different methods are listed in Table 4.10. In this table, sign (v) (p < 0.05) represents that the improvement is of statistic significance, while sign (*) denotes that the improvement is not significant statistically. From the results, it can be seen that both ‘Method 1’ and ‘Method 2’
### Table 4.9: Experimental results using different ANFISs on real world datasets

<table>
<thead>
<tr>
<th>Datasets</th>
<th>Mean ± Standard deviation of ANFISs</th>
<th>Method 0</th>
<th>Method 1</th>
<th>Method 2</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Original ANFIS</td>
<td>Method 0</td>
<td>Method 1</td>
<td>Method 2</td>
</tr>
<tr>
<td>Diabetes</td>
<td>1.527 ± 0.829</td>
<td>1.058 ± 0.497</td>
<td>0.989 ± 0.359</td>
<td>1.011 ± 0.451</td>
</tr>
<tr>
<td>Plastic</td>
<td>2.003 ± 0.246</td>
<td>1.843 ± 0.105</td>
<td>1.836 ± 0.093</td>
<td>1.828 ± 0.078</td>
</tr>
<tr>
<td>Quake</td>
<td>1.264 ± 0.641</td>
<td>0.542 ± 0.248</td>
<td>0.458 ± 0.175</td>
<td>0.498 ± 0.225</td>
</tr>
<tr>
<td>Laser</td>
<td>12.087 ± 4.739</td>
<td>3.757 ± 2.724</td>
<td>3.476 ± 1.069</td>
<td>3.279 ± 1.262</td>
</tr>
<tr>
<td>AutoMPG6</td>
<td>12.770 ± 1.431</td>
<td>5.120 ± 1.038</td>
<td>4.776 ± 1.015</td>
<td>4.987 ± 0.843</td>
</tr>
<tr>
<td>Delta-ail</td>
<td>3.53 × 10^{-4} ± 1.09 × 10^{-4}</td>
<td>1.78 × 10^{-4} ± 1.06 × 10^{-5}</td>
<td>1.73 × 10^{-4} ± 8.87 × 10^{-6}</td>
<td>1.75 × 10^{-4} ± 9.49 × 10^{-6}</td>
</tr>
<tr>
<td>Friedman</td>
<td>5.177 ± 0.633</td>
<td>3.004 ± 0.409</td>
<td>2.900 ± 0.335</td>
<td>2.930 ± 0.405</td>
</tr>
<tr>
<td>Dee</td>
<td>1.017 ± 0.339</td>
<td>0.870 ± 0.225</td>
<td>0.824 ± 0.188</td>
<td>0.839 ± 0.191</td>
</tr>
<tr>
<td>Delta-elv</td>
<td>0.0034 ± 6.195 × 10^{-4}</td>
<td>0.0020 ± 1.69 × 10^{-4}</td>
<td>0.0018 ± 7.11 × 10^{-5}</td>
<td>0.0018 ± 5.90 × 10^{-5}</td>
</tr>
<tr>
<td>ANACALT</td>
<td>1.209 ± 0.966</td>
<td>0.994 ± 0.768</td>
<td>0.999 ± 0.675</td>
<td>0.986 ± 0.681</td>
</tr>
<tr>
<td>Average</td>
<td>3.706 ± 0.982</td>
<td>1.719 ± 0.601</td>
<td>1.626 ± 0.391</td>
<td>1.635 ± 0.412</td>
</tr>
</tbody>
</table>
provide improvements of statistical significance compared with the original ANFIS model. However, as shown in the last column of Table 4.10, all p values are larger than 0.05, indicating that there is no statistical improvements between the two algorithms with different chromosomes. This can be expected as the experimental results on RMSEs also showed that this is no clear winner between ‘Method 1’ and ‘Method 2’.

<table>
<thead>
<tr>
<th>Dataset</th>
<th>Method 1 v.s. Original ANFIS</th>
<th>Method 2 v.s. Original ANFIS</th>
<th>Method 1 v.s. Method 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diabetes</td>
<td>0.0043 (v)</td>
<td>0.0108 (v)</td>
<td>0.6948 (*)</td>
</tr>
<tr>
<td>Plastic</td>
<td>0.0035 (v)</td>
<td>8.3728e-04 (v)</td>
<td>0.5797 (*)</td>
</tr>
<tr>
<td>Quake</td>
<td>1.36e-06 (v)</td>
<td>2.52e-06 (v)</td>
<td>0.3557 (*)</td>
</tr>
<tr>
<td>Laser</td>
<td>7.96e-10 (v)</td>
<td>9.67e-10 (v)</td>
<td>0.4834 (*)</td>
</tr>
<tr>
<td>AutoMPG6</td>
<td>1.17e-18 (v)</td>
<td>1.46e-18 (v)</td>
<td>0.0558 (*)</td>
</tr>
<tr>
<td>Delta-ail</td>
<td>1.27e-08 (v)</td>
<td>1.73e-08 (v)</td>
<td>0.1894 (*)</td>
</tr>
<tr>
<td>Friedman</td>
<td>9.61e-15 (v)</td>
<td>6.22e-16 (v)</td>
<td>0.4926 (*)</td>
</tr>
<tr>
<td>Dee</td>
<td>0.0046 (v)</td>
<td>0.0033 (v)</td>
<td>0.5649 (*)</td>
</tr>
<tr>
<td>Delta-elv</td>
<td>2.10e-12 (v)</td>
<td>1.52e-12 (v)</td>
<td>0.6828 (*)</td>
</tr>
<tr>
<td>ANACALT</td>
<td>0.0165 (v)</td>
<td>0.0111 (v)</td>
<td>0.1954 (*)</td>
</tr>
</tbody>
</table>

4.4.3.3 Comparison with other machine learning methods

As with the experiments on synthetic data, the proposed approach is also compared with five conventional machine learning methods: LinR, SVR, CART, RF, and E-ANFIS. Different from those earlier experiments (where triangular membership functions and a very simple clustering method were used), to enrich the experimental investigation, Gaussian membership functions and fuzzy c-means clustering are utilised here, in implementing the proposed ANFIS interpolation methods. The results are listed in Table 4.11 with the best highlighted in bold.

The proposed approach outperforms the others in a substantial majority of cases. For the three particular cases (of LinR on the Quake dataset, SVR on Dee, and RF on AutoMPG6) where an existing method shows the best outcome, the accuracy of the proposed approach is close. In particular, the proposed approach with ANFIS based
Table 4.11: Accuracy (Mean ± Standard deviation) of different methods on real data

<table>
<thead>
<tr>
<th>Dataset</th>
<th>LinR</th>
<th>SVR</th>
<th>CART</th>
<th>RF</th>
<th>E-ANFIS</th>
<th>Method 1</th>
<th>Method 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diabetes</td>
<td>0.533 ± 0.100</td>
<td>0.441 ± 0.052</td>
<td>0.779 ± 0.130</td>
<td>0.391 ± 0.052</td>
<td>1.172 ± 1.100</td>
<td><strong>0.362 ± 0.045</strong></td>
<td>0.377 ± 0.050</td>
</tr>
<tr>
<td>Plastic</td>
<td>1.623 ± 0.044</td>
<td>2.285 ± 0.037</td>
<td>2.245 ± 0.128</td>
<td>1.886 ± 0.069</td>
<td>1.865 ± 0.348</td>
<td>1.620 ± 0.046</td>
<td><strong>1.603 ± 0.056</strong></td>
</tr>
<tr>
<td>Quake</td>
<td><strong>0.194 ± 0.006</strong></td>
<td>0.206 ± 0.007</td>
<td>0.243 ± 0.015</td>
<td>0.195 ± 0.008</td>
<td>0.259 ± 0.153</td>
<td>0.198 ± 0.006</td>
<td>0.199 ± 0.007</td>
</tr>
<tr>
<td>Laser</td>
<td>6.934 ± 1.337</td>
<td>15.522 ± 0.435</td>
<td>12.87 ± 2.685</td>
<td>7.680 ± 0.801</td>
<td>5.644 ± 2.636</td>
<td>4.547 ± 1.632</td>
<td><strong>4.030 ± 1.539</strong></td>
</tr>
<tr>
<td>AutoMPG6</td>
<td>3.569 ± 0.685</td>
<td>3.336 ± 0.353</td>
<td>4.044 ± 0.559</td>
<td><strong>3.282 ± 0.331</strong></td>
<td>5.625 ± 1.275</td>
<td>3.628 ± 0.696</td>
<td>3.575 ± 0.572</td>
</tr>
<tr>
<td>Delta-ail</td>
<td>1.55 × 10⁻⁴ ±</td>
<td>1.59 × 10⁻⁴ ±</td>
<td>1.91 ± 10⁻⁴ ±</td>
<td>1.66 ± 10⁻⁴ ±</td>
<td>1.64 ± 10⁻⁴ ±</td>
<td><strong>1.50 × 10⁻⁴ ±</strong></td>
<td>1.51 × 10⁻⁴ ±</td>
</tr>
<tr>
<td></td>
<td>1.48 × 10⁻⁶</td>
<td>1.66 × 10⁻⁶</td>
<td>7.33 × 10⁻⁶</td>
<td>5.13 × 10⁻⁶</td>
<td>3.86 × 10⁻⁵</td>
<td><strong>1.45 × 10⁻⁶</strong></td>
<td>1.46 × 10⁻⁶</td>
</tr>
<tr>
<td>Friedman</td>
<td>2.795 ± 0.049</td>
<td>2.771 ± 0.047</td>
<td>7.224 ± 0.483</td>
<td>2.771 ± 0.156</td>
<td>2.408 ± 1.325</td>
<td>2.041 ± 0.075</td>
<td><strong>2.030 ± 0.052</strong></td>
</tr>
<tr>
<td>Dee</td>
<td>0.424 ± 0.023</td>
<td><strong>0.416 ± 0.021</strong></td>
<td>1.016 ± 0.063</td>
<td>0.482 ± 0.035</td>
<td>0.810 ± 0.366</td>
<td>0.477 ± 0.048</td>
<td>0.486 ± 0.064</td>
</tr>
<tr>
<td>Delta-elv</td>
<td>1.51 × 10⁻³ ±</td>
<td>1.53 ± 10⁻³ ±</td>
<td>1.95 ± 10⁻³ ±</td>
<td>1.51 ± 10⁻³ ±</td>
<td>1.55 ± 10⁻³ ±</td>
<td><strong>1.48 × 10⁻³ ±</strong></td>
<td><strong>1.48 × 10⁻³ ±</strong></td>
</tr>
<tr>
<td></td>
<td>1.17 × 10⁻⁵</td>
<td>1.23 × 10⁻⁵</td>
<td>5.19 × 10⁻⁵</td>
<td>1.26 × 10⁻⁵</td>
<td>1.78 × 10⁻⁴</td>
<td><strong>1.03 × 10⁻⁵</strong></td>
<td><strong>1.09 × 10⁻⁵</strong></td>
</tr>
<tr>
<td>ANACALT</td>
<td>0.405 ± 0.020</td>
<td>0.333 ± 0.021</td>
<td>0.299 ± 0.038</td>
<td>0.292 ± 0.043</td>
<td>0.357 ± 0.100</td>
<td>0.280 ± 0.029</td>
<td><strong>0.279 ± 0.028</strong></td>
</tr>
<tr>
<td>Average</td>
<td>1.648 ± 0.227</td>
<td><strong>2.531 ± 0.097</strong></td>
<td>2.873 ± 0.409</td>
<td>1.698 ± 0.149</td>
<td>1.814 ± 0.811</td>
<td>1.316 ± 0.258</td>
<td><strong>1.258 ± 0.236</strong></td>
</tr>
</tbody>
</table>

4.4. Experimentation and Validation
chromosome representation gives by far, the best mean value of the overall RMSE averaged across the ten datasets, and the proposed with rule based chromosome representation achieves the second best (as shown in the last row of Table 4.11). This superiority in performance remains to be true taking into consideration the standard deviations. Note however, that in terms of the overall averaged standard deviation measure, the classical SVR has the least value, demonstrating its excellent stability.

