

DEVELOPMENT OF AN EFFICIENT ALGORITHM FOR MODEL STRUCTURE  
SELECTION IN SYSTEM IDENTIFICATION

MD FAHMI BIN ABD SAMAD @ MAHMOOD<sup>1</sup>  
ABD SAMAD BIN HASAN BASARI<sup>2</sup>  
HISHAMUDDIN BIN JAMALUDDIN<sup>3</sup>

<sup>1</sup> Faculty of Mechanical Engineering, UTeM

<sup>2</sup> Faculty of Information and Communication Technology, UTeM

<sup>3</sup> Faculty of Mechanical Engineering, UTM

<sup>1</sup> [mdfahmi@utem.edu.my](mailto:mdfahmi@utem.edu.my), <sup>2</sup> [abdsamad@utem.edu.my](mailto:abdsamad@utem.edu.my), <sup>3</sup> [hishamj@fkm.utm.my](mailto:hishamj@fkm.utm.my)

System Engineering

## ACKNOWLEDGEMENTS

Praise be to Allah the Cherisher and Sustainer of the Worlds for all His blessings. My gratitude to the management group of my working institution, Universiti Teknikal Malaysia Melaka, specifically to the management of Fakulti Kejuruteraan Mekanikal. Also thanks to Center of Research and Innovation Management. Thanks for the financial support, through UTeM short-term grant PJP/2012/FKM(20C)/S01117 also others who helped with the completion of the project in any way.

To my wife, parents and family members, thanks for continuous motivation in the undertaking of this “journey”. I wish the same for future “journeys”, insyaAllah.

## ABSTRACT

System identification is a field of study involving the derivation of a mathematical model to explain the dynamical behaviour of a system. One of the steps in system identification is model structure selection which involves the selection of variables and terms of a model. Several important criteria for a desirable model structure include its accuracy in future prediction and model parsimony. A parsimonious model structure is desirable in enabling easy control design. Two methods of model structure selection are closely looked into and these are deterministic mutation algorithm (DMA) and forward selection procedure. The DMA is known to be originated from evolutionary computation whereas forward selection procedure may be listed under the study of regression. They have close similarities in characteristics, more specifically known as forward search in model structure selection. However, both also function in a population-based optimization and statistical approaches, respectively. Due to the closeness, this research attempts to clarify the advantages and disadvantages of both methods through model structure selection of difference equation model in system identification. Simulated and real data were used. To allow for fair comparison, DMA was altered so as to equalize its strength, where applicable, to that of forward selection procedure. It was found out that DMA not only has the advantage of simpler procedure but it also superceded the performance of forward selection procedure, even with a handicapped alteration.

## ABSTRAK

Pengenalpastian sistem merupakan satu bidang kajian bagi menerbitkan model matematik untuk memperihal kelakunan dinamik sesuatu sistem. Satu daripada langkah dalam pengenalpastian sistem adalah pemilihan struktur model yang mana melibatkan pemilihan pemboleh ubah dan sebutan bagi sesuatu model. Beberapa kriteria penting bagi struktur model yang diinginkan ialah kejituan ramalan masa hadapan dan keringkasan model. Struktur model yang ringkas diinginkan untuk membolehkan reka bentuk kawalan yang mudah. Dua kaedah pemilihan struktur model dilihat dengan lebih mendalam dan ini adalah algoritma mutasi berketentuan (AMB) dan prosedur pemilihan ke depan. AMB diketahui berasal daripada Komputasi Evolusi manakala prosedur pemilihan ke depan boleh dikategorikan di bawah kajian regresi. Kedua-duanya mempunyai persamaan yang rapat dalam ciri, secara khususnya dikenali sebagai carian ke depan dalam pemilihan struktur model. Bagaimanapun, kedua-duanya berfungsi dalam optimisasi berasaskan populasi dan pendekatan statistik, masing-masing. Disebabkan kerapatan ini, penyelidikan ini cuba menjelaskan kelebihan dan kekurangan kedua-dua kaedah melalui pemilihan struktur model persamaan perbezaan dalam pengenalpastian sistem. Data simulasi dan sebenar digunakan. Untuk membenarkan perbandingan yang adil, AMB diubahsuai untuk membolehkan persetaraan kekuatannya, di mana sesuai, kepada prosedur pemilihan ke depan. Didapati bahawa AMB bukan sahaja mempunyai kelebihan dengan prosedur yang lebih ringkas tetapi juga mengatasi prestasi prosedur pemilihan ke depan, walaupun dengan ubahsuaian yang merendahkan kemampuan asalnya.

