

Parameter Estimation of Bouc–Wen Hysteretic Systems  
using SawTooth Genetic Algorithm

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## Abstract

This paper deals with the identification of a generic Bouc-Wen hysteretic system. It utilizes the so-called Sawtooth Genetic Algorithm that combines variable population size and periodic partial reinitialization of the population. It is shown that, although the complexity of the problem is significant, the Sawtooth GA can rapidly provide very accurate results for engineering purposes.

**Keywords:** Bouc-Wen, hysteretic systems, identification, parameter estimation, genetic algorithms.

## 1 Introduction

The Bouc-Wen hysteretic i.e. memory-dependent model is a versatile and efficient means to account for hysteretic phenomena. It was first introduced by Bouc [1] in 1967, but it was Wen [2] in 1976 who extended the model and demonstrated its versatility by producing a variety of hysteretic patterns, which were enhanced later by Baber and Noori [14] to incorporate non-symmetric behaviour and degradation phenomena.

From the mathematical view point it is a very concise model governed by a single non-linear differential equation that can be easily applied to several hysteretic phenomena in the fields of magnetism, electricity, materials and elasto-plasticity of solids. Examples include the response of R/C sections, steel sections, bolted connections, base isolators such as Lead Rubber Bearings (LRB), Friction Pendulum Systems (FPS) etc.

The standard form of a Single-Degree-Of-Freedom Bouc-Wen model includes eight parameters that govern the size and shape of the hysteretic loops. It is shown that some plausible assumptions can reduce the number of parameters to six;

however, the parameters may increase if the model is extended to include other phenomena, such as strength deterioration, stiffness degradation and pinching. Estimation of these parameters is the objective of this present work.

## 2 Bouc-Wen hysteretic model

### 2.1 Formulation

Considering a SDOF system, the restoring force can be written as:

$$F(t) = a \cdot \frac{F_y}{u_y} \cdot u(t) + (1-a) \cdot F_y \cdot z(t) \quad (1)$$

Where,  $F_y$  is the yield force,  $u_y$  is the yield displacement,  $a$  is the ratio of post-yield to pre-yield (elastic) stiffness and  $z(t)$  is a dimensionless hysteretic parameter obeying a single non-linear differential equation:

$$\dot{z}(t) = \frac{1}{u_y} \left[ A - |z(t)|^n \cdot (\gamma \cdot \text{sign}(\dot{u}(t) \cdot z(t)) + \beta) \right] \cdot \dot{u}(t) \quad (2)$$

Where,  $A, \beta, \gamma, n$  are dimensionless quantities controlling the behaviour of the model. In particular, small values of  $n$  ( $n > 0$ ) correspond to a smooth transition from the elastic to the plastic branch, whereas for large values of  $n$  ( $n > 10$ ) the transition becomes abrupt approaching that of a bilinear model. Parameter  $A$  was introduced in the original paper, but later it became evident that it is redundant. Parameters  $\beta, \gamma$  control the size and shape of the hysteretic loop.

If we denote  $K_0$  as the initial stiffness, then the restoring force, expressed by equation (1), can be analysed into two springs connected in parallel; the first spring is the post-yielding spring and the second is the hysteretic spring, as shown in Figure 1. The part of the force which corresponds to the hysteretic spring can be denoted as  $F^*$ .

With suitably selected values of parameters  $\beta, \gamma$  the model can produce hysteretic loops with strain hardening, as shown for example in Sues et al. [9]. However, since these parameters do not have a physical meaning, it is preferable for engineering purposes to introduce a dedicated strain-hardening spring connected in parallel with the springs of Figure 1, as proposed for example by Sivaselvan and Reinhorn [7]. Therefore, herein we will only consider the case of strain-softening systems, which allows for further simplification of the model.