Table 4.12 shows the running time performance of different methods (given in the ‘Mean ± Standard deviation’ form), in which each line is obtained by averaging the running time over different datasets. It can be observed that the standard deviations of the two proposed methods ('Method 1’ and 'Method 2’) and the 'E-ANFIS' method are relatively larger than that of the rest. The running time of an algorithm on different dataset with different numbers of input variables may vary, and for the ANFIS-based approaches, the running time is more sensitive to the change of the number of input variables. For datasets with more input variables, these algorithms will produce a large rule-base in the resulting ANFIS, and operating on this large rule-base will consume much more time than coping with datasets containing less input variables. This leads to the relatively larger standard deviation of the ANFIS-based methods.

From Table 4.12, similar observations as per those on the synthetic data case studies can be drawn: The proposed methods are faster than E-ANFIS, but slower than the rest, since the evolutionary process incurs more computation. Between the two proposed methods themselves, it is clear that the implementation with ANFIS-based chromosome representation consumes more time. Again, this is expected, reflecting the result of theoretical analysis on computational complexity.

4.4.3.4 Effects of sparsity in training data

This particular experimentation is conducted to investigate the performance of different ANFISs in response to the use of different percentages of training data, instead of just the 20% and 80% split. To focus on the discussion about the performance of varying the amount of training data, only the results on the ‘Quake’ dataset are shown here, as given in Figure 4.8.
Table 4.12: Average running time (seconds) of different methods on real data

<table>
<thead>
<tr>
<th>Methods</th>
<th>Running time</th>
</tr>
</thead>
<tbody>
<tr>
<td>LinR</td>
<td>1.46 ± 0.15</td>
</tr>
<tr>
<td>SVR</td>
<td>13.34 ± 15.57</td>
</tr>
<tr>
<td>CART</td>
<td>2.38 ± 1.85</td>
</tr>
<tr>
<td>RF</td>
<td>3.47 ± 2.5</td>
</tr>
<tr>
<td>E-ANFIS</td>
<td>225.3 ± 171.65</td>
</tr>
<tr>
<td>Method 1</td>
<td>35.15 ± 20.2</td>
</tr>
<tr>
<td>Method 2</td>
<td>64.91 ± 36.55</td>
</tr>
</tbody>
</table>

It can be seen that in general, the RMSE values decrease as the percentage of training data increases, independent of which learning method is used. Importantly, also independent of what percentage of training data is utilised, the three interpolated ANFISs all remarkably outperform the ‘Original ANFIS’ (until training data reaches 90%). Furthermore, the RMSE values of the three interpolated ANFISs generally decline much less rapidly than the RMSE of the ‘Original ANFIS’, indicating that the interpolated ANFISs are less sensitive to the decrease of training data. Indeed, the performances of these three methods using 30% data are very close to those using 90% data. When the available data percentage is 20%, the results are of course the same as discussed in the preceding sub-section, with the three interpolated ANFISs significantly beating the ‘original ANFIS’ and the two GA-based methods outperforming ‘Method 0’. When only 10% of data is available for training, the performances of the interpolated methods degrade but still beat the ‘Original ANFIS’ trained with the conventional method substantially. Most interestingly, even in this case, either of the two proposed methods retains its superior performance over ‘Method 0’, especially when rule based chromosome representation is used. Overall, the proposed ANFIS interpolation algorithms via evolutionary computation achieve a much better result while using less training data than the existing techniques.

4.4.3.5 Effects of crossover and mutation probability

The crossover probability $p_c$ and mutation probability $p_m$ are two important parameters in the evolutionary process. Generally, larger crossover probability and smaller mutation probability are a common choice for most evolutionary problems.
4.5. Summary

In the above-reported experimental investigations, these two parameters are set to $p_c = 0.8, p_a = 0.2$ respectively. In order to examine the effects on performance of using different $p_c$ and $p_m$, these probabilities are varied from 0.1 to 0.9 (with step=0.1) in this experimentation. This part of the experimental studies is focussed on the use of the entire ANFIS based chromosome representation since the number of the individual rule-based chromosome in each sub-population is very small (only 5 in the experiments, so the results of using different $p_c$ and $p_m$ do not differ much in the first place). The resulting box-plot over the ‘Quake’ dataset is shown in Figure 4.9 and Figure 4.10. In conformation with common knowledge in evolutionary computation, the results reveal that larger $p_c$ as well as smaller $p_m$ give a better value for both the median and the interquartile range.

4.5 Summary

This chapter has presented a new ANFIS interpolation approach via evolutionary computation (implemented with GAs), in an effort to improve the learning of ANFIS when there is significant shortage of training data for the problem concerned. The concept of ‘ANFIS interpolation’ means the interpolation of an entire inference system, or a whole group of rules in the target region. This is enabled with the assistance of well-trained ANFISs in the neighbouring regions. Two forms of chromosome
representation are considered: one encoding individual rules and the other expressing an entire possible ANFIS. The proposed approach has been tested on both three function modelling problems with synthetic data and real world regression problems involving 10 benchmark datasets, demonstrating its ability in significantly improving the inference performance when compared with existing techniques.
4.5. Summary

Compared with the ANFIS interpolation approach proposed in Chapter 3 (based on group-based rule interpolation), this evolutionary approach has the following new contributions:

1. Unlike the initial approach which terminates when a group of rules are interpolated, this improved ANFIS interpolation is implemented within the framework of a genetic algorithm which iteratively updates the interpolated rules. This is the fundamental contribution from which the following two innovative technical developments have been made.

2. Two types of chromosome representations are designed to perform the GA process, resulting in two slightly different evolutionary algorithms that have been systemically compared in this chapter.

3. As an ANFIS can be equivalently interpreted as a set of fuzzy rules, the fitness of each single rule based chromosome is very hard to measure. In order to solve this problem, the concept of ‘score table’ has been developed in this chapter, from which the performance of all rule type chromosomes are clearly exhibited.

Further to the above systematic evaluation with benchmark datasets, the proposed approaches are also applied to dealing with the problem of image super resolution. Particularly, Chapter 5 will use full training data to test the performance of the learned ANFIS mappings under the condition where sufficient training data is available.
Chapter 5

Image Super Resolution with Full Training Data via Multiple Learned ANFIS Mappings

In most existing learning based super resolution algorithms, the mappings from low resolution space to its corresponding high resolution space is learned using non-fuzzy techniques [43, 149, 171]. However, image super resolution is a highly ill-posed problem where an observed low resolution (LR) image patch can be generated from any of the many possible high resolution (HR) patches. Therefore, it would be intuitive to introduce imprecision (or fuzzy) techniques to the learning based image super resolution (ISR) tasks. Hither to little work in this direction has been developed [6]. However, an interesting approach has been proposed recently for fuzzy rule based ISR [122] whose basic idea is to develop a set of fuzzy rules describing the required non-linear mappings. These fuzzy rules are learned from the low resolution and high resolution (LR-HR) image pairs of a given training data set, and in this learning process, the most important part is how to decide the rule parameters.

Based on the fact that ANFIS has been proven to be a powerful tool for generating effective fuzzy rules, it would be interesting to investigate its potential to help resolve the image super resolution problem. This chapter introduces the work for an ANFIS to learn its parameters to perform the ISR task with full training data. A new algorithm for single frame image super resolution using multiple learned ANFIS mappings is
developed. In particular, a large number of LR-HR patch pairs from a collection of natural images are generated and used as training data, from which multiple ANFIS mappings from LR space to HR space can be formulated. Those learned ANFIS mappings are tested against a range of natural images and over different scale factors.

The rest of this chapter is organised as follows. Section 5.1 outlines the framework of the proposed ANFIS based image SR approach. Section 5.2 details the proposed approach, performing ISR by an integrated use of the learned ANFIS mappings and a number of pre-processing and post-processing techniques. Experimental results against a number of natural images are shown in Section 5.3, demonstrating the effectiveness of the proposed method. Section 5.4 provides a summary of the reported work in this chapter.

5.1 Framework of Proposed Approach

This section describes the framework of the proposed image super resolution algorithm, which involves two phases: (1) Offline learning, where multiple ANFIS mappings are learned via a large amount of LR-HR image patch pairs. (2) Online application, where the learned multiple ANFIS mappings are used to generate the corresponding HR image from an input LR image.

The flowchart of the proposed algorithm is shown in Figure 5.1. At the learning stage, an external database of LR and HR image pairs is used as the training set. Then each image pair in the training set is divided into small LR-HR patch pairs with a fixed size. Next, the resulting patch pairs are grouped into different clusters using a K-means clustering method, and for each cluster, an ANFIS mapping is learned using the standard ANFIS learning process. When in use (after training), a given input LR image is firstly divided into image patches with the same size as the patches in training stage. For each patch, the most relevant ANFIS mapping is then selected to perform SR, resulting in its corresponding HR patch. By combining all the HR patches, a reconstructed image is obtained. Following this, a non-local means (NLM) filter (which works by exploiting the image’s non-local self similarity) and a iterative back projection (IBP) operator are employed to refine the reconstructed image. This process will be repeated for several times and will finally output the estimated HR image.
5.1. Framework of Proposed Approach
5.2 Implementation of the Proposed Approach

This section presents the implementation details of the framework outlined in Section 5.1. The learning process is introduced in 5.2.1, while the testing process as well as the pre-processing and post-processing techniques utilized in this work are presented in 5.2.2.

5.2.1 Learning of multiple ANFIS mappings

5.2.1.1 Training set generation

At the beginning of the training stage, the training data set, which is a set of image patch pairs of both HR and LR resolutions, is generated. A (prescribed) large number of sharp natural images $\{Y^h\}$ are firstly collected and used to form the training database, including various types of scenes (e.g. people, animals, buildings and plants) with fine textures. Some representative images are shown in Figure 5.2.

