Single parent mating in genetic algorithm for real robotic system identification

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Article Info	ABSTRACT
	System identification (SI) is a method of determining a mathematical model for a system given a set of input-output data. A representation is made using a mathematical model based on certain specified assumptions. In SI, model structure selection is a step where a model structure perceived as an adequate system representation is selected. A typical rule is that the final model must have a good balance between parsimony and accuracy. As a popular search method, genetic algorithm (GA) is used for selecting a model structure. However, the optimality of the final model depends much on the effectiveness of GA operators. This paper presents a mating technique named single parent mating (SPM) in GA for use in a real robotic SI. This technique is based on the chromosome structure of the parents such that a single parent is sufficient in achieving mating that eases the search for the optimal model. The results show that using three different objective functions (Akaike information criterion, Bayesian information criterion and parameter magnitude–based information criterion 2) respectively, GA with the mating technique is able to find more optimal models than without the mating technique. Validations show that the selected models using the mating technique are acceptable.

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1. INTRODUCTION

System identification (SI) is known as a field of study where an optimal mathematical model, relating the variables and terms of a system, is determined. This is done by using the input-output data from the system. By developing the model, better control of the system may be achieved [1], [2]. There are two types of system modelling i.e. continuous-time and discrete-time modelling. Noting that data acquisition in industry or laboratory is made by instants of time, discrete-time modelling is commonly seen. There are 4 main steps in SI and these are data acquisition, model structure selection, parameter estimation and, lastly, model validation. The description of an optimal model is one that has adequate accuracy in predicting the response of the system but at the same time, is parsimonious in form. A parsimonious model structure, that contain fewer variables and/or terms, is desirable because the analysis and control of the system becomes easier [3].

To identify an optimal model for a system within a short time and cost, high efficiency in modelling is needed. Therefore, researchers have turned to meta-heuristic methods, including evolutionary computation as a method to allow optimal search for the system's model [4]–[8]. Evolutionary computation, more specifically genetic algorithm (GA), has proven its strength and endurance, and able to reduce computational

burden. GA has become an interesting area of investigation among researchers for many applications such as wireless sensor network energy optimization [9], control of vehicles [10], [11], modelling of disease severity [12], scheduling in medical field [13], aeronautics and robotics [14].

Although GA has been adopted in SI, its efficiency is still lacking which can be observed from long processing time, premature convergence or non-optimal setting of GA operators that causes loss of computation time and restricted global performance. Premature convergence to local optima is one of the most frequent difficulties that arise when applying GA to complex problem. It occurs when genetic operators can no longer generate offsprings that are fitter than their suboptimal parents. Premature convergence is associated with the loss of diversity in the population. However, too much population diversity can lead to a dramatic deterioration of GA efficiency [15].

Aside from the common operators of GA selection, crossover and mutation and although, relatively rare, researchers have started looking into mating after selection to enhance GA. An example include the introduction of a self-adaptive mating based on parent similarity or fitness [15]. Another example introduces gender and kinship to the individuals in GA [16]. The idea is also adopted in [17] and used together with tabu search in [18].

With proper mating technique, the "marriage" of the parents must be able to explore new search space of solution, producing more varied offsprings (hence, in the context of SI, may mean system model) that cannot be achieved by common procedure of GA. This paper aims at introducing and implementing a new mating technique, named single parent mating (SPM), which is simpler yet effective, for a real robotic SI. The technique is shown to be capable of exploring new search space of solutions, thus producing more optimal and valid models according to three different objective functions (OF). The sections are divided as: section 2 explains the method of study including the mechanism of the mating proposal, section 3 reveals the results along with validation analysis and section 4 concludes the findings of the paper.

2.   RESEARCH METHOD
2.1. GA with mating technique
GA is known as an optimization method that takes the metaphor of species evolution [19]. In traditional GA, the search for an optimal model is made through three important processes: selection, crossover and mutation [20], [21]. The selection process copies good chromosomes into a mating pool - some may be copied a number of times. Common crossover operates by the mating of two or more parents taken randomly from the mating pool once the selection process is completed. However, there is a possibility that the 2 selected parents have the same features causing the process to produce similar offsprings to parents and thus suppressing the evolution.

