A New Approach to Improve the Overall Accuracy and the Filter Value Accuracy of the GM(1,1) New-Information and GM(1,1) Metabolic Models

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***Abstract*—Grey system theory has many facets, one of which is the so-called GM(1,1) model, used for predicting and forecasting. This paper proposes a novel way of improving the overall relative accuracy of the new-information grey model, and the metabolic grey model, and also by improving the filter value accuracy. By incorporating a weight sequence that is populated by a genetic algorithm to minimize the error of the simulated values. The least square parameters (-*a*) and *b*, can then be scaled by the values contained in the weight sequence, until a satisfactory result is obtained. If a high level of accuracy can be attained for the simulation values of the model, and also for the filter value, it will ultimately allow for greater forecasting ability.**

I. Introduction

Grey modelling provides a very affective methodology for predicting and forecasting, and is one of the more popular facets of Grey System Theory (GST), proposed by J.L. Deng in the 1980s [1]. GST has a varied and extensive applicability in real world scenarios, such as economy, agricultural production, disaster prediction, industrial analysis, etc. From the established GM(1,1) model, many enhancements and improvements have been made, as is evident in the literature. In [4] the authors applied a weighted least square method to estimate the parameters for the new-information model. In [6] the precision of the GM(1,1) was improved upon by rebuilding the background values based on the monotonic rise of the accumulated generating sequence. In [8] a *total* least squares method was used to improve the GM(1,1) model, based on the analysis that the additive matrix B also contained errors. In [9] an improvement on the computation was made, allowing for quicker model creation with the same level of accuracy as the traditional GM(1,1) model. In [10] a weighted approach was applied to the original data sequence. This paper proposes yet another enhancement, one which improves the overall accuracy of the GM(1,1) variants; the new-information model and the metabolic model. And by also improving the filter value accuracy, by adjusting the least square parameters via the use of a weight sequence, which is populated by a genetic algorithm (GA) based on the simulated error values. Increases in accuracy can be achieved as will be demonstrated.

By employing the evolutionary tacit of a GA, one is able to create a weight sequence that enables the GM(1,1) model to converge to a near optimal solution, in terms of error reduction. A near optimal, rather than an absolute solution, because a near optimal solution in this context allows for the encapsulation of minor granules of noise and uncertainty, which can be seen as the representation for the variance of the raw data sequence. This noise is minimal, but allows for a truer representation of describing the data and is stipulated by the fitness function.

The notion of a GA was first proposed by John Holland, in 1975 [2] and is an optimization algorithm. In which he described the approach as an abstraction of biological evolution. Having a randomly initialized population, each candidate of the population is evaluated and scored. The fitter the candidate, the higher the likelihood of its genes being passed onto successive generations thereafter. The additional use of *crossover* and *mutation* allows for the possibility of creating ever fitter candidates and by proxy, fitter populations. Successive generations will then breed, producing ever more fitter candidates, and the process is repeated until a solution (if such a solution exists) is converged upon, or a maximum number of generations is reached. The crossover operator allows for large jumps to be made in the search space, whereas, the mutation operator allows for tiny increments, and by doing so allows for variance to enter the fray. The combination of the two operators provides for an affective approach in finding an optimal solution or a near optimal solution.

Section II will now go on to describe the standard GM(1,1) model and its variants, the new-information grey model and the metabolic grey model. Section III will describe the GA. Section IV will demonstrate the new approach of improving the accuracy of the new-information grey model, and the metabolic grey model, and in turn the accuracy of the filter value. Section V will contain the conclusion and discuss possible future works and extensions.

II. The GM(1,1) Forecasting Model

A. GM(1,1) Model

GM(1,1) is an acronym for Grey Model(First Order, One Variable). A GM is created by transforming the raw data sequence into a new data set, by means of the accumulated generating sequence (1-AGO) [7].

Assume that

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$$X^{(0)} = \left(x^{(0)}(1), x^{(0)}(2), ..., x^{(0)}(n)\right),$$

is a non-negative sequence of raw data, where $x^{(0)}(k) \geq 0, k = 1, 2, ..., n$, and $X^{(1)}$ is the 1-AGO sequence of $X^{(0)}$ with

$$X^{(1)} = \left(x^{(1)}(1), x^{(1)}(2), ..., x^{(1)}(n)\right),$$

where

$$x^{(1)}(k) = \sum_{i=1}^{k} x^{(0)}(i) \tag{1}$$

$k = 1, 2, ..., n$ and $Z^{(1)}$ is the mean generated sequence of consecutive neighbors of $X^{(1)}$ given by