![Example images used for training.](image)

Those sharp images are considered as HR images in the training set, and the corresponding LR version $\{X^l\}$ of the HR images $\{Y^h\}$ are simulated by implementing the following steps for each HR image: 1) Down sample the HR image with a scale factor of $s$; 2) Up scale the down sampled images to a certain desired size by bicubic interpolation, so that the LR and the desired HR images are of the same size but the former are of lower resolution (which may mean they contain less information).
5.2. Implementation of the Proposed Approach

Then, the LR-HR image pairs \( \{(X^l, Y^h)\} \) are divided into overlapping patch pairs with a size of \( q \times q \), denoted as \( Q = \{(x^l, y^h)\} \). After vectorization, each patch is a column vector \( x^l \in \mathbb{R}^{q^2} \), \( y^h \in \mathbb{R}^{q^2} \) containing \( q^2 \) pixels (each pixel is denoted by \( x^i \) and \( y^i \) respectively). After that, the LR-HR image patch pairs \( Q \) can be used to train the multiple ANFIS mappings.

5.2.1.2 Multiple ANFISs learning

The above resulting patch pairs \( Q = \{(x^l, y^h)\} \) are subsequently partitioned into \( P \) clusters with centroids \( V \) by the use of conventional K-Means clustering algorithm:

\[
V = \{v^*_p = (v^i_p, v^h_p), p = 1, 2, \cdots, P\}
\] (5.1)

For each cluster, a mapping from the LR image patch to the HR patch is trained over an ANFIS network. The learning procedure is summarised as Algorithm 5.1.

**Algorithm 5.1: Learning multiple ANFIS mappings.**

**Input:**
- A set of sharp HR natural images \( \{Y^h\} \);
- Scale factor \( s \);

**// Training set Generation**

1. for each \( Y^h \) do
2.     Down sample \( Y^h \) with scale factor \( \frac{1}{s} \), resulting in \( Y^i \);
3.     Up sample \( Y^i \) with scale factor \( s \) using bicubic interpolation algorithm, resulting in \( X^i \);
4. end

5. Generate LR-HR image pairs \( \{(X^l, Y^h)\} \);
6. Divide \( \{(X^l, Y^h)\} \) into \( q \times q \) patch pairs \( Q = \{(x^l, y^h)\} \) with overlaps;
7. Vectorize patch pairs to pixel pairs such that \( x^l \in \mathbb{R}^{q^2}, y^h \in \mathbb{R}^{q^2} \);

**// Multiple ANFISs Learning**

8. Partition \( Q \) into \( P \) clusters by K-Means with centroids \( V = \{(v^i_p, v^h_p)\} \);
9. for each cluster do
10.    learn an ANFIS mapping \( \mathcal{A}_p \);
11. end

**Output:**
- Learned multiple ANFIS mappings \( \{\mathcal{A}_p\} \);
- Centroids \( V = \{(v^i_p, v^h_p)\} \).
5.2. Implementation of the Proposed Approach

5.2.2 Image SR with learned ANFIS mappings

In the testing stage, a given new LR image can be reconstructed using the trained ANFIS mappings. This process is implemented with the following three sub-stages: pre-processing, inference with learned mappings and post-processing.

5.2.2.1 Pre-processing

Denote the given testing LR image as \( X \in \mathbb{R}^{m \times n} \), where \( m \) is the image length and \( n \) is the image width, and denote the desired HR image as \( Y \in \mathbb{R}^{M \times N} \), so there exists the relationship that \( M = sm, N = sn \). For training convenience, in the learning stage the LR images of the LR-HR training image pairs are simulated by down sampling then up sampling the HR image, so the resulting LR images are also of big size \( M \times N \). However, the real input LR image is with smaller size \( m \times n \). Therefore, similar with the training stage, the input testing LR image will be pre-processed using pixel based interpolation method before inferencing using the learned ANFIS mappings.

Existing representative pixel based interpolation algorithms include the nearest neighbour interpolation, the linear interpolation, the bilinear interpolation and the bicubic interpolation \([89]\). Amongst them, the bicubic interpolation \([56, 82]\) is the most commonly used one that increases the image pixels by interpolating existing ones using bicubic basic functions, so is employed in the proposed work.

5.2.2.2 Inference with learned ANFIS mappings

After pre-processing, the resulting large size image (also denoted by \( X \) here) will be subsequently enhanced using the learned ANFIS mappings obtained from the learning stage. More specifically, the large size image \( X \) is firstly divided into image patches of size \( q \times q \) with overlaps. Here, the patch size \( q \) is the same as that used during the training process, and the image patches \( x \in \mathbb{R}^{q \times q} \) are also vectorized for computation convenience. Then, for every vectorized image patch \( x \in \mathbb{R}^{q^2} \), an appropriate ANFIS mapping is selected subject to the following constraint:

\[
p = \min_p \| x - v_p^j \|_2^2
\]  \hspace{1cm} (5.2)
where $v^l_p$ is the first part of the centroid $v^c$ in Equation (5.1). And the $p$th ANFIS mapping $\mathcal{A}_p$ is selected to estimate the corresponding HR image patch. For each image patch $x$, the basic idea for inferencing can be expressed by:

$$\text{If } x \text{ is close to } v^l_p \text{ then } y = \mathcal{A}_p(x).$$

(5.3)

where $y \in \mathbb{R}^{q^2}$ is the corresponding HR patch. The behaviour of the function $\mathcal{A}_p(.)$ is inference using the $p$th ANFIS mapping from input LR patch to HR patch. Now, as the LR patch is $q^2$-dimensional ($x$ is a vector with $q^2$ pixels), the antecedent part of Equation (5.3) can be viewed as a conjunction of $q^2$ atomic clauses:

$$\text{If } x \text{ is close to } v^l_p \approx \begin{cases} 
\text{If } x^1 \text{ is close to } v^l_{p1} \\
\text{If } x^2 \text{ is close to } v^l_{p2} \\
\cdots \\
\text{If } x^{q^2} \text{ is close to } v^l_{pq^2}
\end{cases}$$

(5.4)

Similarly, the consequent part of Equation (5.3) can be rewrite as:

$$\begin{align*}
y^1 &= \mathcal{A}_p(x^1) \\
y^2 &= \mathcal{A}_p(x^2) \\
\cdots \\
y^{q^2} &= \mathcal{A}_p(x^{q^2})
\end{align*}$$

(5.5)

where $y^i$ denotes arbitrary pixel in patch $y$. Each $\mathcal{A}_p(x^i)$ is expressed by:

$$\mathcal{A}_p(x^i) = \sum_{j=1}^{C} w_j \cdot y^i_j, \quad p = 1, 2, \cdots, P, \quad i = 1, 2, \cdots, q^2.$$  

(5.6)

where $C$ stands for the number of rules in an ANFIS. Each ANFIS mapping $\mathcal{A}_p(x^i)$ is composed of a set of linear rules, with the following format: If $x^i$ (the input pixel) is $A_j$, then $y^i_j = p_j x + r_j$. As with the work of [122], the Gaussian function defined as Equation (2.3) is herein chosen as the membership function to describe $A_j$ and to obtain the firing strength of the fuzzy rules in each ANFIS network under training. By combining all the estimated HR image patches, a potential HR image results.
5.2. Implementation of the Proposed Approach

5.2.2.3 Post-processing

Two post-processing techniques are employed in the testing stage, including a non-local means filter that aims to suppress the artefacts and noise caused in the inference process, and a iterative back projection algorithm that ensuring the fidelity of the obtained HR image with the LR image.

A. Non-Local Means (NLM)

To smooth the combination process, the NLM filter is used to suppress undesirable artefacts, as well as to reduce the noise in the ANFIS-constructed HR image. The non-local means algorithm is first developed in [17] for the purpose of image denoising. Generally, the denoised pixel $y_i$ is updated as the weighted average of the similar pixels $\{y_j\}$ whose neighbourhoods are similar to its neighbourhood. The denoising process can be expressed as follows:

$$y_i = \sum_{j \in S} w_{ij} y_j$$  \hspace{1cm} (5.7)

where $S$ denotes a certain searching window centred at $y_i$, the weight $w_{ij}$ is defined as follows:

$$w_{ij} = \frac{1}{Z} \exp\left(-\frac{\|p_i - p_j\|^2_{2,a}}{a^2 h^2}\right)$$  \hspace{1cm} (5.8)

where $p_i$ and $p_j$ are two image patches centred at $y_i$ and $y_j$ respectively. Such design of the weight relies on the similar degree between $p_i$ and $p_j$, larger similar degree will lead to larger weight. $a > 0$ denotes the standard deviation of the Gaussian kernel function, and the parameter $h$ controls the decay of the exponential function. $Z$ is a normalisation constant defined as:

$$Z = \sum_j \exp\left(-\frac{\|p_i - p_j\|^2_{2,a}}{a^2 h^2}\right)$$  \hspace{1cm} (5.9)

The underlying idea of NLM can be illustrated as shown in Figure 5.3. In the simple example shown in this figure, the central pixel of patch $p_i$ is updated as the weighted average of itself and its similar pixels. Here, ‘similar pixels’ are identified as the central pixels of patches $p_{j1}, p_{j2}$ and $p_{j3}$. As can be observed in the figure, patches $p_{j1}$ and $p_{j2}$ are very similar with patch $p_i$, so are assigned with larger weights ($w_1$ and $w_2$), while patch $p_{j3}$ which is rather different to $p_i$ is assigned with a small weight ($w_3$).
5.3. Experimentation and Validation

B. Iterative Back Projection (IBP)

Finally, the iterative back projection method [62] is employed to ensure the fidelity with the LR image, contributing to the reduction of the reconstruction error. The IBP is implemented as the following iterative equation:

\[ Y^{t+1} = Y^t + \lambda \ast I(X - D(Y^t)) \]  \hspace{1cm} (5.10)

where \( t \in 0, 1, \cdots, T \), \( T \) is the maximum number of iterations. \( Y^0 \) is initialized as \( Y^0 = Y \). \( \lambda \) is the step size, \( I(\cdot) \) and \( D(\cdot) \) are interpolation operator and down sample operator, respectively.

By iteratively implementing the inference and post-processing sub-stages described above, the final output HR image is obtained. The steps of the proposed testing stage can be summarised as given in Algorithm 5.2.

5.3 Experimentation and Validation

To verify the effectiveness of the proposed approach, experimental comparative studies are carried out and the results are analysed both qualitatively and quantitatively.
Algorithm 5.2: Image super resolution via multiple ANFIS mappings.

**Input:**
- Low resolution image $X$;
- Scale factor $s$;
- Learned ANFIS mappings $\{A_p\}$;
- Centroids $V = \{(v_l^p, v_h^p)\}$.