In this paper, to speed up the search and avoid premature convergence in the population, the algorithm incorporates a mating technique named SPM. The idea is to have 2 parents of completely different characteristics to be mated in order to try out new offsprings for the next generation. In SPM, once the parents are transferred to the mating pool after the selection process, they are copied and inverted to form a new set of parents. Using a binary representation, all bits 1 are changed to 0 and vice versa. The mating is achieved by pairing the original parent with its inverted self, hence the name SPM. The mating emphasizes how the pair of chromosomes is made, not how their informations are exchanged, as information exchange is carried out through crossover. Figure 1 illustrates that there are 24 possible offsprings with SPM when applied together with uniform crossover, as illustration. By this way, bigger search space is explored, diversity of the population is maintained and higher variability of offsprings is accomplished in the next generation. Figure 2 shows the procedure of GA using the mating technique.

2.2. Real robotic system
The real data comes from a flexible robot arm system available from [22]. The flexible robot arm has 1,024 data points of an input (measured reaction torque of the robotic structure) and an output (the acceleration of the flexible arm). Markovsky *et al.* [23], [24] selected lag 4 for a linear model identification of the system. Yassin *et al.* [25], it is identified that the system's suitable specification is maximum order of input lag=2 and maximum order of output lag=4, also within a linear form.

2.3. Simulation setup
In this study, the chromosomes in GA represent specific models for SI. The models, in the form of nonlinear autoregressive with exogenous input (NARX) models, are represented using binary representation where 1 is presence of term and 0 for omission of term. Adopting some literature results, the specification of the search space is as: maximum nonlinearity=2, maximum order of output lag=4, maximum order of input lag=4 and time delay=1. This specification makes up 44 terms to be selected for model structure and the

number of possible models to choose from is 2^{44}-1>10^{13}. Once a model structure is selected, the parameters are estimated using the least squares method. Then, they are evaluated based on the minimization of a specific optimality measurement a.k.a. OF in identifying the system. Three different types of OF i.e. Akaike information criteria (AIC), Bayesian information criteria (BIC) and parameter magnitude-based information criteria 2 (PMIC2) are used to evaluate the models throughout evolution. AIC and BIC may be referred from e.g. [26] while PMIC2 is demonstrated in [27] and [28].

The specification of GA is as: population size=200 and 100, maximum generation=300, bit-flip mutation probability=0.01 and single-point crossover probability=0.6. The study uses roulette-wheel selection and the elitism strategy. In the elitism strategy, the chromosome that is evaluated as the best is brought forward, unchanged, into the population of the next iteration (generation). The processes are repeated until termination (maximum generation).

Prior study conducted using the mating technique with single-point crossover on simulated data sets revealed that the method found more optimal models by setting its implementation in the range of 10% to 20% of population, inclusively. Hence, in this study, GA is carried out using two specific percentages of the parents in the mating pool where the mating pool is the same size as the population. The percentages tested were 0% and 15%. As an example, for a 15% SPM, 15% of the parents in the mating pool are copied and inverted. This makes another set of parents of size 15% of population. Mating was done between the parents and its inverted selves (making up 30% of a population). The remaining 70% comes from the initial mating pool. With this setting, it may be noted that 0% represents GA without mating. For each percentage, 15 runs of GA on the real robot arm system data set are made.
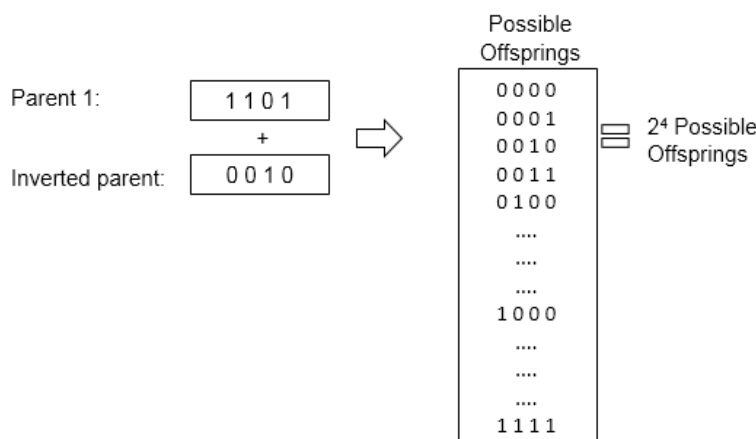