$$Z^{(1)} = \left(z^{(1)}(1), z^{(1)}(2), ..., z^{(1)}(n)\right),$$

where

$$z^{(1)}(k) = 0.5x^{(1)}(k) + 0.5x^{(1)}(k-1) \tag{2}$$

$k = 1, 2, ..., n$. If $\hat{a} = [a, b]^T$ is a sequence of parameters, and

$$B = \begin{bmatrix} -z^{(1)}(2) & 1 \\ -z^{(1)}(3) & 1 \\ \cdot & \cdot \\ \cdot & \cdot \\ \cdot & \cdot \\ -z^{(1)}(n) & 1 \end{bmatrix}, \qquad Y = \begin{bmatrix} x^{(0)}(2) \\ x^{(0)}(3) \\ \cdot \\ \cdot \\ \cdot \\ x^{(0)}(n) \end{bmatrix}$$

Then the least square estimate of the grey differential equation

$$x^{(0)}(k) + az^{(1)}(k) = b, \tag{3}$$

satisfies

$$\hat{a} = \left[B^T B\right]^{-1} B^T Y, \tag{4}$$

then

$$\frac{dx^{(1)}}{dt} + ax^{(1)} = b, \tag{5}$$

is called the *whitenization* of the grey differential equation presented in (3). The solution to the time response function of the whitenization function is given by

$$x^{(1)}(t) = \left[x^{(1)}(0) - \frac{b}{a}\right] e^{-at} + \frac{b}{a}. \tag{6}$$

The time response sequence of the grey differential equation presented in (3) is given by

$$x^{(1)}(k+1) = \left[x^{(1)}(0) - \frac{b}{a}\right] e^{-ak} + \frac{b}{a}, k = 1, 2, ..., n. \tag{7}$$

The restored values of $x^{(0)}(k)$ can be given by

$$\hat{x}^{(0)}(k+1) = \alpha^{(1)}\hat{x}^{(1)}(k+1) = \hat{x}^{(1)}(k+1) - \hat{x}^{(1)}(k). \tag{8}$$

The parameters *(-a)* and *b* are referred to as the *development coefficient* and the *grey action quantity*. The new method for improving the accuracy involves scaling these parameter values according to the values contained in the weight sequence; scaling either *(-a)* or, *(-a)* AND *b*, by the same weight. The parameter *(-a)* describes the development states of $\hat{X}^{(1)}$ and $\hat{X}^{(0)}$, and represents the variance and dynamic nature of the system. Parameter *b* is referred to as the grey action quantity value, and is obtained from the background values (behavioral sequence). It indicates the environmental effects on the system. In general, the variables that act upon the system should be external or predefined, but as this is a GM of the first order and a single variable, the background values are instead used. As a result, the model built only uses the system's behavioral variants [7].

B. GM(1,1) Variations

Sub-sequences of the original data sequence can sometimes be used when creating GM(1,1) models. Depending on which sub-sequences are used will determine different parameter values.

Assume that

$$X^{(0)} = \left(x^{(0)}(1), x^{(0)}(2), ..., x^{(0)}(n)\right).$$

Taking $x^{(0)}(n)$ as the origin of the time axis, then it can be stated that when $t < n$ it is a reference to the *past*, and $\hat{x}^{(0)}(t)$ is referred to as the simulation value. When $t = n$ it is a reference to the *present*, and $\hat{x}^{(0)}(t)$ is referred to as the filter value. And when $t > n$, it is a reference to the future, and $\hat{x}^{(0)}(t)$ is referred to as the prediction value.

As the main purpose of GM is to make accurate predictions, it is understandable that having a high level of accuracy at the moment when $t = n$, will allow for greater ability in predicting and forecasting. As is the case with prediction models in general, high levels of accuracy can be achieved for predictions closer to the origin. That is to say, the further away from $t = n$, the more diminished the accuracy will become. This justifies the sentiment that having a high accuracy for the filter value will allow for the immediate value for $t > n$ to have a high level of accuracy.

C. The New-Information Grey Model

Let $x^{(0)}(n+1)$ be a new piece of information added to the end of the sequence. When it is inserted, the resultant GM is built upon the following sequence

$$X^{(0)} = \left(x^{(0)}(1), x^{(0)}(2), ..., x^{(0)}(n), x^{(0)}(n+1)\right).$$

The magnitude of the original sequence is increased, but data contained in the sequence is constantly up to date.