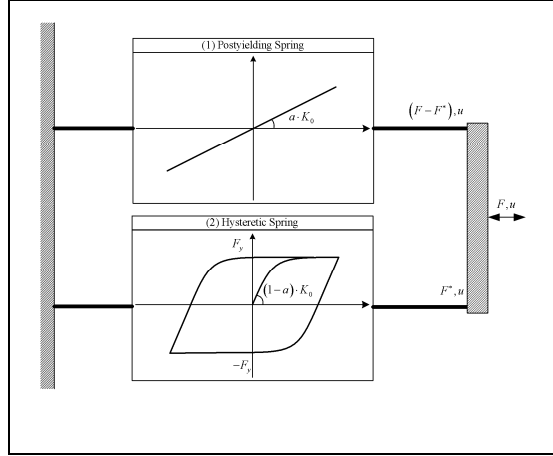


Figure 1: The restoring force analysed in a post-yielding and a hysteretic spring.

For the case of strain-softening systems, some conditions such as the initial stiffness and the hysteretic yield force allow for the decrement of the parameters. In order to calculate the initial stiffness, we impose a small displacement  $\Delta u$  into the system. From equation (1), the resulting restoring force can be written as:

$$\Delta F = \Delta \left[ a \cdot \frac{F_y}{u_y} \cdot u + (1-a) \cdot F_y \cdot z \right] = a \cdot \frac{F_y}{u_y} \cdot \Delta u + (1-a) \cdot F_y \cdot \Delta z \quad (3)$$

From the differential form of equation (2) by noting that  $A \gg z^n$  as the initial value of  $z$  is zero, one obtains:

$$\Delta z = \frac{A}{u_y} \Delta u \quad (4)$$

Combining equations (3) and (4), the following relation is obtained:

$$\Delta F = a \cdot \frac{F_y}{u_y} \cdot \Delta u + (1-a) \cdot F_y \cdot \frac{A}{u_y} \Delta u \quad (5)$$

The initial stiffness may be denoted as  $k_i = \Delta F / \Delta u$ , therefore:

$$k_i = a \cdot \frac{F_y}{u_y} + (1-a) \cdot \frac{F_y}{u_y} \cdot A \quad (6)$$

From equation (6), it is evident that if the initial stiffness of the system is equal to  $K_0 = F_y / u_y$ , then the parameter  $A$  should be equal to 1.

In addition, the yield force of the hysteretic spring should be equal to  $F_y$ . For example, if we consider only the hysteretic spring (i.e. by setting  $a = 0$ ) when it has passed yielding, the restoring force is expressed as:

$$F_{\max} = F_y \cdot z_{\max} \quad (7)$$

From equation (7) it results that the parameters of the model should be chosen in such a way that  $z_{\max} = \pm 1$ . Considering monotonic loading, the hysteretic spring yields and parameter  $z$  takes its maximum value which remains constant. Therefore,  $\dot{z}(t) = 0$  and from equation (2) one obtains:

$$\left\{ \begin{array}{l} \dot{u}(t) = 0 \\ or \\ A - |z(t)|^n \cdot (\gamma \cdot \text{sign}(\dot{u}(t) \cdot z(t)) + \beta) = 0 \end{array} \right\} \quad (8)$$

Moreover, in the general case:

$$z_{\max} = \pm \left( \frac{A}{\gamma \cdot \text{sign}(\dot{u}(t) \cdot z(t)) + \beta} \right)^{\frac{1}{n}} \quad (9)$$

In the case of monotonic loading,  $\dot{u}(t)$  and  $z(t)$  share the same sign. Therefore, from equation (9) and by noting that  $A = 1$  and  $z_{\max} = \pm 1$ , one obtains:

$$1 = \left( \frac{1}{\gamma + \beta} \right)^{\frac{1}{n}} \Rightarrow \gamma + \beta = 1 \quad (10)$$

Moreover, when the hysteretic spring yields and parameter  $z$  is constant, from equation (1) it is obtained:

$$\Delta F = \Delta \left[ a \cdot \frac{F_y}{u_y} \cdot u + (1-a) \cdot F_y \cdot z \right] = a \cdot \frac{F_y}{u_y} \cdot \Delta u \quad (11)$$

The post-yielding stiffness may be denoted as  $k_f = \Delta F / \Delta u$ , therefore:

$$k_f = a \cdot \frac{F_y}{u_y} = a \cdot K_0 \quad (12)$$

Equation (12) is consistent with the physical meaning of  $a$  as the ratio of post-yield to pre-yield (elastic) stiffness. Therefore, the conditions  $A = \beta + \gamma = 1$  allow for the simplification of the strain-softening model while providing consistency with the physical meaning of the chosen parameters. Moreover, this is achieved without any restrictions in the ability of the model to simulate hysteresis.