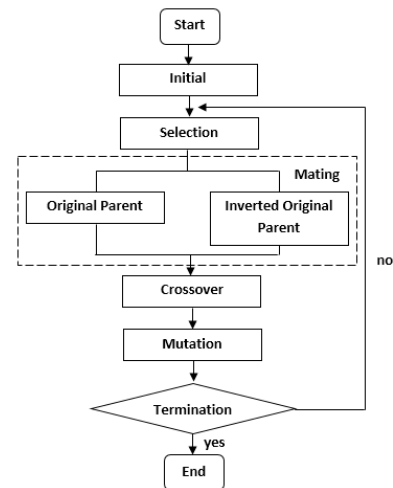Figure 1. Possible offsprings with single parent mating (SPM)   Figure 2. GA with SPM

3. RESULTS AND DISCUSSION

3.1. Model structure selection

Finding an optimal model, that has adequate accuracy of prediction yet parsimonious in its structure, is aimed through the minimization of the OF. Figure 3 shows the average OF value of the best chromosome versus generation when using 0% SPM technique (that represents no mating and labelled "0" in legend) and 15% SPM technique (labelled "0.15") for the real flexible robot arm data with 200 population size. Based on Figure 3(a), the graph of 15% SPM started at a high value but then decreased rapidly until the 100th generation when using AIC. It then settled rather consistently until the 300th generation. The decrement when using 0% SPM was rather slow until the maximum generation. The OF value of 15% SPM is better (lower) than 0% SPM throughout the evolution. Closer investigation revealed that GA with 15% SPM managed to find the same, presumably, the most optimal model in all its runs while with 0% SPM, the very same model is found in only 5 runs. The model has 8 regressors with an OF of -10745. Some of the models in 0% SPM gives higher OF of -10741. The best model from 15% SPM is written as:

$$y(t) = 3.158y(t-1) - 4.439y(t-2) + 3.13y(t-3) - 0.982y(t-4)$$
$$+0.019u(t-1) - 0.029u(t-2) + 0.055u(t-3) - 0.030u(t-4) \tag{1}$$

Figures 3(b) to 3(c) show that the results using BIC and PMIC2 have quite the same pattern as graph in Figure 3(a). The graphs show that 15% SPM is better than 0% SPM, noted by achieving lower OF average of the best chromosomes, and, additionally, by shorter time. Similar to the observation when using AIC, with BIC, GA with 15% SPM found the same most optimal model (according to BIC) in all runs with an OF of -10707 whilst 0% SPM found it in 8 runs. Some of the models in 0% SPM gives higher OF of -10694. The model found with BIC has 7 regressors and is:

$$y(t) = 3.128y(t-1) - 4.367y(t-2) + 3.058y(t-3) - 0.952y(t-4)$$
$$+0.004u(t-1) + 0.026u(t-3) - 0.015u(t-4) \tag{2}$$