## TABLE OF CONTENTS

CHAPTER	TITLE	PAGE
	TITLE PAGE	i
	ACKNOWLEDGEMENT	ii
	ABSTRACT	iii
	ABSTRAK	iv
	TABLE OF CONTENTS	v
	LIST OF TABLES	viii
	LIST OF FIGURES	x
	LIST OF APPENDICES	xii
<b>1</b>	<b>INTRODUCTION</b>	<b>1</b>
	1.1 Introduction	1
	1.2 Problem Statement	2
	1.3 Research Objectives	3
	1.4 Research Scopes	3
	1.5 Research Methodology	5
<b>2</b>	<b>LITERATURE REVIEW</b>	<b>8</b>
	2.1 System Identification	8
	2.1.1 Data Acquisition	9
	2.1.2 Model Structure Selection	10
	2.1.2.1 Types of Model	10
	2.1.2.2 Considerations and Requirements	12

2.1.3	Parameter Estimation	13
2.2	Model Structure Selection Methods	15
2.3	Evolutionary Computation	17
2.3.1	Historical Background	18
2.3.2	Characteristics and Related Issues	19
2.4	Regression	22
<b>3</b>	<b>FORWARD SELECTION PROCEDURE</b>	<b>24</b>
3.1	Introduction	24
3.2	Partial Correlation Coefficient	25
3.3	Tests of Significance for Partial Correlation	26
3.4	Use of p-value for Hypothesis Testing	27
3.5	Parameter Estimation	28
<b>4</b>	<b>DETERMINISTIC MUTATION ALGORITHM</b>	<b>30</b>
4.1	Introduction	30
4.2	Foundations of Deterministic Mutation Algorithm	31
4.2.1	Theoretical Justification	31
4.2.2	Main Procedure	32
4.3	Application of DMA in Model Structure Selection	36
4.4	Objective Function for Model Structure Selection	37
4.5	Comparison to Forward Selection Procedure	38
<b>5</b>	<b>RESULTS AND DISCUSSION</b>	<b>40</b>
5.1	Simulation Study	40
5.2	Hald Data Modelling	40
5.2.1	Forward Selection Procedure for Hald Data Modelling	42
5.2.1.1	Implementation Setups	44
5.2.1.2	Modelling Result	

5.2.2	Deterministic Mutation Algorithm	45
5.2.2.1	Constant Term is Not Compulsory	46
5.2.2.2	Constant Term is Absent	48
5.2.2.3	Constant Term is Compulsory	50
5.2.3	Comparison of Modelling Performance	52
5.3	Simulated Data Modelling	53
5.3.1	Modelling Result of Forward Selection Procedure	56
5.3.2	Modelling Result using Deterministic Mutation Algorithm	57
5.3.2.1	Constant Term is Not Compulsory	57
5.3.2.2	Constant Term is Compulsory	60
5.3.3	Comparison of Modelling Performance	63
<b>6</b>	<b>CONCLUSIONS AND RECOMMENDATIONS</b>	<b>64</b>
6.1	Conclusion	64
6.2	Recommendations for Future Work	65
	<b>ACHIEVEMENT</b>	<b>66</b>
	<b>REFERENCES</b>	<b>67</b>
	<b>APPENDICES</b>	<b>76</b>

## LIST OF TABLES

TABLE NO.	TITLE	PAGE
2.1	Methods Applied to Model Structure Selection	15
2.2	Comparisons Among Evolutionary Algorithms	20
3.1	Simplification of Test of Significance for Partial Correlation	27
3.2	Selection of Hypothesis Acceptance	28
4.1	Characteristic Difference between Deterministic Mutation Algorithm and Forward Selection Procedure	39
5.1	Raw Hald Data	41
5.2	Parameters and Values for Use of 'stepwise' Command	43
5.3	Result of Variable Selection for Hald System Identification using Forward Selection Procedure	44
5.4	Statistics of Variable Selection for Hald System Identification using Forward Selection Procedure	44
5.5	Associated Model Coefficient for Hald System Identification using Forward Selection Procedure	45
5.6	Result of Variable Selection for Hald System Identification using Deterministic Mutation Algorithm (Constant Term is Not Compulsory)	47
5.7	Result of Variable Selection for Hald System Identification using Deterministic Mutation Algorithm (Constant Term is Absent)	49
5.8	Result of Variable Selection for Hald System Identification using Deterministic Mutation Algorithm (Constant Term is Compulsory)	51