## 2.2 Identification

The identification of Bouc-Wen hysteretic systems poses a challenging problem. Many researchers have applied a variety of methods, such as genetic algorithms, differential evolution [11], extended Kalman filters, reduced gradient methods, Simplex methods [5], [9] etc.

The performance of these methods, with respect to both efficiency and accuracy, is in most cases problematic for the broad spectrum of hysteretic models that predict the response of inelastic structures. Genetic algorithms provide a promising solution for the identification problem for two main reasons: first, GAs use only “payoff” data i.e. no derivative data, for the evolution of the population and second, they feature an inherent capability for massive parallel computing. In light of this, in this work a new variant genetic algorithm proposed by Koumousis and Katsaras [6], namely Sawtooth GA, is applied to the identification problem of a SDOF Bouc-Wen hysteretic system.

## 3 Genetic Algorithms

### 3.1 General

Genetic algorithms (GAs) were introduced by John Holland at the University of Michigan in the 1960s. Holland’s introduction of generic algorithms was based on a population of chromosomes with crossover, inversion and mutation. Since then, many variations of GAs have been introduced and used successfully in many fields. Today, genetic algorithms together with evolution strategies and evolutionary programming form the field of evolutionary computation with a wide range of efficient solutions in many engineering problems.

One of the most important applications of GAs is optimization. GAs are widely considered very good global optimizers that can quickly search a huge space and provide good candidate solutions in a reasonable amount of time. However, their performance in discovering the actual local or global optimum is limited; therefore, GAs are often coupled with a local optimizer, such as “steepest ascend” hill climbing etc., which takes over when the progress of the GA degrades.

### 3.2 Saw-tooth GA

Recently, Koumouis and Katsaras [6] introduced a new genetic algorithm scheme that uses variable population size and partial reinitialization in a synergistic way to enhance performance. This approach was compared to standard or pure-GA and other GAs that use reinitialization of the population, such as the micro-GA or  $\mu$ GA, first suggested by Goldberg [10], with very good results.

The population size follows a predefined scheme, shown in Figure 2:

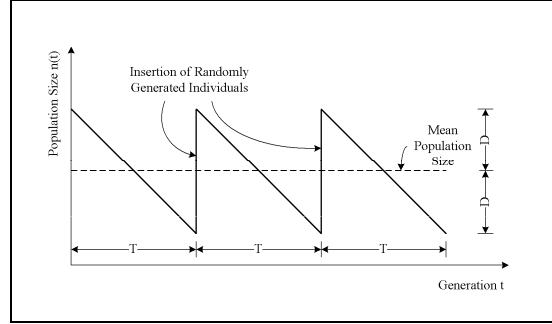


Figure 2: Population variation scheme.

The scheme is characterized by amplitude  $D$  and period of variation  $T$ . Thus, at a specific generation  $t$ , the population size  $n(t)$  is determined as:

$$n(t) = \text{int} \left\{ \bar{n} + D - \frac{2 \cdot D}{T-1} \cdot \left[ t - T \cdot \text{int} \left( \frac{t-1}{T} \right) - 1 \right] \right\} \quad (13)$$

Where  $\bar{n}$  is the mean population size. From the parametric studies with a large testbed of unimodal and multimodal problems, it became evident that strong reinitialization of the population, i.e. large values of  $D/\bar{n}$ , was beneficial for the performance of the GA. Moreover, moderate periods with values of  $T/\bar{n}$  (around 0.50) seem to perform well [6].