D. The Metabolic Model

Let $x^{(0)}(n+1)$ be a new piece of information added to the end of the sequence, but unlike the new-information model, $x^{(0)}(1)$ is deleted. The reasoning being, the older the element in the sequence, the less the significance it has in the prediction ability in the overall GM. The metabolic model is built upon the following sequence

$$X^{(0)} = \left(x^{(0)}(2), x^{(0)}(n), ..., x^{(0)}(n+1)\right).$$

The magnitude will stay the same throughout, all the while the data contained in the sequence is kept up-to-date, and relevant.

III. The Genetic Algorithm

GAs have been utilized in the creation of grey modelling before, as is evident in the literature [5][3]. Previous works have established a GA to find an optimal value to use instead of 0.5. The GA in this paper was created to populate a weight sequence based on the error of the simulated values. Given a sequence of raw data, and then creating a new-information and a metabolic grey model from that sequence, the newly created simulated values are then used in the GA. The goal of the GA is to create a scaling weight so that the simulated value can be readjusted to minimize the error between the actual value and the simulated value. This is repeated for all values in the sequence, where

$$\hat{X}^{(0)} = \left(\hat{x}^{(0)}(i)\right)_{i=1,}^{n}$$

is the simulated sequence, and

$$\omega = \left(\omega_{(1)}, \omega_{(2)}, ..., \omega_{(3)}\right),$$

is the weight sequence. The results of which are recorded and given by

$$W^{(0)} = \left(\omega_{(1)}\hat{x}^{(0)}(1), \omega_{(2)}\hat{x}^{(0)}(2), ..., \omega_{(n)}\hat{x}^{(0)}(n)\right).$$

The simulated values are then scaled against their associated weight. At this point, it is noteworthy to mention that the readjustment it meaningless, as the values have been manipulated to show better accuracies. Where the novelty of this paper lies, is that the values from the weight sequence are now applied to the parameter values, scaling them accordingly. Scaling either parameter *(-a)* or, *(-a)* AND *b*, by each weight value, and then recreating the GM model based on the new parameter values, an improvement on the overall accuracy and filter value can be made.

The fitness function of the GA was to reward candidates that provided an error of between -0.0002 and 0.0002. The reasoning for not wanting to create a weight that provided an absolute error of zero, was so that tiny granules of noise could still be allowed to exist in the system. This noise would represent the fluctuations between elements in the sequence. An exhaustive approach could be used, but the GA incorporates the essence of heuristics. The GA would create an initial random population of float values between the range of $[-1, 2]$, and process each candidate via the fitness function. The higher the score for the candidate the the higher the likelihood of reproducing and passing on its genes to future populations. After successive generations, the GA would present, and select at random the fittest members of the population for each of the simulated $\hat{X}^{(0)}$ values.

IV. Demonstration of the New Approach

The paper will now demonstrate the new approach, but firstly a new-information GM(1,1) and a metabolic GM(1,1) model must be created, based upon the same initial sequence. This will provide a basis for comparing the effectiveness of the new approach. Given the initial sequence (as presented in [7])

$$X^{(0)} = \left(x^{(0)}(i)\right)_{i=1}^{5} = (2.874, 3.278, 3.337, 3.390, 3.679).$$

To make use of the new-information model, an additional *new* element has to be added to the sequence, we are now presented with

$$X^{(0)} = \left(x^{(0)}(i)\right)_{i=1}^{6} = (2.874, 3.278, 3.337, 3.390, 3.679, \mathbf{3.85}),$$

and as such

$$B = \begin{bmatrix} -4.513 & 1 \\ -7.821 & 1 \\ -11.184 & 1 \\ -14.719 & 1 \\ -18.483 & 1 \end{bmatrix}, \qquad Y = \begin{bmatrix} 3.278 \\ 3.337 \\ 3.390 \\ 3.679 \\ 3.85 \end{bmatrix}$$

therefore the parameter values are given as follows

$$\hat{a} = [B^T B]^{-1} B^T Y = \begin{bmatrix} -0.0429054276246188 \\ 3.02008082902633 \end{bmatrix}$$

The corresponding time response sequence is

$$\begin{cases} \hat{x}^1(k+1) = 73.26324901 \cdot e^{-ak} - 70.38924901 \\ \hat{x}^0(k+1) = \hat{x}^1(k+1) - \hat{x}^1(k) \end{cases}$$

The results of the new-information model are presented in Table I. The average relative error of the entire model is

$$\Delta = \frac{1}{5}\sum_{k=2}^{6}\Delta = 1.4767\%$$

TABLE I. NEW INFORMATION GM(1,1)