5.9	Result of Variable Selection for Simulated System Identification using Forward Selection Procedure	56
5.10	Statistics of Variable Selection for Simulated System Identification using Forward Selection Procedure	57
5.11	Result of Variable Selection for Simulated System Identification using Deterministic Mutation Algorithm (Constant Term is Not Compulsory)	59
5.12	Variables, Terms and Parameter Values of Regressors at Step 4 of Deterministic Mutation Algorithm	59
5.13	Result of Variable Selection for Hald System Identification using Deterministic Mutation Algorithm (Constant Term is Compulsory)	62
5.14	Multiple Correlation Coefficient vs Number of Variables and Constant Term using Different Methods	63

## LIST OF FIGURES

FIGURE NO.	TITLE	PAGE
1.1	Flow Chart of Research Methodology	5
1.2	Flow Chart of Efficient Algorithm Development	6
2.1	System Identification	9
4.1	Pseudocode for Deterministic Mutation Algorithm	36
5.1	Significance of 'penter' and 'premove' Parameters	43
5.2	Statistics of Modelling of Hald Data using Original DMA (a) Sum of OF Value of Population versus Generation Number (b) System Output and Predicted Output versus Data Number at Termination	46
5.3	Best Chromosome in Modelling of Hald Data using Original DMA (a) Best OF Value versus Generation Number (b) EI versus Generation Number	47
5.4	Statistics of Modelling of Hald Data using Original DMA and Without Constant Term (a) Sum of OF Value of Population versus Generation Number (b) System Output and Predicted Output versus Data Number at Termination	48
5.5	Best Chromosome in Modelling of Hald Data using Original DMA and Without Constant Term (a) Best OF Value versus Generation Number (b) EI versus Generation Number	49
5.6	Statistics of Modelling of Hald Data using Altered DMA (a) Sum of OF Value of Population versus Generation Number (b) System Output and Predicted Output versus Data Number	

	at Termination	50
5.7	Best Chromosome in Modelling of Hald Data using Altered DMA (a) Best OF value versus Generation Number (b) EI versus Generation Number	51
5.8	Multiple Correlation Coefficient vs Number of Variables using Different Methods	52
5.9	Plots of Input and Output Realizations	55
5.10	Statistics of Modelling of Simulated Data using Original DMA (a) Sum of OF Value of Population versus Generation Number (b) System Output and Predicted Output versus Data Number at Termination	58
5.11	Best Chromosome in Modelling of Simulated Data using Original DMA (a) Best OF Value versus Generation Number (b) EI versus Generation Number	58
5.12	Statistics of Modelling of Simulated Data using Altered DMA (a) Sum of OF Value of Population versus Generation Number (b) System Output and Predicted Output versus Data Number at Termination	61
5.13	Best Chromosome in Modelling of Simulated Data using Altered DMA (a) Best OF Value versus Generation Number (b) EI versus Generation Number	61
5.14	Multiple Correlation Coefficient vs Number of Variables and Constant Term using Different Methods	63

**LIST OF APPENDICES**

<b>APPENDIX</b>	<b>TITLE</b>	<b>PAGE</b>
A	Deterministic Mutation Algorithm	75
B	Hald Result Data using Deterministic Mutation Algorithm (Constant Term is Not Compulsory)	80
C	Hald Result Data using Deterministic Mutation Algorithm (Constant Term is Absent)	81
D	Hald Result Data using Deterministic Mutation Algorithm (Constant Term is Compulsory)	82
E	Simulated Data Result using Deterministic Mutation Algorithm (Constant Term is Not Compulsory)	83
F	Simulated Data Result using Deterministic Mutation Algorithm (Constant Term is Compulsory)	85

## CHAPTER 1

### INTRODUCTION

#### 1.1 Introduction

System identification is a method of determining a mathematical model for a system given a set of input-output data of the system (Johansson, 1993). There are four main steps involved in system identification and these are data acquisition, model structure selection, parameter estimation and model validation (Söderström and Stoica, 1989; Ljung, 1999). As one of the stage in system identification, the model structure selection stage refers to the determination of the variables and terms to be included in a model. Basically, an optimum model is described as having adequate predictive accuracy to the system response yet parsimonious in structure. A parsimonious model structure is preferred since, with less number of variables and/or terms, system analysis and control becomes easier.