Selecting these linear models as the optimal ones within the space of nonlinear model choices agree with [25]. When using PMIC2, models with lower OF value is found in 4 runs with 15% SPM than the lowest of 0% SPM. The best model of PMIC2 contains 29 regressors. It contains several nonlinear terms and the linear ones are $y(t-2)$, $y(t-3)$ and $y(t-4)$ with an OF value of 7.032, compared to 21.692 - the lowest when using 0% SPM.
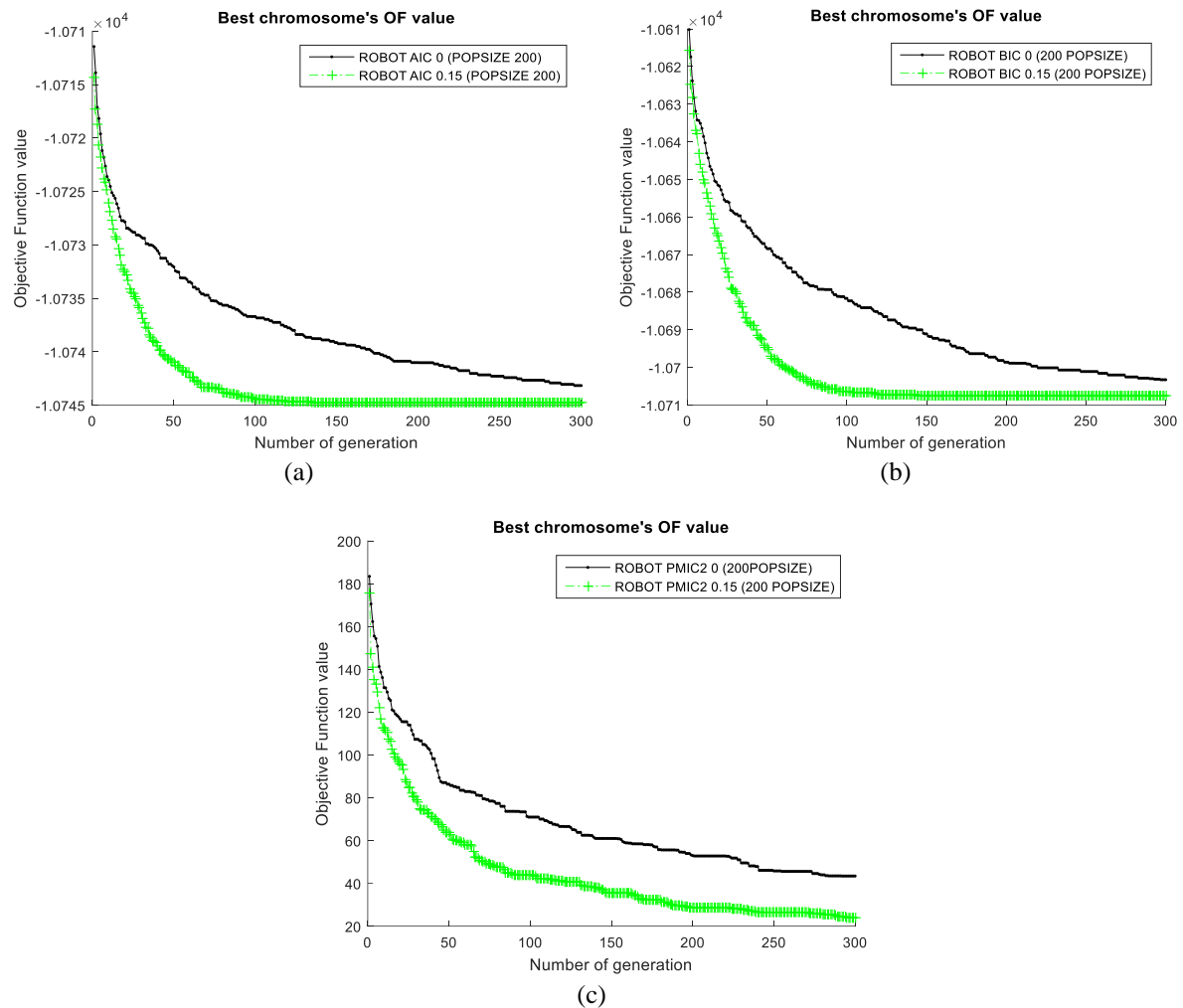

(a)

(b)

(c)

Figure 3. Best chromosome's OF value for robot arm with 200 population size (a) AIC model, (b) BIC model, and (c) PMIC2 model