No.	Original Data	Simulated Data	Errors	Relative Errors (%)	Accuracy (%)
2	3.278	3.2118	0.0662	2.02	97.98
3	3.337	3.3526	-0.0156	0.47	99.53
4	3.39	3.4996	-0.1096	3.23	96.77
5	3.679	3.6530	0.0260	0.71	99.29
6	3.85	3.8131	0.0369	0.96	99.04

Using the same initial sequence which created the new-information model, it is now used to create the metabolic model. For this to adhere to the nature of the metabolic approach, the first element in the sequence is deleted, and as a result, we are presented with the following sequence (as presented in [7])

$$X^{(0)} = \left(x^{(0)}(i)\right)_{i=1}^{5} = (3.278, 3.337, 3.390, 3.679, 3.85)$$

and as such

$$B = \begin{bmatrix} -4.9465 & 1 \\ -8.31 & 1 \\ -11.8445 & 1 \\ -15.609 & 1 \end{bmatrix}, \qquad Y = \begin{bmatrix} 3.337 \\ 3.390 \\ 3.679 \\ 3.85 \end{bmatrix}$$

$$\hat{a} = [B^T B]^{-1} B^T Y = \begin{bmatrix} -0.0515989937970014 \\ 3.03885124063102 \end{bmatrix}$$

The corresponding time response sequence is

$$\begin{cases} \hat{x}^1(k+1) = 62.17141085 \cdot e^{-ak} - 58.89341085 \\ \hat{x}^0(k+1) = \hat{x}^1(k+1) - \hat{x}^1(k) \end{cases}$$

The results of which are presented in Table II. The average relative error of the entire model is

$$\Delta = \frac{1}{4}\sum_{k=2}^{5}\Delta = 1.1385\%$$

TABLE II. METABOLIC GM(1,1)

No.	Original Data	Simulated Data	Errors	Relative Errors (%)	Accuracy (%)
2	-	-	-	-	-
3	3.337	3.2923	0.0447	1.34	98.66
4	3.39	3.4666	-0.0766	2.26	97.74
5	3.679	3.6502	0.0288	0.78	99.22
6	3.85	3.8435	0.0065	0.17	99.83

We should not only be concerned with the average relative error of both models, but also the relative error for the filter value at $t = n$, which in this case is element $\hat{x}^{(0)}(6)$. It can be seen in Table II, the filter value for the metabolic model (0.17%) has a lower relative error than the new-information model (0.96%), and therefore a higher level of accuracy. Also, the metabolic model has a lower average relative error (1.1385%) than that of the new-information model (1.4767%). The new approach is now applied to both models to show that improvements can be made to overall accuracy, and to the filter value accuracy.

A. The New Approach, Applied to the New-Information Model

By taking the simulated values contained in Table I, the GA was applied to each element in the sequence, providing a scaling weight for each element. Table III shows the weights along with the *new* errors and relative errors for the new-information model.

TABLE III. THE GENETIC ALGORITHM APPLIED WEIGHTS ON THE NEW INFORMATION MODEL

No.	Simulated Data	Weight	New Simulation	Errors	Relative Errors (%)
2	3.2118	1.0205913	3.278	0.0001	0.0021
3	3.3526	0.99537826	3.337	-0.0001	0.0025
4	3.4995	0.96866274	3.390	0.0001	0.0039
5	3.6529	1.0071266	3.679	0.0000	0.0010
6	3.8131	1.0096848	3.850	0.0000	0.0005

The weights are now scaled against the original parameters values of the new-information model in succession for both *(-a)* and *b*, the results of which can be seen in Table IV. The values contained in Table V are the results of the weights being applied to parameter *(-a)* only.

B. The New Approach, Applied to the Metabolic Model

The process is now repeated on the values contained in Table II for the metabolic GM(1,1) model, the results of which can be seen in Table VI.

TABLE VI. THE GENETIC ALGORITHM APPLIED WEIGHTS ON THE METABOLIC MODEL

No.	Simulated Data	Weight	New Simulation	Errors	Relative Errors (%)
2	-	-	-	-	-
3	3.2923	1.0136282	3.337	-0.0001	0.0037
4	3.4666	0.97787666	3.390	0.0001	0.0029
5	3.6502	1.0079083	3.679	0.0000	0.0009
6	3.8435	1.001712	3.850	0.0000	0.0011

The weights are then applied to the original parameters of the new metabolic model in succession for both *(-a)* and *b*, the results of which can be seen in Table VII. The values contained in Table VIII are the results of the weights being applied to parameter *(-a)* only.