// Pre-processing
1. Do Bicubic interpolation for $X$;
2. repeat
   // Inference with learned ANFIS mappings
3. Divide $X$ into $q \times q$ patches $\{x\}$ with overlaps;
4. for each patch $x$ in $X$ do
5.    Select an ANFIS mapping $A_p$ with minimum cost using Equation (5.2);
6.    Estimate corresponding HR patch $y = A_p(x)$;
end
7. Integrate $\{y\}$ to get $Y$;
// Post-processing
8. Apply NLM method, for every pixel $y_i$ in $Y$: $y_i = \sum_{j \in S} w_{ij} y_j$;
9. Apply iterative back projection: $Y^{t+1} = Y^t + \lambda \cdot I(X - D(Y^t))$;
10. $X \leftarrow Y$;
11. until maximum iteration reached;

**Output:**
Estimated high resolution image $\hat{Y}$.

5.3.1 Experimental setup

In this experiment-based investigation, 6 typical natural images each with a size of $256 \times 256$ are used as the original HR images (ground truth), and the corresponding testing LR images are simulated by down-sampled HR ones using a scale factor of 2 and 3. Parameters in the implemented system are empirically set as follows: the image patch size $q = 9$; the number of clusters $P = 6$, which is also the number of the ANFIS mappings; the number of fuzzy rules in each ANFIS is set to $C = 9$; and in the training of ANFIS, 10,000 data samples (image patch pairs) are used. All the experiments are performed on a laptop with an Intel Core i7-6700 CPU @ 2.6 GHz and 16GB RAM, using MATLAB R2015a.

The performance of the proposed approach is compared with the bicubic interpolation [56], the standard fuzzy rule based method [122], and the popular sparse
representation method [150]. The results of only using the ANFIS mappings without post-processing are also provided. For the colour images used, they are firstly converted into the YCbCr space from the original GRB space, and since the human eyes are more sensitive to the intensity channel (Y), the proposed approach is only applied on the intensity channel.

5.3.2 Evaluation index

To quantitatively access the performance of the proposed work, the Peak Signal-to-Noise Ratio (PSNR) and the Structure SIMilarity (SSIM) indexes are computed. PSNR assesses the reconstruction performance through calculating the Euclidean distance between the original HR image $Y$ and the estimated HR image $\hat{Y}$, in which the Mean Square Error (MSE) between them is firstly calculated:

$$MSE = \frac{\|Y - \hat{Y}\|^2}{MN}$$

$$PSNR = 10 \log_{10} \left( \frac{255^2}{MSE} \right)$$

where $M, N$ are the image length and width respectively, and $\| \cdot \|_F$ stands for the Frobenius norm of matrix. SSIM reflects the degree of structural similarity between the original and the estimated HR image, which is defined by

$$SSIM = \frac{4\mu_Y\mu_{\hat{Y}}\sigma_{Y\hat{Y}}}{(\mu_Y^2 + \mu_{\hat{Y}}^2)(\sigma_Y^2 + \sigma_{\hat{Y}}^2)}$$

where $\mu_Y$ and $\mu_{\hat{Y}}$ are the mean value of the original and that of the estimated HR image, respectively; $\sigma_Y$ and $\sigma_{\hat{Y}}$ are their respective standard deviations; and $\sigma_{Y\hat{Y}}$ is the co-variation of $Y$ and $\hat{Y}$. A larger PSNR means a better result with the best being $+\infty$, while the range of the SSIM index is $[0, 1]$ with its best being 1.

5.3.3 Results and discussion

Visual comparisons on the use of different algorithms are shown in Figure 5.4 ($s = 2$) and Figure 5.5 ($s = 3$), in which the detailed image of a small random patch is provided in the second row of each. Qualitatively, these results show that the system implementing the proposed approach produces images with less artefacts and sharper
Figure 5.4: Visual comparison of results from different methods on image 'Butterfly' with scale factor being 2 – From left to right: (a) HR image. (b) Bicubic. (c) Fuzzy Rule. (d) Sparse Representation. (e) ANFIS. (f) ANFIS & Post-processing.
Figure 5.5: Visual comparison of results from different methods on image ‘Child’ with scale factor being 3 – From left to right:
(a) HR image. (b) Bicubic. (c) Fuzzy Rule. (d) Sparse Representation. (e) ANFIS. (f) ANFIS & Post-processing.
### Table 5.1: SR results of different algorithms with scale factor = 2

<table>
<thead>
<tr>
<th>Image</th>
<th>Index</th>
<th>Algorithm</th>
<th></th>
<th></th>
<th></th>
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<tr>
<td></td>
<td></td>
<td>Bicubic</td>
<td>Fuzzy Rule [122]</td>
<td>Sparse [150]</td>
<td>ANFIS</td>
<td>ANFIS &amp; NLM</td>
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<td>Lena</td>
<td>PSNR</td>
<td>32.79</td>
<td>34.13</td>
<td>35.04</td>
<td>33.92</td>
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<td></td>
<td>SSIM</td>
<td>0.901</td>
<td>0.911</td>
<td>0.930</td>
<td>0.920</td>
<td>0.932</td>
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<tr>
<td>Child</td>
<td>PSNR</td>
<td>33.96</td>
<td>35.44</td>
<td><strong>36.36</strong></td>
<td>35.56</td>
<td>36.24</td>
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<tr>
<td></td>
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<td>0.937</td>
<td>0.951</td>
<td>0.948</td>
<td><strong>0.953</strong></td>
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<td>Girl</td>
<td>PSNR</td>
<td>33.87</td>
<td><strong>35.37</strong></td>
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<td>Butterfly</td>
<td>PSNR</td>
<td>27.46</td>
<td>30.36</td>
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<td></td>
<td>SSIM</td>
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<td>Hat</td>
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<td></td>
<td>SSIM</td>
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<td>0.898</td>
<td>0.921</td>
<td>0.907</td>
<td><strong>0.922</strong></td>
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<tr>
<td>House</td>
<td>PSNR</td>
<td>32.10</td>
<td><strong>34.65</strong></td>
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<td>32.78</td>
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<td></td>
<td>SSIM</td>
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<td><strong>0.910</strong></td>
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<tr>
<td>Average</td>
<td>PSNR</td>
<td>31.99±2.39</td>
<td>33.85±1.91</td>
<td>34.17±1.77</td>
<td>33.15±2.27</td>
<td><strong>34.27±1.69</strong></td>
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<td></td>
<td>SSIM</td>
<td><strong>0.908±0.0183</strong></td>
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<td>0.924±0.0186</td>
<td><strong>0.937±0.0185</strong></td>
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Table 5.2: SR results of different algorithms with scale factor = 3

<table>
<thead>
<tr>
<th>Image</th>
<th>Index</th>
<th>Algorithm</th>
<th>Bicubic</th>
<th>Fuzzy Rule [122]</th>
<th>Sparse [150]</th>
<th>ANFIS</th>
<th>ANFIS &amp; NLM</th>
</tr>
</thead>
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<tr>
<td>Lena</td>
<td>PSNR(dB)</td>
<td>30.10</td>
<td>31.50</td>
<td>31.05</td>
<td>30.76</td>
<td>31.33</td>
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<td></td>
<td>SSIM</td>
<td>0.827</td>
<td>0.856</td>
<td>0.851</td>
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<td>0.859</td>
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<td>Child</td>
<td>PSNR(dB)</td>
<td>30.11</td>
<td>31.41</td>
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<td>31.08</td>
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<td>SSIM</td>
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<td>0.869</td>
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<tr>
<td>Girl</td>
<td>PSNR(dB)</td>
<td>32.57</td>
<td>33.27</td>
<td>33.31</td>
<td>33.23</td>
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<td>33.52</td>
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<tr>
<td></td>
<td>SSIM</td>
<td>0.877</td>
<td>0.888</td>
<td>0.895</td>
<td>0.893</td>
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<td>0.900</td>
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<tr>
<td>Butterfly</td>
<td>PSNR(dB)</td>
<td>24.05</td>
<td>26.41</td>
<td>25.44</td>
<td>25.04</td>
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<td>27.07</td>
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<td></td>
<td>SSIM</td>
<td>0.808</td>
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<td>0.889</td>
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<td>Hat</td>
<td>PSNR(dB)</td>
<td>29.20</td>
<td>30.62</td>
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<td>0.844</td>
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<td>0.854</td>
</tr>
<tr>
<td>House</td>
<td>PSNR(dB)</td>
<td>29.54</td>
<td>32.36</td>
<td>30.30</td>
<td>30.05</td>
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<td>30.96</td>
</tr>
<tr>
<td></td>
<td>SSIM</td>
<td>0.835</td>
<td>0.859</td>
<td>0.848</td>
<td>0.839</td>
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<td>0.860</td>
</tr>
<tr>
<td>Average</td>
<td>PSNR(dB)</td>
<td>29.26±2.81</td>
<td>30.93±2.39</td>
<td>30.25±2.62</td>
<td>29.99±2.71</td>
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<tr>
<td></td>
<td>SSIM</td>
<td>0.832±0.0248</td>
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<td>0.857±0.0219</td>
<td>0.848±0.0267</td>
<td></td>
<td>0.873±0.0185</td>
</tr>
</tbody>
</table>
5.3. Experimentation and Validation

details, especially around content boundaries (such as those on the hat brims and eyebrow). The reconstructed images by the proposed approach (in Figure 5.4(f) and Figure 5.5(f)) appear to be closer to the original HR ones (in Figure 5.4(a) and Figure 5.5(a)). The results also illustrate that those resulting images using only multiple ANFIS mappings without post-processing contain irregular artefacts and have block effects, decreasing the visual quality. The joint use of the multiple ANFIS mappings and the post-processing algorithms can effectively suppress or even eliminate such displeasing artefacts, generating HR images with better visual effects.

The results of quantitative comparisons with scale factors 2 and 3 are given in Table 5.1 and Table 5.2 respectively. Best results, corresponding to the maximum values in each line, are listed in bold. It can be observed that the system implementing the proposed approach outperforms the rest in all but two or three cases. Furthermore, the mean value and standard deviation of the PSNR and SSIM indices show the robustness of the proposed system. Additionally, the quantitative comparisons once again illustrate that using multiple ANFIS mappings alone may lead to the reconstructed images containing irregular artefacts and block effects. The integrated use of both multiple ANFIS mappings and post-processing techniques can effectively suppress or in certain cases, eliminate the displeasing artefacts.

It is known that for images, especially structured images with rich details, adopting one single and universal learned mapping for SR is impossible [171]. The above experimental comparisons demonstrate that through K-Means clustering and learning relevant mapping on each cluster, the proposed approach is able to exploit the advantage of selecting the most appropriate mapping with respect to different image patches and hence, to reduce the possibility of introducing addition noise. This strategy improves the system’s representation capability over different types of region, thereby contributing to the increase in reconstruction accuracy.

The number of clusters (denoted by $P$) is an important parameter in the K-means clustering algorithm, which is set to be $P = 6$ empirically in the above experimentation. In order to investigate how the algorithm may behave when the value of $P$ varies, experiments with different $P$ values (from 3 to 9) are conducted here. The performance (PSNR) and training time are shown in Figure 5.6 and Figure 5.7 respectively. It can be seen from the curve of Figure 5.6 that the PSNR values do not vary much when different numbers of clusters ($P$) are used (although the PSNR value when $P = 6$ is slightly better), showing the robustness of the proposed
algorithm. From Figure 5.7 it can be observed that the algorithm costs the longest training time when $P = 3$. This is because it takes longer to train an ANFIS model with more training data than to do so with less training data. Thus, despite the number of clusters is small, it is more time consuming. At the beginning, the training time reduces as the number of clusters increases. However, when this number increases to a certain point ($P = 6$), the algorithm will involve the training of many models, but consumes as much time as training a few models with a large amount of data. As such, after that point the training time changes slowly. Therefore, by trading off the reconstruction accuracy and the computational cost, the number of clusters is set to be $P = 6$ in this work.