Next, another test is made by reducing the population size to 100. This affects GA in a way that less parents are inverted, making the effectiveness of SPM questionable. Figure 4 shows the average results. Based on Figure 4(a), it is seen again that, throughout evolution, the OF of the best model in 15% SPM is lower than that of 0% SPM. The decrement of 15% SPM is rapid until it found a model with a very low OF

whilst the decrement of 0% SPM is slow. 5% SPM found the same model as with 200 population size (1) in all its runs while 0% SPM found the very same, presumably, the most optimal model in 10 runs. Figures 4(b) to 4(c) show the OF average of the best chromosomes when using BIC and PMIC2, respectively. The pattern with PMIC2 is not exactly the same as with AIC and BIC but the outcome is the same. In all the OFs, 15% SPM found models with lower OF than 0% SPM throughout evolutions. With BIC, 0% SPM found, presumably, the most optimal model in 7 runs whilst 15% SPM found the same model in all its runs. This is the same model when using 200 population size (2). When using PMIC2, 8 runs in 15% SPM ended with final models of lower OF than the best model found using 0% SPM in all its runs. The best model contains several nonlinear terms and the linear ones are $y(t-1)$ and $y(t-3)$. This model has a higher OF than the one with 200 population size i.e. 15.583.

All the results obtained with 200 and 100 population size indicate that the population in 15% SPM contain more genetic diversity, allowing more optimal models to be found quicker. It indicates that bigger search space was explored and higher variety of offsprings was found in the next generation, compared to no mating. When a population is unable to produce offsprings of higher variability than their parents, an algorithm becomes trapped in local optima. This may have caused 0% SPM to be stuck with the near-optimals.