Traditionally, model structure selection is performed by determining a finite set of models, typically within a certain maximum specification, and enumeratively testing all the models for predictive accuracy and parsimony. The decision of selection is based on certain information criterion where some established criterions are Akaike's information criterion, B-information criterion and  $\phi$ -information criterion (Veres, 1991). Another method reported is the regression methods such as the backward elimination, forward selection or inclusion and stepwise regression method. These methods involve

testing of different models guided by an analysis of each model's squared multiple correlation coefficient,  $R^2$  and partial  $F$ -test value (Draper and Smith, 1998). In another development, a method called orthogonal least squares is applied in model structure selection (Korenberg *et al.*, 1988; Billings and Yang, 2003a). Despite these encouraging developments, these methods require heavy statistical computation. In order to overcome this, researchers turn to search methods those are able to provide a selection method that is simpler and more efficient in terms of cost and time.

The most recent and successful search method applied to system identification is evolutionary computation (EC) (Fleming and Purshouse, 2002). EC is a term known since 1991 to represent a cluster of methods that uses the metaphor of natural biological evolution in its search and optimization approach (Fogel, 2000). Unlike conventional search methods, EC searches from a global perspective i.e. it does not settle with a local optimum solution (Sarker *et al.*, 2002). Its search is guided by an evaluation function, also called objective function (OF), where good information is exploited via genetic operators. Generally, these operators are reproduction, crossover and mutation. This capability enables the determination of optimum solutions to various optimization problems.

## 1.2 Problem Statement

Model structure selection in system identification basically involves the search for an optimum model structure among many alternative models. This can be achieved by using a search method. The characteristic of global search is found in EC where it is able to perform the search for an optimum model by exploiting good information via global manipulation of solutions.

With the continuous demand for an efficient method of model structure selection, two algorithms are looked into in more detail in order to search for a more efficient

method. These two methods are deterministic mutation algorithm (DMA) (Abd Samad *et al.*, 2011) and forward selection procedure. The DMA is known to be originated from evolutionary computation whereas forward selection procedure may be listed under the study of regression. They have close similarities in characteristics, more specifically known as forward search in model structure selection. However, both also function in a population-based optimization and statistical approaches, respectively. Due to the closeness, this research attempts to clarify the advantages and disadvantages of both methods through model structure selection in system identification.

### 1.3 Research Objectives

This study embarks on the following objectives:

- (i) To study the algorithmic foundation of DMA and FSI in system modelling;
- (ii) To write computer programs of DMA and FSI for system modelling;
- (iii) To assess the performance of DMA and FSI on difference equations;
- (iv) To study the advantages and disadvantages of DMA and FSI with respect to studied circumstances.
- (v) To develop potential areas of DMA, where FSI is found to perform better, for more efficient algorithm

### 1.4 Research Scopes

Due to wide development of study in the field of system identification, the research is limited to the following scopes:

- (i) Two sets of data are to be used. One is real-world data obtained from literature and the other one is a simulated discrete-time difference equation models.

Discrete-time models (also called time series model) become a practical choice with the assumption that the output of a system is a realization of the variables at instants of time. The assumption is also inline with typical data acquisition practice. In the group of discrete-time models, difference equation model is the simplest interpretation of a system's process. A study of difference equation models has shown that difference equation models are representative of many other types of models (Chen and Billings, 1989). A common linear model structure for discrete-time systems is the ARX (AutoRegressive with eXogenous input) model. A nonlinear ARX (NARX) model is to be used to represent a nonlinear discrete-time system.

- (ii) Data in simulated difference equation model consists of less than two input and/or output variables.

The testing of the algorithm is to be made on data those are in the form of single input-single output set. It does not, however, restrict its applicability to data of more than two variables since the application of EC to this type of data only requires minor rearrangement of data and is not considered as a new subject (Ahmad *et al.*, 2002).