![Figure 5.6: PSNR index of using different P (number of clusters in K-means algorithm) on Lena image with scale factor being 2.](image)

5.4 Summary

In this chapter, a single frame image super resolution approach using ANFIS has been proposed, with sufficient training data provided. It works by employing multiple ANFIS networks that learn the mappings between the LR patches and the HR patches. Different ANFIS mappings are learned from an external database of a large number of LR and HR image patch pairs. For each patch of a new input LR image, the
Figure 5.7: Training time of using different $P$ (number of clusters in K-means algorithm).

most relevant trained ANFIS is selected to perform super resolution. The non-local means filter as well as the iterative back projection algorithm are used to refine the resulting image. Comparative experimental results presented have demonstrated the effectiveness of the proposed approach.

Having shown the effectiveness of the learned ANFIS mappings in dealing with the problem of image super resolution with full training data, the next chapter will evaluate the performance of the interpolated ANFIS mappings, when solving the hyperspectral image super resolution task with sparse training data.
Chapter 6

Hyperspectral Image Super Resolution with Sparse Training Data via ANFIS Interpolation

The proposed ANFIS interpolation approaches have been proven to be successful in dealing with regression tasks over benchmark datasets with insufficient training data, as reported in Chapters 3 and 4. This current chapter presents a systematic application of the proposed ANFIS interpolation techniques for the problem of hyperspectral image super resolution.

Hyperspectral image is wildly used in real world applications, such as terrain detection [32, 45], military surveillance [46] and medical diagnosis [102], owing to its multi-spectral property. The super resolution of hyperspectral images is also very important for providing high quality images for those special applications. As mentioned previously (in Section 2.3.2), the learning based SR methods require an extra training dataset with large number of training images to learn an effective model. However, the special imaging mechanism makes the acquire of sufficient hyperspectral images for training a very difficult task in certain applications. This practical training data shortage problem makes the hyperspectral image super resolution a more difficult task compared with natural image super resolution. In order to deal with this challenging problem, in this chapter, a new hyperspectral image super resolution approach with sparse training data is developed by introducing the proposed ANFIS interpolation techniques.
The rest of this chapter is organised as follows. For academic completeness, Section 6.1 presents a brief introduction to hyperspectral image and an overview of hyperspectral image super resolution methods. Section 6.2 details the proposed ANFIS Interpolation based hyperspectral ISR approach, along with its training and testing phases. Experimental investigation is reported and discussed in Section 6.3, including the experimental setup, performance criteria and the experimental results. Section 6.4 concludes the chapter.

6.1 Hyperspectral Image Super Resolution

In this section, the background knowledge related to the work in this chapter is presented. The concept of hyperspectral image is introduced firstly, then existing typical hyperspectral image super resolution methods are reviewed.

6.1.1 Hyperspectral image (HSI)

Hyper-Spectral Image (HSI) is defined as an image cube with a number of image channels (or image bands). Different with traditional single-channel black-and-white image or three-channel RGB color image, an HSI usually contains dozens or even hundreds of spectral bands (as shown in Figure 6.1). Another equivalent interpretation of HSI is "the hyperspectral imaging sensor acquires a spectral vector with dozens or hundreds of elements from every pixel in a given scene, the result is the so called hyperspectral image" [15].

For a given HSI $X \in R^{M \times N \times L}$, different forms of representation can be used:

- **Spectral representation**: each image pixel in an HSI $X$ can be represented as a vector with $L$ elements: $x \in R^L$, and there are totally $M \times N$ pixels.

- **Spatial representation**: each image band (or channel) is a two dimensional image matrix $X_j \in R^{M \times N}$, with $L$ image bands in total.

Both of these two types of representation are commonly used in processing an HSI, and when processing a single image band (or pixel), the neighbouring bands
6.1. Hyperspectral Image Super Resolution

Figure 6.1: Hyperspectral Image (HSI).

(or pixels) are usually taken into consideration due to the high correlation among neighbouring bands (or pixels).

Different from the traditional three-channel colour images that can be obtained easily using optical cameras, the acquire of hyperspectral images is more complex. HSIs are usually obtained through the use of special imaging equipments such as hyperspectral cameras, which acquires each image band within a certain spectral response interval, such that different image bands in an HSI are acquired with different spectral responses. This special imaging mechanism makes different image bands within the same HSI may show different information, which is very useful in special real world applications. For example, Figure 6.2 shows three band images (band 10, band 100 and band 200) of a terrain HSI named 'cuprite', from which it can be seen that the band images reflect different image details. In band 10, the bottom-left part of the image is almost black, but some textures can be observed in band 100 while in band 200 the image textures are much clearer. These different information provided by different bands will be helpful for the subsequent terrain detection tasks.

6.1.2 HSI super resolution (HSI SR)

Since the wide use of high quality HSIs, the super resolution of HSI is becoming one of the most popular topics in the recent years. Due to the special property of HSI as mentioned above, the HSI super resolution is more complex than the traditional black-and-white images or the RGB ones. Generally, hyperspectral image super
6.1. Hyperspectral Image Super Resolution

Figure 6.2: Band images of an HSI

(a) Band 10

(b) Band 100

(c) Band 200
6.1. Hyperspectral Image Super Resolution

resolution (HSI SR) \([3]\) refers to the techniques that enlarge each band of an given low resolution HSI (LR HSI) to get a high resolution HSI (HR HSI) with HR images in every bands.

The HSI SR approaches in the existing literatures can be approximately classified into three categories: multi-frame HSI SR, single-frame HSI SR, and the fusion-based HSI SR algorithms. In multi-frame HSI SR approaches, multiple low resolution hyperspectral observations from the same scene are detected, geometrically registered and combined to generate one image of high spatial resolution. These multiple observations of the same scene can be obtained from overlapping flight lines, multi-angle data \([21]\), or multiple instances of different time \([170]\). Similar with the traditional multi-frame image SR technique which is introduced previously in Section 2.3, multi-frame HSI SR approaches need sub-pixel level registration for every band, which is much more time consuming than that of the traditional images. Fusion-based approaches fuses the LR HSI with other available image sources of high spatial resolution, acquired by other sensors (e.g. multi-spectral image sensors or panchromatic image sensors mounted on satellites). A large majority of fusion-based methods injects the high spatial information of the panchromatic image into the hyperspectral image bands \([100]\), which is also called HSI pan-sharpening. Another branch of fusion-based approaches is to adopt spatial-spectral fusion between the LR hyperspectral image and an HR multispectral image that can deliver the required spectral information \([151, 160, 174]\).

According to the two forms of HSI representation mentioned in Section 6.1.1, there are generally three classes of approaches in single-frame HSI SR category. 1) Spatial based approaches \([119, 123, 162]\): These approaches use the spatial representation of an HSI in which the given LR HSI is considered as \(L\) LR band images. Those LR band images are then enlarged either independently or collaboratively. 2) Spectral based approaches \([109, 110]\): The spectral based approaches also termed as 'hyperspectral unmixing'. In these approaches, the given LR HSI is decomposed into a number of pixels according to the spectral representation of an HSI. Each pixel is assumed as a linear mixture of several pure image pixels \([61]\). Therefore, through the use of the spectral unmixing techniques \([49, 81]\), the number of pixels of an HSI will be increased such that the image is enlarged. Both of these two kinds of approaches have their advantages and disadvantages. For instance, the spatial based approaches don ot take the spectral information into consideration,
while on the contract, the spectral based approaches also do not consider the spatial correlation among pixels. 3) Spatial-Spectral based approaches [57, 176]: In order to overcome these disadvantages in the spatial or spectral based methods, the third class of HSI SR approaches is proposed, by combining both the spatial and the spectral approaches. These approaches always iteratively conduct the spatial regulation step and the spectral regulation step, in an effort to maintain both the spatial and spectral information.

Current HSI HR approaches usually assume that there exit sufficient training HSIs. However, different from the natural images that usually can be obtained very easily in the daily life by using optical cameras, the hyperspectral images are obtained using special imaging equipments that leads to the process of getting an image very time consuming. Also, usually hyperspectral cameras are carried on special machines such as satellite, aircraft or medical device, resulting in that the acquirement of images are often effected by the weather, noise or other random factors. All these reasons make the acquire of sufficient hyperspectral images a very difficult task. Therefore the proposed ANFIS interpolation method is used in this chapter to perform HSI SR task under sparse training data situations. In this chapter, the spatial based single frame super resolution strategy is employed in the proposed work.

6.2 HSI SR with Sparse Data through ANFIS Interpolation

In this section the proposed approach for HSI SR is described in detail. The whole process is divided into two stages: the training stage and the testing stage. In the training stage, as the same with the image SR with full training data described in Chapter 5, the whole training set are grouped into a small number of sub-sets. Among these subsets, some are with full training data while some are with sparse data. An individual ANFIS mapping is then learned for each subset with full data, while for those with sparse data, the corresponding ANFIS mapping is constructed using the ANFIS interpolation method. In the testing stage, the estimated HR image is obtained by inferencing using these learned or interpolated ANFIS mappings.
6.2. HSI SR with Sparse Data through ANFIS Interpolation

6.2.1 Training stage

The proposed training process is shown in Figure 6.3, and the outline of the training process is shown in Algorithm 6.1.

![Flowchart of the training process](image)

Figure 6.3: Flowchart of the training process
6.2. HSI SR with Sparse Data through ANFIS Interpolation

Algorithm 6.1: Training stage for HSI SR with sparse data.