TABLE IV. THE RESULTS OF THE BOTH PARAMETERS *(-a)* AND *b* BEING SCALED BY EACH WEIGHT VECTOR - THE NEW-INFORMATION MODEL

Weight	Relative Error $\hat{x}^{(0)}(2)$	Relative Error $\hat{x}^{(0)}(3)$	Relative Error $\hat{x}^{(0)}(4)$	Relative Error $\hat{x}^{(0)}(5)$	Relative Error $\hat{x}^{(0)}(6)$	New Parameter a	New Parameter b	Avg. Relative Error (%)
1.0205913	0.04	2.67	5.59	1.65	1.48	-0.0438	3.0823	2.2874
0.99537826	2.48	0.03	2.7	1.24	1.51	-0.0427	3.0061	1.5908
0.96866274	5.15	2.88	0.34	4.27	4.64	-0.0416	2.9255	3.4573
1.0071266	1.31	1.23	4.05	0.11	**0.12**	**-0.0432**	**3.0416**	**1.3609**
1.0096848	1.05	1.5	4.34	0.4	0.19	-0.0433	3.0493	1.4957

TABLE V. THE RESULTS OF PARAMETER *(-a)* BEING SCALED BY EACH WEIGHT VECTOR - THE NEW-INFORMATION MODEL

Weight	Relative Error $\hat{x}^{(0)}(2)$	Relative Error $\hat{x}^{(0)}(3)$	Relative Error $\hat{x}^{(0)}(4)$	Relative Error $\hat{x}^{(0)}(5)$	Relative Error $\hat{x}^{(0)}(6)$	New Parameter a	New Parameter b	Avg. Relative Error (%)
1.0205913	1.9	0.68	3.54	0.32	**0.48**	**-0.0438**	**3.0201**	**1.3853**
0.99537826	2.05	0.42	3.16	0.8	1.07	-0.0427	3.0201	1.4977
0.96866274	2.21	0.14	2.76	1.3	1.68	-0.0416	3.0201	1.6160
1.0071266	1.98	0.54	3.34	0.57	**0.8**	**-0.0432**	**3.0201**	**1.4455**
1.0096848	1.96	0.57	3.38	0.53	**0.74**	**-0.0433**	**3.0201**	**1.4340**

TABLE VII. THE RESULTS OF THE BOTH PARAMETERS *(-a)* AND *b* BEING SCALED BY EACH WEIGHT VECTOR - THE METABOLIC MODEL

Weight	Relative Error $\hat{x}^{(0)}(3)$	Relative Error $\hat{x}^{(0)}(4)$	Relative Error $\hat{x}^{(0)}(5)$	Relative Error $\hat{x}^{(0)}(6)$	New Parameter a	New Parameter b	Avg. Relative Error (%)
1.0136282	0.04	3.76	0.75	1.44	-0.0523	3.0803	1.4969
0.97787666	3.58	0.17	3.26	2.77	-0.0505	2.9717	2.4444
1.0079083	0.54	3.13	0.10	0.76	-0.052	3.0629	1.1346
1.0017126	1.17	2.44	0.60	**0.03**	**-0.0517**	**3.0441**	**1.0597**

TABLE VIII. THE RESULTS OF PARAMETER *(-a)* BEING SCALED BY EACH WEIGHT VECTOR - THE METABOLIC MODEL

Weight	Relative Error $\hat{x}^{(0)}(3)$	Relative Error $\hat{x}^{(0)}(4)$	Relative Error $\hat{x}^{(0)}(5)$	Relative Error $\hat{x}^{(0)}(6)$	New Parameter a	New Parameter b	Avg. Relative Error (%)
1.0136282	1.23	2.44	0.54	**0.15**	**-0.0523**	**3.0389**	**1.0905**
0.97787666	1.51	1.96	1.18	0.68	-0.0505	3.0389	1.3361
1.0079083	1.28	2.36	0.64	**0.01**	**-0.052**	**3.0389**	**1.0750**
1.0017126	1.33	2.28	0.75	**0.13**	**-0.0517**	**3.0389**	**1.1236**