## 4 Analysis

### 4.1 Overview

In this work, a set of identification analyses for the SDOF Bouc-Wen hysteretic system was performed. The analyses were based on simulated noise-free data for various levels of mass and viscous damping; the simplification  $A=1$ ,  $\beta=1-\gamma$ , analyzed in paragraph 2.1, was made for all cases. The excitation used was the well-known El Centro accelerogram. Depending on the mass and viscous damping, the response varied from nearly linear elastic to strongly non-linear with well-defined hysteretic loops.

In this study, the identification was performed as one-stage process, i.e. the full range of values of parameters was used for the whole analysis. In order to increase performance, a multi-stage process that gradually reduces the range of values can be designed.

## 4.2 Response

GAs require the evaluation of the fitness value of a large number of candidate solutions, i.e. chromosomes. This is accomplished by using a fast fourth order Runge–Kutta method with constant step in the integration of the equations of motion together with the non-linear equation for the hysteretic parameter. It was found that this method was sufficiently accurate because of the small time-step and the small demand for accuracy in the calculation of the fitness of a chromosome. However, a more accurate and expensive method, based on Livermore stiff ODE integrator, was also implemented for the calculation of the reference response and for comparison purposes with respect to the simple fourth order Runge–Kutta method. The differences were found to be negligible for all cases.

## 4.3 Objective function

In this study, the mean square error (MSE) of the predicted displacement as compared to the reference time history was used as an objective function. In general, the discrete normalized form of the MSE of a predicted time history  $\hat{x}(t)$  as compared to a reference time history  $x(t)$  can be expressed as:

$$MSE = \frac{100}{n \cdot \sigma_{x_i}^2} \cdot \sum_{i=1}^n (x_i - \hat{x}_i)^2 \quad (14)$$

Where,  $\sigma_x^2$  the variance of the reference time history and  $n$  the number of points used. The reference displacement history of the SDOF model, i.e. the “correct” solution, was calculated for a known set of six parameters, namely  $\gamma$ ,  $n$ ,  $a$ ,  $c$ ,  $F_y$ ,  $u_y$ . The candidate solutions were produced by sets of parameters between a lower and an upper bound. Therefore, the optimization problem can be stated as the minimization of MSE when each parameter  $P_i$  is within the range specified by the following side constraints:

$$P_{i,\min} \leq P_i \leq P_{i,\max} \quad (15)$$

For some parameters, the range of values was chosen to be as wide as possible; for example  $a$  i.e. the ratio of post-yield to pre-yield (elastic) stiffness was set to take values between 0 and 1, inclusively. For other parameters, such as  $u_y$ , the range



was set to be one or two orders of magnitude around the true value. The mass of the system was considered known.

A minimum accuracy of  $10^{-6}$  was set for the predicted values of all parameters. The encoding length (in bits) for each parameter was calculated based on the range of values and the accuracy. Note that, on purpose, the range and accuracy were not chosen in such a way so as to produce a convenient  $2^k$  search space. Therefore, the exact values of the parameters were not included in the search space.

#### 4.4 Selection, crossover and mutation scheme

In order to avoid premature convergence of the GA, Koumoussis and Katsaras [6] propose the use of elitism and tournament or rank selection scheme. The reason for this is that, in general, a population may include individuals with very different fitness values, especially when the amplitude  $D$  is very big. These populations tend to be overrun very fast by the individuals with high fitness, thus degrading the performance of the GA. Therefore, a proper selection scheme, or another technique such as hypermutation is needed to avoid this phenomenon. In this work, however, the selection scheme used was the biased roulette wheel. It was observed that even fitness – proportionate selection schemes, such as the biased roulette wheel paired with elitism can perform well, provided that proper scaling of the fitness values takes place.