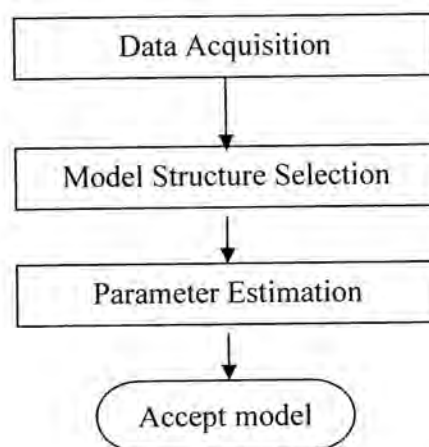
- (iii) The least squares method is used for estimation of system parameters. For simulated models, the disturbances are injected from a uniform distribution. In this circumstance, the least squares method becomes an unbiased method since the disturbances infinitesimally behave as white noise. This form of disturbances also suggests that the noise data are uncorrelated which is suitable for the least squares method. The least squares method also becomes a generalization to other methods like maximum likelihood (Draper and Smith, 1998). The assumption of white



noise is also used for real-world data. The method is widely used in literature and the simplest when the assumption is true.

## 1.5 Research Methodology

The methodology of the research is based on the general flow of system identification which includes data acquisition, model structure selection and parameter estimation as shown in Figure 1.1. The model validation stage which commonly follows parameter estimation is not considered. Every stage is defined and carried out so that the basics of system identification is clearly accomplished and the applicability of the whole conclusion is clarified.



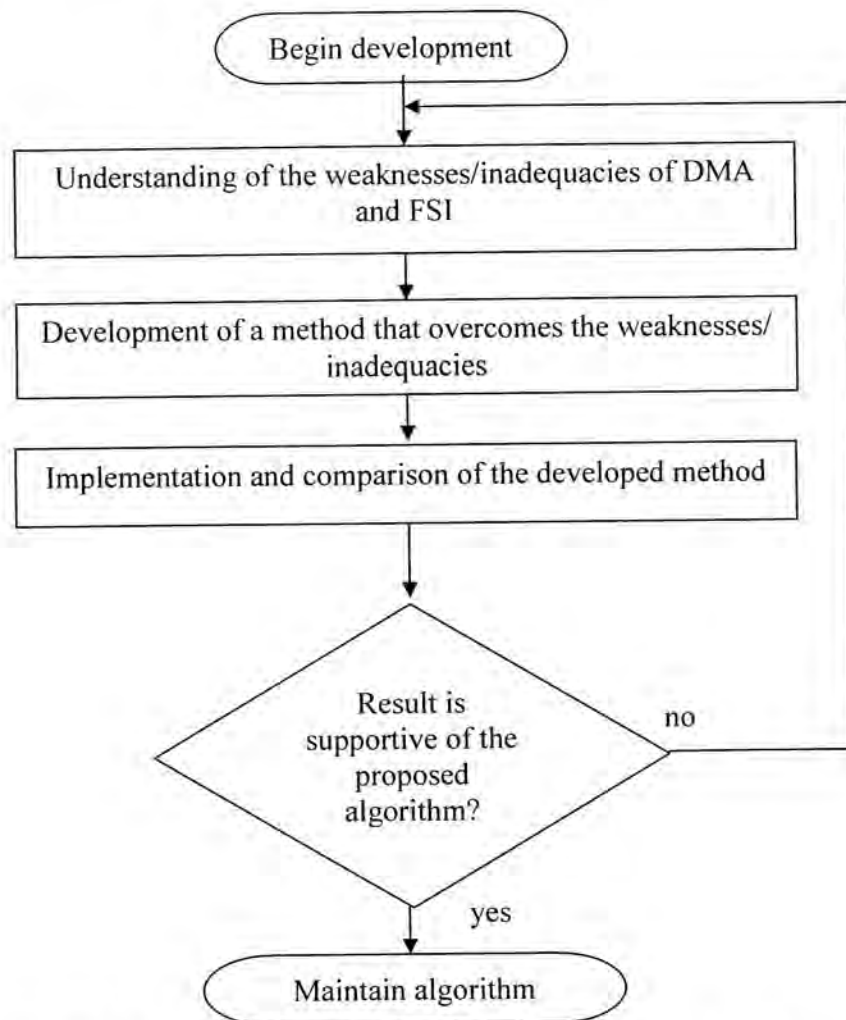
**Figure 1.1** Flow Chart of Research Methodology

The development of an efficient algorithm is related directly to the model structure selection step. The step is broken down into several other steps as follows:

- (i) Identifying and understanding the weaknesses/inadequacies in DMA and FSI.
- (ii) Developing a method that overcomes the weaknesses/inadequacies by modifying/renewing the procedure of an established method.