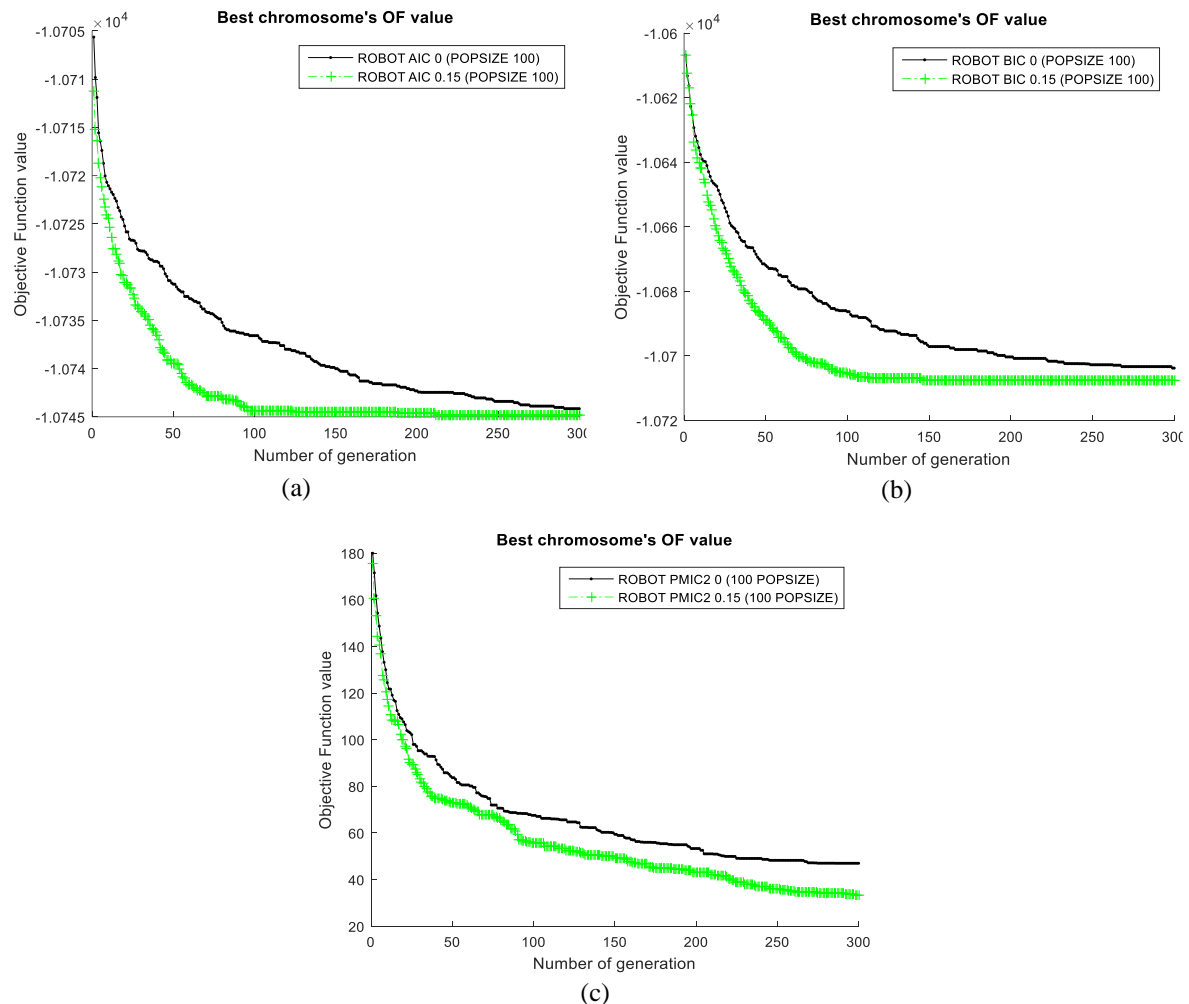

Figure 4. Best chromosome's OF value for robot arm with 100 population size (a) AIC model, (b) BIC model, and (c) PMIC2 model

3.2. Model validation

To complement the whole procedure of SI, correlation tests are used as validation stage to ensure that no other significant terms and/or variables are omitted from the model [29]. Only the models selected using AIC and BIC are discussed since the validation of the PMIC2 models do not provide significant result.

Since the selected models using AIC and BIC are of linear forms, Figure 5 shows the linear correlation tests, consisting of error autocorrelation test ($\phi_{\varepsilon\varepsilon}$) and input-error cross correlation test ($\phi_{u\varepsilon}$), carried out onto the results of the models, respectively. The dotted horizontal lines resemble the bandwidth such that a valid model with 95% confidence should have the lines within the bandwidth. They both look the same and it can be seen that some points lie outside of the bandwidth. The data reveals that there are small differences between Figures 5(a) and 5(b) where the biggest difference in $\phi_{\varepsilon\varepsilon}$ test is at lag -16 while in $\phi_{u\varepsilon}$ test, the biggest difference is at lag -1. Nonetheless, the result is similar to the ones found in [30] where the authors commented that it is difficult to achieve perfect results for real life cases, and that sufficiently good, as can be seen, is acceptable. These validation deficiencies may be inherent from wrong selection of lag orders or nonlinearity. Including the noise terms will improve the model as carried out in [25].
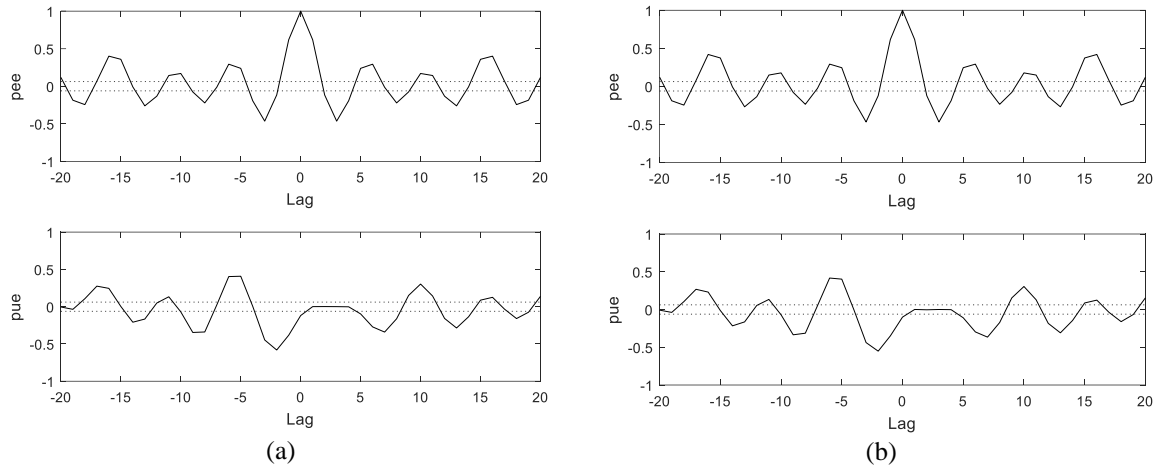