In order to perform proper scaling, a large value, i.e.  $MSE_{\max} = 10^6$ , was set as an upper bound for the MSE of chromosomes. The reason is twofold; first, it is not rare phenomenon to observe overflow of double precision variables during the calculation of the MSE. The overflow is captured by the error handler of the routine and the maximum value of MSE is assigned to the chromosome. Second, if the MSE of a chromosome nearly overflows the double data type, then after scaling, the fitness values of all other chromosomes are almost the same. This may lead to loss of promising chromosomes as they fail to produce offspring. Scaling was performed using the linear method proposed by Goldberg [12] with  $C_{mult} = 2$ , where  $C_{mult}$  is the desired number of expected copies for the best individual.

A single-point crossover scheme with probability 0.7 was adopted. The mutation scheme included jump mutation with probability  $1/N$  and creep mutation with probability  $(L_{bit}/N)/N_{par}$ , where  $N$  is the current population size,  $L_{bit}$  is the length of the chromosome in bits and  $N_{par}$  is the number of parameters.

#### 4.5 Computational details

For the purposes of the GA analysis, a long period ( $>2 \cdot 10^{18}$ ) random number generator of L'Ecuyer with Bays-Durham shuffle and added safeguards [13] was

used. The typical chromosome length was 132 bits. The population size followed a predefined saw-tooth scheme with mean value  $\bar{n} = 25$ , amplitude  $D = 15$  and period  $T = 15$ .

Three cases of mass were considered, with five cases of viscous damping each. Viscous damping was equal to 0%, 5%, 10%, 20% and 30% of critical value. Each of the 15 cases was run 100 times; each run evolved for 3000 generations, followed by hill climbing for the best individual.

The following table (Table 1) presents the true values and the range of the parameters used in the GA analysis:

Parameter	True Value	$c_{true} < 10$		$c_{true} > 10$	
		Lower Bound	Upper Bound	Lower Bound	Upper Bound
$\gamma$	0.900	0.000	1.000	0.000	1.000
$n$	2.000	1.000	10.000	1.000	10.000
$c$	varies	0.000	10.000	10.000	20.000
$a$	0.100	0.000	1.000	0.000	1.000
$F_y$	2.860	0.100	10.000	0.100	10.000
$u_y$	0.111	0.001	1.000	0.001	1.000

Table 1: True values and range of parameters.

## 4.6 Software

For the purposes of this study, a custom computer program with full graphical interface and a GA library was developed. The software, shown in Figure 3, allowed visual inspection of the progress of the analysis and produced a full log for further processing.

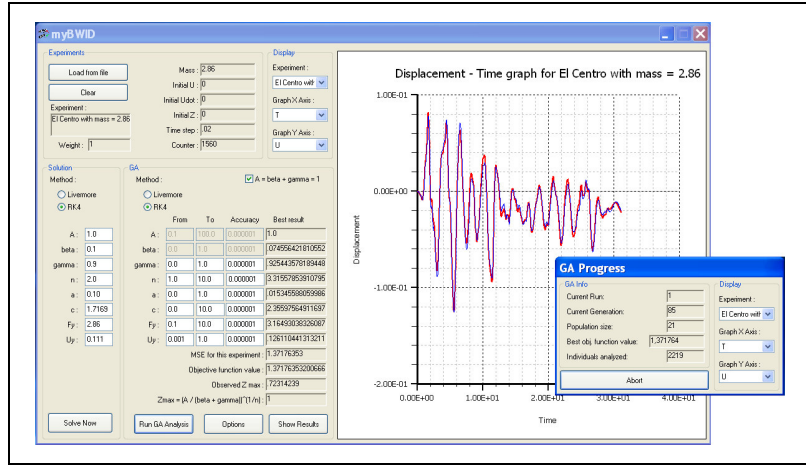


Figure 3: Screenshot of developed software

## 5 Results

### 5.1 Reduced set of parameters

The following tables summarize the predicted parameters for the best individual of all 100 runs:

Parameter	$c = 0.0000$	$c = 0.8585$	$c = 1.7169$	$c = 3.4338$	$c = 5.1507$
$\gamma$	0.924316	0.968751	0.812500	0.875000	0.937500
$n$	2.125000	2.037659	1.984375	1.914062	2.054688
$c$	0.039673	0.781249	1.728515	3.417663	5.161133
$a$	0.103516	0.101562	0.093749	0.090317	0.109375
$F_y$	2.835431	2.797363	2.818928	2.923047	2.840869
$u_y$	0.110510	0.108557	0.108375	0.113192	0.110754