- (iii) Evaluating the performance of the developed method among its original method.
- (iv) Repeating steps (i) to (iii) for further development of the developed method until a satisfactory algorithm is established.

The flow chart of the steps for algorithm development is provided in Figure 1.2. The first three steps above are repeated until an algorithm that is more superior than its original method is established. Although one might choose to see this methodology as a continuous flow by keep modifying the algorithm, it is presented here as ending with a final algorithm within the time-frame of the research.



**Figure 1.2** Flow Chart of Efficient Algorithm Development

With regards to the comparison of algorithms during the testing on simulated and real-life problem, several common performance indicators were discussed those were predictive accuracy and model parsimony. Besides these measures, results are also compared to original model.

## CHAPTER 2

### LITERATURE REVIEW

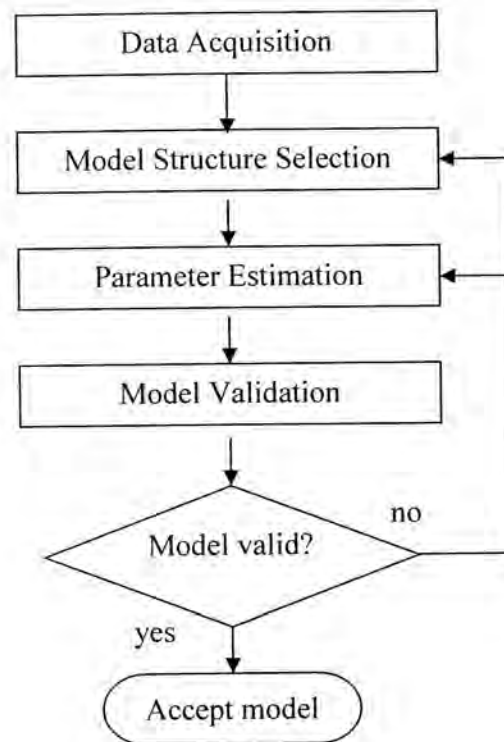
#### 2.1 System Identification

System identification is a method of recognizing the characteristics of a system, thus producing a quantitative input-output relationship that explains or resembles the system's dynamics. The procedure involves the interpretation of observed or measured data into physical relationship, often and easily interpreted in the form of mathematical models (Johansson, 1993).

System identification is also normally related to modelling. There are two types of modelling and these are *a priori* modelling and *a posteriori* modelling (Johansson, 1993). An *a priori* modelling stresses the construction of a mathematical model of a system based on the knowledge of the scientific interdependence of variables whether mechanical, electrical, chemical or others. An *a posteriori* modelling, on the other hand, does not require any theoretical knowledge of the system. The construction of a model in an *a posteriori* modelling is also referred to as black-box modelling. In black-box modelling, the variables enter the model independently via a prediction procedure.

The procedure of identification can be divided into several distinctive steps. These steps are data acquisition, model structure selection, parameter estimation and model validation. The flow chart is shown in Figure 2.1 Throughout the years, system

identification has evolved largely in terms of procedures and methods in the steps above, mainly in model representation and parameter estimation stages. Examples of practical nonlinear system identification can be found in Billings and Fadzil (1985) and Thomson *et al.* (1996).



**Figure 2.1** System Identification

### 2.1.1 Data Acquisition

Many real-world systems, for example, in the fields of mechanics, electricity, chemistry, economics, biology and ecology, are dynamic systems. In dynamic systems, the response of the system depends not only on its input but also its internal state. Although these systems warrant a continuous-time model rather than a discrete-time model, it is practical that data acquisition is performed under the assumption that the variables or terms are interconnected by instants of time. Variables refer to different

components of a system like inputs, outputs and disturbances while terms refer to different dimension or transformation of variables.

## 2.1.2 Model Structure Selection

Model structure selection stage can be divided into two sequential steps:

- (i) Selection on the type of model to represent the system.
- (ii) Construction of the correct or optimum model structure.

In today's literature, various types of models are proposed for system modelling. The following sub-subsection explains the characteristics and recent developments of various types of models. This is followed by a sub-subsection on some considerations in selecting the type of model and constructing an optimum model structure.