TABLE IX. SUMMARY OF THE RESULTS FOR THE STANDARD NEW-INFORMATION MODEL AND THE METABOLIC MODEL

Model Type	Parameter a	Parameter b	Filter value $\hat{x}^{(0)}(5)$	Filter Value $\hat{x}^{(0)}(6)$
New-Info. Model	-0.0429054276246188	3.02008082902633	3.6530	3.8131
Metabolic Model	-0.0515989937970014	3.03885124063102	3.6502	3.8435
Model Type	**Errors $\epsilon(5)$**	**Errors $\epsilon(6)$**	**Relative Error (%) Δ_5**	**Relative Error (%) Δ_6**
New-Info. Model	0.026	0.0369	0.71	0.96
Metabolic Model	0.0288	0.0065	0.78	0.17

C. The Results

The paper will now describe the results of applying the new approach on both the new-information grey model, and the metabolic grey model. Table IX allows the reader to easily see the results of the filter values, errors, relative error and the accuracy for the standard new-information and the standard metabolic model in one summarized table. This provides as means to allow the reader to see the significance of the improvements.

The average relative error for the new-information model and the metabolic model, were given as 1.4766% and 1.1385%, respectively. This simple fact states that the metabolic model, overall, has less error and therefore higher accuracy than the new-information model. The relative error for filter value of $\hat{x}^{(0)}(5)$ for the new-information model is 0.71%, which out preforms the metabloic model, which has a relative error of 0.78%. However, as both sequences made use of a sixth element, the filter value for $\hat{x}^{(0)}(6)$ in this case is more important, as it is the moment when $t = n$. In which case, the

new information model has a relative error of 0.96%, whereas, the metabolic model has a relative error of 0.17%. This fact, coupled with the overall average relative error, means that the metabolic model in this instance is better suited for forecasting and predicting.

If the reader now refers to the values contained in Table IV, Table V, Table VII and Table VIII, one can see, in certain instances, a better result for the overall relative error and filter values, especially filter value $\hat{x}^{(0)}(6)$. The values highlighted in red bold text show the instances where an improvement has been made, for both the new-information model and the metabolic model. The highlighted instances state that when *that* particular weight is used in either scaling both parameters *(-a)* AND *b*, or just parameter *(-a)*, an improvement can be made for the overall average relative error, and an increase in the overall accuracy, and an increase for the filter value for $\hat{x}^{(0)}(6)$; for both the new-information model and the metabolic grey model. Echoing the sentiment of an improvement of the filter value when $t = n$, will allow for greater predictability thereafter for the immediate forecasted value.

It's noteworthy to mention that better gains are achieved when the weight values are used to scale parameter *-a* only, for both the new-information and metabolic models. As parameter *-a* is the development coefficient, and describes the development states of $X^{(1)}$ ans $\hat{X}^{(0)}$, representing this variance by a scaled value will possibly allow for greater efficiency, as seems to be the case.

V. Conclusion

The work presented in this paper proposes a novel way of improving the average relative errors, and thereby improving the overall accuracy for the new-information grey model and the metabolic grey model. Model selection is decided upon by the user, but the standard metabolic model seems to provide superior forecasting ability (according to the data sequence used). By using the approach presented in this paper, by applying it on either the new-information or metabolic model, one can improve the overall accuracy and filter value accuracy, whilst reducing the average relative error. According to the literature, genetic algorithms have been used before in the creation of grey models. However, they have been concentrated on finding optimal values for the α parameter, which in most cases is set to 0.5. By using a genetic algorithm for scaling the parameters, especially $(-a)$, greater improvements gains can be achieved for the standard models. The heuristic approach that a genetic algorithm applies, allows one to make use of the fitness function to evaluate possible candidates for the weight sequence. By rewarding candidates whose fitness function results are favorable, each successive population has ever fitter candidates. The allowance for noise to be factored into the fitness function, represents the *natural* noise fluctuations of the raw data. Hence, why scaling only parameter $(-a)$, the development coefficient, will often lead to better gains, as this parameter is representative of the variance contained in the data sequence. It has been shown, that using certain weights for scaling the parameters can produce better results, overall AND for the filter value for when $t = n$.

A. Future Work

The fitness function of the GA could be adjusted, so that either more noise could be incorporated into the system, or less noise. This adjustment could be regulated by an additional GA, and the results examined to see if additional improvements can be gained. Also, by inspecting the connotation associated with parameter *b*, one could derive a better scaling procedure to ensure that parameter *b* stays true to the data. Given a weight sequence before applying it to the parameters for scaling, it may be research worthy to investigate if one can easily identify which values will most likely improve upon the overall accuracy. As is shown in the results not all values from the weight sequence improve upon the accuracy of the models, this is only realized after the model is created. It would be far more efficient and effective if one could, with a high level of precision dictate which values of the weight sequence would improve upon the standard values for the accuracy overall.

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