Table 2: Predicted values of parameters for case I ( $m=2.86$ )

Parameter	$c = 0.0000$	$c = 1.9195$	$c = 3.8390$	$c = 7.6780$	$c = 11.5170$
$\gamma$	0.976563	0.703125	0.898438	0.861328	0.906250
$n$	2.085655	1.914063	1.958007	1.914062	2.019531
$c$	0.000000	2.187500	3.750000	7.623291	11.532879
$a$	0.101563	0.107422	0.097167	0.097655	0.102882
$F_y$	2.894043	2.700382	2.884375	2.889209	2.840869
$u_y$	0.113496	0.102704	0.111240	0.111640	0.110265

Table 3: Predicted values of parameters for case II (m=14.3)

Parameter	$c = 0.0000$	$c = 2.7146$	$c = 5.4292$	$c = 10.8584$	$c = 16.2875$
$\gamma$	0.921875	0.859375	1.000000	0.812501	0.968995
$n$	2.125000	2.072265	2.177185	1.914062	2.018982
$c$	0.097656	2.890625	5.625000	10.879517	16.250000
$a$	0.101563	0.101563	0.102142	0.097961	0.097655
$F_y$	2.836186	2.803783	2.865039	2.826367	2.923047
$u_y$	0.111057	0.108740	0.113802	0.108307	0.114168

Table 4: Predicted values of parameters for case III (m=28.6)

The following tables summarize the error in the prediction of the parameters for the best individual of all 100 runs:

Parameter	$c = 0$	$c = 0.05 \cdot c_{cr}$	$c = 0.10 \cdot c_{cr}$	$c = 0.20 \cdot c_{cr}$	$c = 0.30 \cdot c_{cr}$
$\gamma$	2.702%	7.639%	9.722%	2.778%	4.167%
$n$	6.250%	1.883%	0.781%	4.297%	2.734%
$c$	-	8.998%	0.677%	0.470%	0.203%
$a$	3.516%	1.562%	6.251%	9.683%	9.375%
$F_y$	0.859%	2.190%	1.436%	2.204%	0.669%
$u_y$	0.442%	2.200%	2.365%	1.974%	0.222%

Table 5: Error (%) in the prediction of parameters for case I (m=2.86)

Parameter	$c = 0$	$c = 0.05 \cdot c_{cr}$	$c = 0.10 \cdot c_{cr}$	$c = 0.20 \cdot c_{cr}$	$c = 0.30 \cdot c_{cr}$
$\gamma$	8.507%	21.875%	0.174%	4.297%	0.694%
$n$	4.283%	4.297%	2.100%	4.297%	0.977%
$c$	-	13.962%	2.318%	0.713%	0.138%
$a$	1.563%	7.422%	2.833%	2.345%	2.882%
$F_y$	1.190%	5.581%	0.852%	1.021%	0.669%
$u_y$	2.249%	7.474%	0.217%	0.576%	0.662%

Table 6: Error (%) in the prediction of parameters for case II (m=14.3)

Parameter	$c = 0$	$c = 0.05 \cdot c_{cr}$	$c = 0.10 \cdot c_{cr}$	$c = 0.20 \cdot c_{cr}$	$c = 0.30 \cdot c_{cr}$
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$\gamma$	2.431%	4.514%	11.111%	9.722%	7.666%
$n$	6.250%	3.613%	8.859%	4.297%	0.949%
$c$	-	6.484%	3.606%	0.194%	0.230%
$a$	1.563%	1.563%	2.142%	2.039%	2.345%
$F_y$	0.833%	1.966%	0.176%	1.176%	2.204%
$u_y$	0.052%	2.036%	2.525%	2.426%	2.854%

Table 7: Error (%) in the prediction of parameters for case III (m=28.6)