### 2.1.2.1 Types of Model

The most common classification of models is based on whether the model represents time-invariant or time-varying systems. For time-invariant systems, difference equation models are usually preferred. For time-varying systems, among popular choices are cascaded block model, neural network, wavelet network and cellular automata.

Difference equation models can be divided into linear and nonlinear models. For a general representation of various classes of linear difference equation model, an ARMAX (AutoRegressive Moving Average with eXogenous input) model is used. It includes the representation of AutoRegressive model, Moving Average model and all other combinations with or without an exogenous variable. It is written as follows:

$$y(t) = a_1 y(t-1) + \dots + a_{n_y} y(t-n_y) + b_0 u(t-d) + b_1 u(t-d-1) + \dots + b_{n_u} u(t-d-n_u+1) + c_0 e(t) + c_1 e(t-1) + \dots + c_{n_e} e(t-n_e) \quad (2.1)$$

where  $y(t)$ ,  $u(t)$  and  $e(t)$  are output, input and noise, respectively at time  $t$ ;  $n_y$ ,  $n_u$  and  $n_e$  are the maximum orders of lag for output, input and noise, respectively,  $a_1, a_2, \dots, a_{n_y}$ ,  $b_0, b_1, \dots, b_{n_u}$ ,  $c_1, c_2, \dots, c_{n_e}$  are the parameters of the model and  $d$  is the time delay that explains the processing time before an input affects the output of the system.

Nonlinear models give much richer possibilities in describing systems and have better flexibility when inferring from a finite data set. Nonlinear models are used when higher degree variables are used to describe a system. Examples of nonlinear difference equation model include NARX (Nonlinear AutoRegressive with eXogenous input), NARMAX (Nonlinear ARMAX) and NOE (Nonlinear Output Error) models. Their polynomials can be identified by their linear counterparts with addition of higher degree terms (Ljung, 1999). The NARMAX model is a general representation for finite nonlinear difference systems with obvious advantages over functional series expansions (Billings, 1984). It is also proven to provide a general representation of various classes of nonlinear systems including bilinear, output-affine and rational models (Chen and Billings, 1989). Another important feature of the NARMAX model is that it is linear-in-the-parameters allowing easy implementation of parameter estimation.

Linear and nonlinear functions can also be present simultaneously in a cascaded form. The most easily distinguished nonlinear model representation in the class of cascaded block models are the Wiener and Hammerstein models (Johansson, 1993; Ljung, 1999). They both differ in a way that in a cascaded block diagram, the input to a Wiener model goes through a linear process followed by a nonlinear transformation, while in Hammerstein model, the flow goes through the nonlinear process first.

Neural network is a type of nonlinear model. Originally, the neural network is developed with the metaphor of brain synapses. A typical artificial neural network is

characterized by nodes or also called neurons to represent the inputs, outputs and intermediate variables. These are linked by connection weights,  $w$  and the computation is made by a predefined activation function. There are many types of neural network such as feedforward, back-propagation and recurrent network (Billings *et al.*, 1991; Negnevitsky, 2002). A popular class of neural network is radial basis function network (Billings and Zheng, 1995; Rashid *et al.*, 2004). Among types of radial basis functions are thin-plate-spline function, Gaussian function, multiquadric function and inverse multiquadric function. In another development, Liu *et al.* (1999) proposed the construction of a variable neural network which allows the number of basis functions to vary along the design process. By utilizing wavelet frame decomposition in its activation function, the model is known as wavelet network. A development of wavelet network configuration can be referred in Billings and Wei (2005).

A cellular automata (CA) is mainly composed of three parts: a discrete lattice, a neighbourhood and a set of rules. The discrete lattice becomes the platform for CA pattern while the neighbourhood and the rules dictate the pattern or vice versa. The cells of a neighbourhood are characterized by its time and space while the rules determine the connections between the cells as a term of a mathematical model. Its usefulness is significant in pattern recognition and image processing application. Current researches are on detection of the neighbourhood structure and extraction of rules using forward orthogonal least squares algorithm (Billings and Yang, 2003a) and using genetic algorithm (GA) (Yang and Billings, 2000a; 2000b; Billings and Yang, 2003b).

### **2.1.2.2 Considerations and Requirements**

When choosing a model type, certain considerations need to be accounted. Most literature stresses on the purpose of modelling (Johansson, 1993; Ljung, 1999). The purposes may vary from establishing a simple regulating model to understanding a system's complete dynamics. In Goodwin and Payne (1977), the characteristics of an