**Input:**
Training HSI dataset: \( \{X^l, Y^h\} \);
Scale factor: \( s \);
Interpolation method mode: \( \text{Method} \);

1. \( S = \emptyset \);
2. Divide training dataset into \( P \) sub-sets \( \{ P_i; i = 1, 2, \cdots, P \} \) with centroids \( \{ V_i; i = 1, 2, \cdots, P \} \);
3. \( \text{for } i = 1 \text{ to } i = P \text{ do} \)
   4. \( \text{if } P_i \text{ contains sufficient data} \)
      5. \( \text{Train ANFIS } \mathcal{A}_i \text{ with standard training method;} \)
      6. \( \text{else} \)
      7. \( S \leftarrow \{ S, i \}; \)
   8. \( \text{end} \)
9. \( \text{end} \)
10. \( \text{for each } i \in S \text{ do} \)
    11. \( \text{Choose 2 closest ANFISs } \mathcal{A}_{i1} \text{ and } \mathcal{A}_{i2} \text{ as source ANFISs;} \)
    12. \( \text{Generate rule dictionary } D \text{ by extracting rules from } \mathcal{A}_{i1} \text{ and } \mathcal{A}_{i2}; \)
    13. \( \text{switch } \text{Method} \text{ do} \)
        14. \( \text{case } 0 \text{ do} \)
            15. \( \text{Interpolate ANFIS } \mathcal{A}_i \text{ using 'Method 0';} \)
        16. \( \text{case } 1 \text{ do} \)
            17. \( \text{Interpolate ANFIS } \mathcal{A}_i \text{ using 'Method 1';} \)
        18. \( \text{case } 2 \text{ do} \)
            19. \( \text{Interpolate ANFIS } \mathcal{A}_i \text{ using 'Method 2';} \)
    20. \( \text{end} \)
21. \( \text{end} \)

**Output:**
Multiple learned ANFIS mappings \( \{ \mathcal{A}_i \} \);
Centroids \( \{ V_i \} \).

6.2.1.1 Training dataset generation

The training dataset consists of a number of low resolution and high resolution hyperspectral image pairs \( \{X^l, Y^h\}\), with a scale factor \( s \). Here each \( X^l \in \mathbb{R}^{m \times n \times L} \), each \( Y^h \in \mathbb{R}^{M \times N \times L} \), the length of LR-HSI \( X^l \) and that of HR-HSI \( Y^h \) have the relationship \( M = sm \), and similarly the relation between the width of \( X^l \) and that of \( Y^h \) is \( N = sn \). The training dataset can be generated as the following steps: 1) A number of high quality HR HSIs are collected, forming the \( \{ Y^h \} \); 2) For each \( Y^h \), its corresponding low resolution image pair \( X^l \) is constructed as follows: every band of \( Y^h \) (denoted as \( Y_j^h, j = 1, \ldots, L \)) is firstly down sampled with the scale factor \( s \), and then up sampled
using the bicubic interpolation method; 3) Combine all the image pairs to form the training dataset.

**6.2.1.2 Train ANFIS mappings for source domains**

In the training stage, the previously generated training dataset is firstly divided into several subsets according to the different characteristics of band images. However, the number of training samples between different subsets can be rather imbalanced. That is, for certain subsets there may be sufficient training samples available whilst for others there may not. For those with sufficient training samples, it is easy to learn effective ANFIS mappings. Yet, for those without sufficient samples, it can be rather difficult to derive quality models. Denote the subsets with full training data as source domains, the subsets with sparse training data as target domains. The proposed approach adopts different strategies for source domains and target domains. In source domains, the ANFIS mappings are directly trained. While in target domains, the relevant mappings are interpolated by the support of two source ANFIS mappings in source domains.

Suppose that the given training dataset is divided into $P$ subsets $\{P_i\}$, and the index set of the subsets with sparse training data is denoted by $S$. For the subsets with sufficient training data (i.e. $\{P_i; i \notin S\}$), the learning of ANFIS mappings adopts the standard ANFIS learning method which is described in Chapter 5, so is omitted here.

**6.2.1.3 Interpolate ANFIS mappings for target domains**

For those subsets with sparse data, the interpolation procedure of ANFIS mappings is described in detail as follows. For an arbitrary subset with sparse data $P_i, i \in S$, two closest ANFISs is selected firstly as source ANFISs according to the distances $d_j$ between the center of the sparse training data $V_i, i \in S$ and the center of the subsets with full training data $V_j, j \notin S$. The distance $d_j$ is calculated as:

$$d_j = \sqrt{(V_i - V_j)^2}$$  \hspace{1cm} (6.1)

where the ANFISs related to the two subsets with the smallest distances $d_j$ are chosen as the two source ANFISs, denoted as $\mathcal{A}_{i1}$ and $\mathcal{A}_{i2}$. With the two source ANFISs,
and the sparse training data in \( P_i \), the ANFIS mapping \( \mathcal{A}_i \) can be interpolated using the proposed ANFIS interpolation method.

**Rule dictionary generation**

According to the proposed ANFIS interpolation method, the first step is to generate a rule dictionary, which is used to store the extracted fuzzy rules from the source ANFISs \( \mathcal{A}_{1i} \) and \( \mathcal{A}_{2i} \). For the present application of HSI SR, assuming that the \( i \)th rule can be expressed in the following format:

\[
R_i : \text{if } x \text{ is } A_{ii}, \text{ then } y_i = p_i x + r_i
\]  

(6.2)

where \( x \) denotes an input pixel from an arbitrary band of the LR HSI, \( A_{ii} \) is the corresponding fuzzy set, \( y_i \) represents the output of the \( i \)th rule (which contributes to the final outcome of the HR HSI being constructed). The rule dictionary \( D = \{D_a, D_c\} \) is generated by reorganising the above extracted fuzzy rules, with the antecedent part \( D_a \) and the consequent part \( D_c \) each collecting all the antecedents and consequents of those rules. Thus, \( D_a \) consists of the antecedent parts of all the rules:

\[
D_a = \{A_1, A_2, \cdots, A_n\}
\]

(6.3)

where \( n \) is the number of rules in the rule dictionary. And the consequent part \( D_c \) consists of the consequents of the rules, where each column denotes the linear coefficients in the consequent part of a certain rule:

\[
D_c = \begin{bmatrix}
p_1 & p_2 & \cdots & p_n \\
r_1 & r_2 & \cdots & r_n
\end{bmatrix}
\]

(6.4)

**Interpolation using three ANFIS interpolation methods**

There are totally three ANFIS interpolation methods proposed in this thesis, including the initial one described in Chapter 3 (termed as ‘Method 0’), and the GA based two methods introduced in Chapter 4 with either the rule type chromosome (termed as ‘Method 1’) or the ANFIS type chromosome (termed as ‘Method 2’).

For ‘Method 0’, the small number of training data in \( P_i \) is divided into \( C \) clusters using the K-means algorithm. For the centre of each cluster, a new fuzzy rule is interpolated by exploiting the LLE algorithm. Then, by aggregating all interpolated
rules, an intermediate ANFIS results. Finally the intermediate ANFIS is fine-turned to get the final interpolated output.

Similar with ‘Method 0’, in ‘Method 1’ and ‘Method 2’, the small number of training data in $P_i$ are also divided into $C$ clusters using the K-means algorithm. The centre of each cluster is used as a seed for generating a number of individuals, which are utilized as observations for interpolating a number of new rules subsequently. Those interpolated rules form the initial population, either in individual rule form (Method 1) or in gathered form (Method 2). Then the initial population will be evolved through a GA process and finally output the interpolated ANFIS mapping.

6.2.2 Testing stage

Given a test LR HSI $X \in \mathbb{R}^{m \times n \times L}$, the testing stage is to test the performance of the learned or interpolated ANFIS mappings $\{\alpha_i\}$. At the beginning, a preprocessing step is conducted to up scale the LR HSI to the same size with the desired HR HSI using bicubic interpolation, resulting in $X \in \mathbb{R}^{M \times N \times L}$. Next, the image details will be enhanced by the ANFIS mappings. Particularly, each image band $X_j \in \mathbb{R}^{M \times N}$ is firstly vectorized as a vector format, which is also denoted by $X_j$ and here $X_j \in \mathbb{R}^{MN}$. A corresponding ANFIS mapping is then selected to perform inference for this band, by solving the following optimization formula:

$$i = \min_i \| X_j - V_i \|_2^2$$  \hspace{1cm} (6.5)

where $\{V_i\}$ denotes the centroids of the subsets from the training stage, and the $i$th ANFIS $\alpha_i$ is chosen as the relevant mapping for inference. Therefore the corresponding HR image band $Y_j$ can be obtained by:

$$Y_j = \alpha_i(X_j)$$  \hspace{1cm} (6.6)

Finally, the post-processing technique (Iterative Back Projection, IBP) is used here to finish the testing stage and then produce the estimated HR HSI. Note that different with the post-processing process in Chapter 5 where a NLM filter is also employed, here only the IBP operator is utilized to perform the post-processing. This is in order to avoid that the details of the resulting images are over-smoothed by the NLM filter, so that the differences between the results of the interpolated and non-interpolated ANFIS models can be clearly shown. The testing stage is summarized as Algorithm 6.2.
6.3. Experimentation and Discussion

This section presents and discusses the results of experimental comparison. Section 6.3.1 gives the basic experimental settings, Section 6.3.2 introduces the performance criteria for hyperpectral image SR used in the thesis, and Section 6.3.3 presents the experimental results over the CAVE HSI dataset.

6.3.1 Experimental setup

The CAVE dataset [20] is used here for the HSI SR experiments. The CAVE dataset contains 31 HSIs of a wide variety of real-world materials and objects, each of which consists of 31 image bands, covering the range of wavelength from 400nm to 700nm. In the experiments, 26 HSIs are used as the training dataset, and the remaining 5 images are used for testing. The training dataset is manually divided into $P = 5$ sub-datasets based on the fact that different image bands of HSIs usually have different characteristics, and the characteristics of the neighbouring bands are usually similar. The division of the 5 sub-datasets is as follows, the first 1 to 6 bands of all HSIs in the training dataset form the first sub-dataset ($P_1$), then every 6 neighbouring bands of all HSIs in the training dataset form a sub-dataset ($P_i, i = 2, 3, 4$), the last sub-dataset ($P_5$) contains the remaining 7 image bands.
6.3. Experimentation and Discussion

Assume that the second and the fourth sub-datasets are with sparse data, the other 3 sub-datasets are with full training data. The simulation of the sparse sub-datasets is done by manually delete a large portion of randomly selected image pixels. So in this experiments the ANFIS mappings $A_1, A_3, A_5$ are learned by the standard ANFIS learning method with full training data, while the ANFIS mappings $A_2, A_4$ are interpolated with sparse training data. The partition of bands that forms the 5 subsets are illustrated in Figure 6.4.

![Figure 6.4: Illustration of the 5 subsets](image)

In the experiments, the LR HSIs are enlarged with the scale factor $s = 2$ and $s = 3$ respectively. Similarly with the proposed ANFIS interpolation method described in Chapter 3 and Chapter 4, the triangular membership function is employed in this super resolution problem. Some parameters used in the experiments are set as follows. The number of rules in each ANFIS is set to $C = 6$. In the interpolation process, the number of closest rules is set to $K = 3$.

Five methods are compared in the experiments: 1) Experiments with full training data for all the subsets, which is used as a reference model denoted as 'M-full' hereafter; The other four methods are with sparse training data in some of the subsets. 2) Experiments with sparse training data using the original ANFIS learning method without interpolation, denoted as 'M-sparse' hereafter; 3) Experiments with sparse training data using the initial ANFIS interpolation method, denoted
6.3. Experimentation and Discussion

as ‘Method 0’ hereafter; 4) Experiments with sparse training data using the rule chromosome based evolutionary ANFIS interpolation method, denoted as ‘Method 1’ hereafter; 5) Experiments with sparse training data using the ANFIS chromosome based evolutionary ANFIS interpolation method, denoted as ‘Method 2’ hereafter.