Figure 5. Linear correlation tests for best model in 15% SPM (a) AIC model (1) and (b) BIC model (2)

Cross validation is also carried out on the results, as shown in Figure 6 and Figure 7, where the predicted output is superimposed to the real output and the error (difference of value between the two) plotted. With the range of real output data from -0.7883 to 0.7891, the highest error is 0.0147 whilst the average error is 0.0043 in Figure 6. From Figure 7, the highest error is 0.0151 whilst the average error is 0.0042. These errors are small and they show that the models selected by GA using AIC and BIC incorporating the mating technique are valid and acceptable. Furthermore, the mean square error of the models are 2.620×10^{-5} and 2.632×10^{-5} for AIC and BIC models, respectively. These data are comparable to the ones from [30] who obtained 2.69×10^{-5} and 2.72×10^{-5} for training data set and testing data set, respectively.
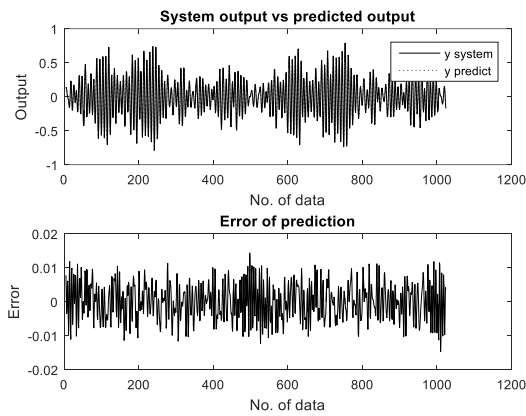

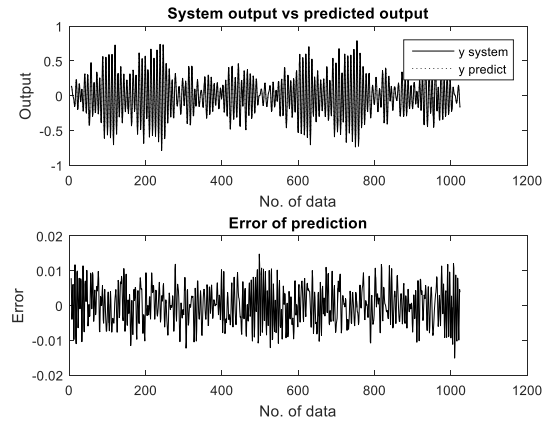Figure 6. Superimposition of predicted output of model using AIC with 15% SPM onto real output

Figure 7. Superimposition of predicted output of model using AIC with 15% SPM onto real output

4.   CONCLUSION

The aim of this paper is to show the effectiveness of SPM for GA in optimization of a real discrete-time SI. Three types of OFs are used and according to all OFs, GA with SPM is able to find more optimal models, and additionally, quicker than without mating. In all runs, the models found using the mating technique have either lower or equal OF value than the runs without mating, indicating that the selected models are parsimonious yet with adequate accuracy. In validating the models, correlation tests are done to the selected models. Although the correlation tests show that the models do not fulfill the 95% confidence bandwidth completely, which is expected to be due to inherent noise of real data, superimposition of the predicted output from the models with the real output value provide convincing validation. Even when using a small population size, the technique is shown to be capable of reaching into untested territory of the search space. Using the mating technique, new points are able to be explored thus enabling the search for optimal models to become more promising than the traditional procedure of GA. From application perspective, future work may focus on changing the phenotype-to-genotype conversion for a more effective search of optimal models while from the method's perspective, other crossover and selection types may be tested together with SPM to see whether faster convergence may be achieved.

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