The following table (Table 8) summarizes the MSE for the best individual of all 100 runs for each case:

	$c = 0$	$c = 0.05 \cdot c_{cr}$	$c = 0.10 \cdot c_{cr}$	$c = 0.20 \cdot c_{cr}$	$c = 0.30 \cdot c_{cr}$
$m = 2.86$	0.014390%	0.044956%	0.016365%	0.001775%	0.001615%
$m = 14.3$	0.005248%	0.026854%	0.004543%	0.002519%	0.000335%
$m = 28.6$	0.003343%	0.003093%	0.003270%	0.000871%	0.002052%

Table 8: MSE (%) of the best individual for all cases

From the above it is evident that, although the predicted values of the parameters may differ from the true values considerably, the GA was always able to find sets of parameters with very low MSE (lower than 0.05%). The response graph of these chromosomes almost coincides with the reference graph. This phenomenon can be attributed to the fact that changes in different parameters can produce similar change in the whole response, depending on the excitation and the characteristics of the model.

Taking into consideration the wide range of the parameters, the predicted values were consistently close to the true values. One can notice that parameter  $a$  (ratio of post-yield to elastic stiffness), yield force  $F_y$  and yield displacement  $u_y$ , are better identified in case III which produces the more well-defined hysteretic loops. This is expected since these parameters are related to geometric properties of the hysteretic loop.

## 5.2 Full set of parameters

In order to demonstrate the redundancy of the parameters, a set of analyses was conducted for case I (m=2.86) and five cases of viscous damping, taking into consideration the full set of parameters. Parameter  $A$  was set to take values between 0.1 and 100.0 inclusively while parameter  $\beta$  was set to take values between 0.0 and 1.0, inclusively. The population size followed a modified saw-tooth scheme with

mean value  $\bar{n} = 50$ , amplitude  $D = 40$  and period  $T = 25$ . All other options were held the same as the ones used for the analyses of the reduced set of parameters.

The following table summarizes the predicted parameters for the best individual of all 100 runs:

Parameter	$c = 0.0000$	$c = 0.8585$	$c = 1.7169$	$c = 3.4338$	$c = 5.1507$
$A$	68.781	85.513	53.660	57.859	2.865
$\beta$	0.069	0.125	0.133	0.098	0.062
$\gamma$	0.594	0.469	0.705	0.532	0.779
$n$	1.984	2.195	1.967	1.956	2.195
$c$	0.001	0.957	1.746	3.438	5.234
$a$	0.894	0.913	0.839	0.858	0.236
$F_y$	2.287	2.913	1.986	1.809	1.896
$u_y$	0.727	0.943	0.725	0.633	0.179
$MSE$	0.051 %	0.053 %	0.013 %	0.001 %	0.008 %

Table 9: Predicted values of parameters for case I ( $m=2.86$ ) (full set of parameters)

From the above it is evident that, again, the GA was able to find sets of parameters with very low MSE. However, the predicted values of the parameters may be significantly different from the true values. In most cases, a large value of  $a$  (ratio of post-yield to pre-yield stiffness) was found; in this case, the response of the system approached that of the equivalent linear oscillator.

## 6 Conclusions

A Genetic Algorithm called Sawtooth GA was applied to the demanding task of the identification of a generic Bouc-Wen hysteretic system. The GA combines variable population size and periodic partial reinitialization of the population to enhance performance. It is also coupled with a local optimizer based on the “steepest ascend” hill climbing method.

It was shown that the initial form of the hysteretic system can be simplified by plausible assumptions based on the physical meaning of the parameters. The identification process was implemented with the reduced set of six parameters. Although the range of the parameters was very wide, the GA was able to produce very good solutions in a small amount of time.

During the calculations, it was observed that the performance of Sawtooth GA was similar to micro GA. Both methods were far superior to standard GA. However, the performance of the GA is encumbered because of the big chromosome length. A

multi-stage identification scheme that gradually narrows down the ranges of the parameters would facilitate further the identification process.

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