6.3.2 Performance criteria

Different from the two-dimensional natural images used in Chapter 5, the HSIs are image cubes. Therefore the commonly used measures (PSNR and SSIM) can not be directly used. Instead, the average PANR (A-PSNR), the average SSIM (A-SSIM), as well as the RMSE indices, which are designed for evaluating performance of the HSI SR methods, are employed to quantitatively evaluate the performance of different SR methods. The RMSE (Root-Mean-Squared Error) for this HSI SR problem is defined as:

$$\text{RMSE} = \sqrt{\frac{\| \hat{\mathbf{Y}} - \hat{\mathbf{Y}} \|_F^2}{M \times N \times L}}$$

(6.7)

where $M, N, L$ are the image length, image width and number of image bands respectively, and $\| \cdot \|_F$ stands for the Frobenius norm of matrix. $\mathbf{Y} \in \mathbb{R}^{L \times MN}$ and $\hat{\mathbf{Y}} \in \mathbb{R}^{L \times MN}$ denotes the transformed two dimensional matrices of the ground truth HR image $\mathbf{Y}$ and the estimated HR image $\hat{\mathbf{Y}}$ respectively. The A-PSNR index assesses the model results by computing the average PSNR among all image bands, which is calculated as follows:

$$A-PSNR = \frac{1}{L} \sum_{j=1}^{L} \text{PSNR}_j$$

(6.8)

where $L$ denotes the number of image bands, $\text{PSNR}_j$ is the PSNR value of the $j$th band that is computed using Equation (5.11) and (5.12). Similarly, the A-SSIM (Average Structure SIMilarity) index is the average SSIM among all image bands, which is defined by the following:

$$A-SSIM = \frac{1}{L} \sum_{j=1}^{L} \text{SSIM}_j$$

(6.9)

where $\text{SSIM}_j$ denotes the SSIM of the $j$th image band which is calculated using Equation (5.13). The range of the A-SSIM index is $[0, 1]$. Generally, a smaller RMSE and a lager A-PSNR or A-SSIM means a better result.
6.3. Experimentation and Discussion

6.3.3 Results and discussion

The experimental results of scale factor being 2 are listed in Table 6.1, and that of scale factor being 3 are listed in Table 6.2. The average performance of the 5 testing images are shown in the last row, represented by the ‘Mean ± Standard Deviation (SD)’ form.

Table 6.1: HSI SR results of different algorithms with scale factor = 2

<table>
<thead>
<tr>
<th>Image</th>
<th>Index</th>
<th>Algorithm</th>
<th>M-full</th>
<th>M-sparse</th>
<th>Method 0</th>
<th>Method 1</th>
<th>Method 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Balloons</td>
<td></td>
<td>RMSE</td>
<td>1.482</td>
<td>4.102</td>
<td>1.700</td>
<td>1.547</td>
<td>1.743</td>
</tr>
<tr>
<td>Toy</td>
<td></td>
<td>A-PSNR</td>
<td>44.711</td>
<td>35.871</td>
<td>43.520</td>
<td>44.343</td>
<td>43.304</td>
</tr>
<tr>
<td></td>
<td></td>
<td>A-SSIM</td>
<td>0.9898</td>
<td>0.9839</td>
<td>0.9876</td>
<td>0.9877</td>
<td>0.9879</td>
</tr>
<tr>
<td>Flowers</td>
<td></td>
<td>RMSE</td>
<td>4.431</td>
<td>7.448</td>
<td>4.751</td>
<td>4.519</td>
<td>4.773</td>
</tr>
<tr>
<td></td>
<td></td>
<td>A-PSNR</td>
<td>35.201</td>
<td>30.689</td>
<td>34.595</td>
<td>35.029</td>
<td>34.555</td>
</tr>
<tr>
<td></td>
<td></td>
<td>A-SSIM</td>
<td>0.9540</td>
<td>0.9400</td>
<td>0.9508</td>
<td>0.9507</td>
<td>0.9517</td>
</tr>
<tr>
<td>Painting</td>
<td></td>
<td>RMSE</td>
<td>2.126</td>
<td>2.154</td>
<td>2.146</td>
<td>2.154</td>
<td>2.129</td>
</tr>
<tr>
<td></td>
<td></td>
<td>A-PSNR</td>
<td>41.578</td>
<td>41.467</td>
<td>41.499</td>
<td>41.465</td>
<td>41.568</td>
</tr>
<tr>
<td></td>
<td></td>
<td>A-SSIM</td>
<td>0.9755</td>
<td>0.9737</td>
<td>0.9744</td>
<td>0.9740</td>
<td>0.9751</td>
</tr>
<tr>
<td>Peppers</td>
<td></td>
<td>RMSE</td>
<td>3.349</td>
<td>3.624</td>
<td>3.316</td>
<td>3.251</td>
<td>3.275</td>
</tr>
<tr>
<td></td>
<td></td>
<td>A-PSNR</td>
<td>37.632</td>
<td>36.947</td>
<td>37.719</td>
<td>37.891</td>
<td>37.827</td>
</tr>
<tr>
<td></td>
<td></td>
<td>A-SSIM</td>
<td>0.9338</td>
<td>0.9265</td>
<td>0.9271</td>
<td>0.9285</td>
<td>0.9296</td>
</tr>
<tr>
<td>Average</td>
<td></td>
<td>RMSE ±1.209</td>
<td>2.659</td>
<td>3.857</td>
<td>2.758</td>
<td>2.675</td>
<td>2.759</td>
</tr>
<tr>
<td></td>
<td></td>
<td>A-SSIM ±0.0234</td>
<td>0.9677</td>
<td>0.9614</td>
<td>0.9648</td>
<td>0.9649</td>
<td>0.9658</td>
</tr>
</tbody>
</table>

The average RMSE values are herein taken as the basis upon which to analyse the results. The ‘M-full’ model in Table 6.1 is trained with sufficient training data,
and is used as a reference model. From the last row of Table 6.1, it can be observed that the ‘M-full’ model gives the best result, with the smallest ‘RMSE’ value. The best average results of the other four ANFIS models that are constructed with insufficient training data (‘M-sparse’, ‘Method 0’, ‘Method 1’ and ‘Method 2’) are shown in bold. Compared with the outcome of running the ‘M-full’ model, the result of the ‘M-sparse’ model degrades heavily due to the training data shortage. The average RMSE value increased to 3.857 from the 2.659 of the reference model. Using the same sparse training data, the initial ANFIS interpolation method proposed in Chapter 3 (‘Method 0’) gives much more improved result (with the RMSE value
reduced to 2.758). The evolutionary ANFIS interpolation method with rule-typed chromosome further improves the result. The RMSE value reduced to 2.675, which is very close to that of the reference model trained with full data (2.659).

Similar conclusion goes to the standard deviation values. Due to the lack of sufficient training data, the performance of the 'M-sparse' model is not stable. It gives the largest and also the worst standard deviation (2.208), which is much larger than the SD value of the reference model (1.209). The three interpolation based models provide more stable results, with much closer standard deviation values to the SDs of 'M-full' model.

The super resolution problem with scale factor being 3 is harder than that of scale factor being 2, as more information will be needed to construct the high resolution image. So compared with Table 6.1, the average performance in the last row of Table 6.2 is worse. By analysing the experimental results in Table 6.2, it can be concluded that the 'M-sparse' method performs the worst, giving the largest RMSE values and the smallest A-PSNR and A-SSIM values among the five methods. The three ANFIS interpolation methods significantly improve the super resolution performance. This is verified by the minor difference between the result of the interpolated ANFISs and that of the reference model. For example, the average RMSE value of 'Method 2' (5.334 ± 3.027) is very close to that value (5.246 ± 3.012) produced by the reference method. Comparing the performance among the three interpolated ANFISs themselves ('Method 0', 'Method 1' and 'Method 2'), the two evolutionary ANFIS interpolation methods (especially the one with ANFIS-based chromosome) give better results than the 'Method 0' model.

The visible results are shown in Figure 6.5 - Figure 6.8. In order to show the details of the results using different methods, two randomly selected patches from the resulting images are shown in the second row and third row respectively. It can be observed from these patches that in the resulting image using the original ANFIS with sparse data, there are obvious noise and bad edges, and that running the interpolated ANFISs leads to significant improvement. For example, focusing on the detailed patches of HSI 'Balloons' (as shown in the second and third rows of the Figure 6.8), there are unpleasing circles in the results of 'M-sparse' (ANFIS trained with sparse data). The three interpolation based methods ('Method 0', 'Method 1' and 'Method 2'), especially the two evolutionary interpolation methods ('Method 1' and 'Method 2') obviously eliminate those circles, making the results much closer to that of the 'M-full' model and even the ground truth.
Figure 6.5: Super resolution results using different ANFISs on HSI ‘toy’ with scale factor being 2.
6.3. Experimentation and Discussion

Figure 6.6: Super resolution results using different ANFISs on HSI 'balloons' with scale factor being 2.

(a) Ground Truth
(b) M-Hill
(c) M-planes
(d) Method 1
(e) Method 2
(f) Method 1
6.3. Experimentation and Discussion

Figure 6.7: Super-resolution results using different ANFISs on HSI ‘flowers’ with scale factor being 3.
6.3. Experimentation and Discussion

Figure 6.8: Super-resolution results using different ANFISs on HSI 'balloons' with scale factor being 3.
6.4 Summary

This chapter has presented a novel approach for hyperspectral image super resolution with spare training data, via the use of the proposed ANFIS interpolation technique. This study extends the prior work of Chapter 5 where multiple ANFISs were trained over full training data and mapped with the patches of an LR image to obtain the final HR image. According to the characteristics of different image bands, the training sets are divided into subsets with sufficient or insufficient data. Subsets with sufficient training data are referred to as source domains, where ANFIS models can be produced directly and used as source ANFISs for the interpolation in the target domains, where a large number of training data is missing. The performance of all the three interpolation methods in dealing with the HSI SR problem has been evaluated against five testing HSIs, showing that they provide similar results as those attainable by the reference model with full data in all subsets, while significantly improving upon the outcomes achieved by the ANFISs directly trained with sparse data without interpolation. The next chapter will conclude this thesis and discuss possible future work that may be developed to improve the work in the thesis.
Chapter 7

Conclusion and Future Work

This chapter presents a summary of this thesis as detailed in the preceding chapters. In particular, Section 7.1 summarizes the main contributions made from this research. Having reviewed the theoretical basis of a popular fuzzy inference system (ANFIS), this thesis has proposed a number of improved techniques over it, with both theoretical and practical promising results. The effectiveness of ANFIS with full training data is verified by applying multiple learned ANFIS mappings in the popular super resolution problem. The proposed approaches for interpolation with a rule group and GA based ANFIS interpolation significantly improve the performance of an ANFIS given sparse training data. The practical application of ANFIS interpolation to hyperspectral image super resolution validates its efficacy in addressing real world problems. Whilst the work is promising, Section 7.2 of this chapter points out some initial thoughts for further improving this research, on both the theoretical ‘ANFIS interpolation’ aspect and the practical ‘image super resolution’ aspect.

7.1 Summary of Thesis

The core work presented in this thesis is the concept and implementation of group based fuzzy rule interpolation, which is a novel extension of traditional single rule based FRI approaches. It is able to make a fuzzy inference system (specified in ANFIS within this thesis) to be learned over sparse training data. ANFIS interpolation as having been presented in this thesis follows the general idea of FRI, while possessing a number of specific characteristics:
1. Unlike traditional FRI approaches, which interpolate one single rule to perform fuzzy inference for an unfired observation, a group of fuzzy rules are collectively interpolated covering the entire target domain.

2. Instead of using Mamdani type of rules [108] for knowledge representation, which almost all existing FRI techniques (other than those reported in [31, 95, 153]) take, TSK type of rules [131] is utilised.

3. The proposed approach handles situations that are rather different from those dealt with by traditional FRI techniques, where training data (or more generally the rules) regarding the actual problem domain (namely, the target domain) are extremely sparse, but there are sufficient data (or rules) in the neighbouring domains (or the source domains). That is, the knowledge about the target domain is so poor that traditional FRI methods simply fail to work (with few rules available to carry out interpolation). Combining these characteristics makes it a very difficult task to interpolate a set of accurate rules in an effort to construct a required ANFIS. Of course, if there were a fair amount of training data available in the target domain, then a traditional FRI that works for TSK models would be sufficient to perform interpolation; that is, there would not be a need for the separation of source domains from the target domain in the first place.

Particularly, the main contributions of this thesis include a theoretical part on ‘ANFIS interpolation’ and an application part on ‘image super resolution’.

### 7.1.1 ANFIS interpolation methods

Chapter 3 has presented a primary ANFIS interpolation method, i.e., to use an interpolation scheme based on a group of fuzzy rules to construct an ANFIS with insufficient training data. In this approach, the concept of rule dictionary has been proposed to restore the extracted rules, which acts in the same role as a sparse rule-base in traditional fuzzy rule interpolation. Then a group of new rules are interpolated by exploiting the LLE algorithm for the clustered sparse training data, forming an intermediate ANFIS. It is subsequently used as an initial network, with which the fine turning process can work more efficiently. Systematic experiments have been conducted, demonstrating that the performance of ANFIS with sparse data can
be significantly improved by this primary ANFIS interpolation method. Experiments using different percentages of training data have also been conducted, showing the effectiveness of the proposed interpolation method over extremely sparse data. Furthermore, experiments over an approximate linear function modelling problem have showed that the proposed approach may still work even no training data is available in the target domain.

Based on this primary method, Chapter 4 has presented an alternative ANFIS interpolation approach that implements the interpolation with a GA process. Two strategies of chromosome representation (rule based one and ANFIS based one) have been proposed, forming two different interpolation algorithms. The implementation of algorithm with the ANFIS based chromosomes is easier as there are only one global population involved. While for the algorithm with rule type chromosomes, the whole population is initialized as several sub populations, and the GA process are conducted within these sub populations. Also, a score table has been designed for the convenience of evaluating the rule type chromosomes. Systematic experimental examinations of the proposed approach have been carried out. Experimental results have shown that the proposed method helps boost the regression performance compared to both the original ANFIS and the primary interpolation method. This improved approach has also been compared with several classical machine learning methods, showing its competitiveness in dealing with regression problems.

7.1.2 Real world applications

ANFIS has been applied to perform the image super resolution task in Chapter 5, with sufficient training data provided. The proposed approach can be divided into a learning stage and a testing stage. Multiple nonlinear mappings from the low resolution space to the high resolution space are implemented using ANFIS through a training stage. While in the testing stage, a pre-processing technique is firstly carried out to enlarge input images of a small size, through interpolating LR image pixels. Each patch that is extracted from the pre-processed image is then enhanced by choosing and employing one of the learned ANFIS mappings. Post-processing techniques are finally performed to suppress the displeasing artefacts, resulting in the required HR image as output. The proposed approach has been compared with a number of popular image SR algorithms, and experimental results have revealed
the outstanding performance of the proposed approach over the rest, indicating the superiority of ANFIS in ISR problems when sufficient data is available.

Having shown the effectiveness of ANFIS in dealing with ISR using full training data in Chapter 5, Chapter 6 has investigated the performance of three proposed ANFIS interpolation methods in coping with the hyperspectral image super resolution problem using sparse data. In the training stage, the image cubes are clustered into several subsets according to the different characteristics of image bands. Some bands are with sufficient data while some are with sparse data. The subsets with sufficient training data are then used for learning ANFIS mappings using the same way as in Chapter 5, and for each of the remaining subsets with sparse data, the proposed ANFIS interpolation methods are applied, where two of the learned ANFISs with sufficient data are selected as the source ANFISs. Experimental results have demonstrated that all of the three interpolated models improve the super resolution results for the bands with sparse data.

7.2 Future Work

Although promising, much can be done to further improve the work presented so far in this thesis. The following addresses a number of interesting issues that may help strengthen the current research.

7.2.1 On ANFIS interpolation

In the proposed ANFIS interpolation methods, some preliminary techniques are employed due to their popularity and simplicity, which can be modified with more sophisticated and more powerful alternatives. As stated throughout this thesis, the simplest K-means algorithm is used for clustering; using an automated data clustering method such as those proposed in [16] would help derive more accurate interpolative results. Similarly, instead of using LLE, it is worth examining how other optimisation mechanisms may be adapted for integrated use within the interpolation process. Also, the simplest evolutionary process (genetic algorithm) is utilised, implementing the underlying ideas with more advanced evolutionary algorithms may lead to further strengthened interpolative results. Purely for convenience in implementation, in the
7.2. Future Work

evolutionary ANFIS interpolation method, the sizes of different clusters are herein assumed to be the same, but there is no reason why an adaptive mechanism cannot be introduced to form different cluster sizes, reflecting the amounts of training data scales given per cluster. This may further improve the learning performance. Furthermore, most implementations are based on the use of triangular fuzzy sets, following the common practice in the FRI literature. Nonetheless, this is not necessary, other forms of member functions can be exploited. Whilst it is not expected to adversely affect the performance of the proposed approaches, verifications of this postulation requires future experimental investigation.

Currently, the interpolation methods either terminate once an interpolated ANFIS covering an originally sparse data area is obtained (for the initial ANFIS interpolation approach presented in Chapter 3), or iterates with a fixed number of rules (for the evolutionary ANFIS interpolation in Chapter 4). If the fuzzy rules can be updated dynamically and adaptively with respect to both the rule parameters and the rule numbers, it can be expected that more interpolated ANFIS models may be attained. Thus, it would be very useful to consider extending the existing ideas on dynamic generalization and promotion of interpolated rules as of [113] to create novel ANFIS models on the fly, gaining overall inference efficiency as well as effectiveness. Also, ANFIS is herein chosen as a representative fuzzy inference system to perform the proposed interpolation of FISs. Yet, apart from ANFIS, other inference systems may also suffer from the data shortage problem in the process of model development. Thus, extending the present results of devising and running interpolation based on a group of rules with other fuzzy inference systems would be another interesting piece of further research.

Finally, the proposed approach has been evaluated with several function modelling problems and a range of real world benchmark datasets, plus a practical application for hyperspectral image super resolution. It would be interesting to extend the experimental investigations with more real world tasks and more complicated problems. A particular focus on the practical application of this research may be for image modelling and analysis, especially in the areas of remote sensing [151, 169] and medical diagnosis [91, 104].
7.2.2 On image super resolution

The proposed image super resolution methods (either with full training data or sparse training data) currently work on raw image pixels. However, much research has shown that image features may be significantly more representative than raw image pixels. The gradient and wavelet features which are commonly used in image processing tasks are likely candidates for this. Therefore, extracting and using appropriate image features to train more efficient ANFIS mappings is of great interest to potentially improve the work. Furthermore, as widely recognised in the literature, the use of less but more informative features may do better than utilising all extracted features [68, 140], integrating feature selection techniques (e.g., [42, 69]) into such further developments may boost their efficiency.

Also, all parameters used in the ISR methods are empirically preset in this thesis. For example, the number of ANFIS mappings and the maximum number of fuzzy rules in an ANFIS are set as pre-fixed values by trading off the algorithm’s accuracy and efficiency. However, the best parameters for different images may be various, affected by different image characteristics such as image size, image contents and image types. Thus, how to determine the appropriate parameters adaptively is an issue that needs further investigation, if this process is to be automated with minimal human intervention. Besides, the proposed HSI SR approach has been evaluated against the CAVE dataset only. Yet, there are various hyperspectral image datasets that may have different characteristics from those currently employed in this thesis. Therefore, modifying and testing the ANFIS interpolation aided HSI SR against other representative datasets also forms an important future work.
Appendix A

Publications Arising from the Thesis

A number of publications have been generated from this research carried out within the PhD project. The resultant publications that are in close relevance to the thesis are listed below, including both journal and conference papers.

A.1 Journal Articles

1. Jing Yang, Changjing Shang, Ying Li, Fangyi Li and Qiang Shen, Constructing ANFIS with Sparse Data through Group-Based Rule Interpolation: An Evolutionary Approach. IEEE Transactions on Fuzzy Systems, 2021. DOI: 10.1109/TFUZZ.2021.3049949


A.2 Conference Papers


Appendix B

List of Acronyms

5-FCV  5-Fold Cross-Validation
ANFIS  Adaptive Network-based Fuzzy Inference System
CART  Classification And Regression Tree
CNN  Convolutional Neural Network
CRI  Compositional Rule of Inference
COG  Centre Of Gravity
EC  Evolutionary Computation
EFS  Evolutionary Fuzzy System
FIS  Fuzzy Inference System
FRI  Fuzzy Rule Interpolation
GA  Genetic Algorithm
GP  Genetic Programming
HR  High Resolution
HSI  Hyper-Spectral Image
IBP  Iterative Back Projection
ISR  Image Super Resolution
KEEL  Knowledge Extraction based on Evolutionary Learning
<table>
<thead>
<tr>
<th>Abbreviation</th>
<th>Description</th>
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<tbody>
<tr>
<td>KH</td>
<td>Kóczy and Hirota</td>
</tr>
<tr>
<td>LinR</td>
<td>Linear Regression</td>
</tr>
<tr>
<td>LLE</td>
<td>Local Linear Embedding</td>
</tr>
<tr>
<td>LR</td>
<td>Low Resolution</td>
</tr>
<tr>
<td>LSE</td>
<td>Least Square Estimation</td>
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<tr>
<td>MF</td>
<td>Membership Function</td>
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<tr>
<td>NLM</td>
<td>Non-Local Means</td>
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<tr>
<td>PSNR</td>
<td>Peak Signal-to-Noise Ratio</td>
</tr>
<tr>
<td>PSO</td>
<td>Particle Swarm Optimisation</td>
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<tr>
<td>RD</td>
<td>Rule Dictionary</td>
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<tr>
<td>RF</td>
<td>Random Forest</td>
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<tr>
<td>RMSE</td>
<td>Root-Mean-Squared Error</td>
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<tr>
<td>SD</td>
<td>Standard Deviation</td>
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<tr>
<td>SSIM</td>
<td>Structure SIMilarity</td>
</tr>
<tr>
<td>SVR</td>
<td>Support Vector Regression</td>
</tr>
<tr>
<td>TSK</td>
<td>Takagi-Sugeno-Kang</td>
</tr>
<tr>
<td>T-FRI</td>
<td>Transformation-based Fuzzy Inference System</td>
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Bibliography


