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**myBWID**  
**version 1.0**

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# 1. Introduction

## **1.1 Scope**

This document describes in brief the usage of myBWID version 1.0. The Bouc-Wen model is described in chapter 2. Next, the main features of the program are presented through a number of selected examples.

## **1.2 Program requirements**

The minimum requirements are:

- Operating System: Microsoft® Windows /NT/2000/XP/Vista
- Visual Basic 6 Service Pack 5 runtime libraries.

## **1.3 Abbreviations**

SDOF:           Single Degree of Freedom

ODE:            Ordinary Differential Equation

## **1.4 About myBWID (my Bouc-Wen IDentification) version 1.0**

This program employs evolutionary algorithms for the identification of SDOF Bouc-Wen hysteretic systems. Apart from hysteretic damping, the identification may include viscous type effects. The program was developed and used for research purposes. The main results of this research were published recently [1].

The hybrid evolutionary algorithm described in [1] is implemented within the program. However, other Genetic Algorithms (GAs) including standard GA, microGA, Sawtooth GA [5] etc can also be used. In addition, a greedy ascent hill climber (GAHC) may be employed which greatly improves performance.

Some important notes:

- The software is provided "as is". Make sure to read the terms of usage in the about form.

- At this moment, this manual provides only a small number of guidelines on how to use the software. Future releases of this manual will include the description of more program features.
- The performance of all algorithms described in [1] was measured with respect to the number of function evaluations, not the time needed to conclude the analysis. The program has *not* been designed to provide the fastest execution possible. A number of system parameters have been set in such a way so as to facilitate debugging, although they may entail a significant overhead. These include the frequent redrawing of the response of the current best result and the output of a complete analysis report which describes all stages of execution.
- If you are interested in this work or require further information, do not hesitate to contact professor V.K. Koumouisis ([vkoum@central.ntua.gr](mailto:vkoum@central.ntua.gr)) or A.E. Charalampakis ([achar@mail.ntua.gr](mailto:achar@mail.ntua.gr))

## 2. Bouc Wen Model

### 2.1 General

The Bouc – Wen model is a smooth hysteretic model which is very popular because of its versatility and simplicity. It was first introduced by Bouc in 1967 [2]. In 1976, Wen [3] extended the model and demonstrated its versatility by producing a variety of hysteretic patterns.

### 2.2 Formulation

According to Bouc-Wen model, the restoring force of a SDOF system can be written as:

$$F(t) = a \cdot \frac{F_y}{u_y} \cdot u(t) + (1-a) \cdot F_y \cdot z(t) \quad (7.2.1)$$

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 differential equation with zero initial condition:

$$\dot{z}(t) = \frac{1}{u_y} \left[ A - |z(t)|^n \cdot (\gamma \cdot \text{sign}(\dot{u}(t)) \cdot z(t) + \beta) \right] \cdot \dot{u}(t) \quad (7.2.2)$$

where,  $A, \beta, \gamma, n$  are dimensionless quantities controlling the shape of the hysteresis loop.

The equation of motion for a SDOF system with linear viscous damping  $c$  is given as:

$$m \cdot \ddot{u}(t) + c \cdot \dot{u}(t) + F(t) = f(t) \quad (7.2.3)$$

where,  $u(t)$  is the displacement,  $F(t)$  is the restoring force,  $f(t)$  is the excitation force. Substituting (7.2.1) into (7.2.3) we obtain:

$$m \cdot \ddot{u}(t) + c \cdot \dot{u}(t) + a \cdot \frac{F_y}{u_y} \cdot u(t) + (1-a) \cdot F_y \cdot z(t) = f(t) \quad (7.2.4)$$

Equations (7.2.2) and (7.2.4) are transformed into a state-space form as follows:

$$\begin{cases} x_1(t) = u(t) \\ x_2(t) = \dot{u}(t) \\ x_3(t) = z(t) \end{cases} \quad (7.2.5)$$

$$\begin{cases} \dot{x}_1(t) \\ \dot{x}_2(t) \\ \dot{x}_3(t) \end{cases} = \begin{cases} x_2(t) \\ -\frac{1}{m} \cdot \left[ c \cdot x_2(t) + a \cdot \frac{F_y}{u_y} \cdot x_1(t) + (1-a) \cdot F_y \cdot x_3(t) - f(t) \right] \\ \frac{1}{u_y} \cdot \left[ \left( A - |x_3(t)|^n \cdot \left( \gamma \cdot \text{sign}(x_2(t) \cdot x_3(t)) + \beta \right) \right) \cdot x_2(t) \right] \end{cases} \quad (7.2.6)$$

The above system of three first order non-linear ODEs is solved numerically following Runge-Kutta 4<sup>th</sup> – 5<sup>th</sup> order or Livermore stiff ODE integrator which is based on a “predictor-corrector” scheme [4].

### **2.3 Parameter Constraints**

A number of parameter constraints are necessary. In particular,  $A=1$  and  $\beta + \gamma = 1$  should be imposed for reasons of physical consistency of the model [1]. By default, these constraints are active in the program. You can choose to deactivate the constraints by using the check boxes in the “GA” frame of the main window. However, this is not recommended.

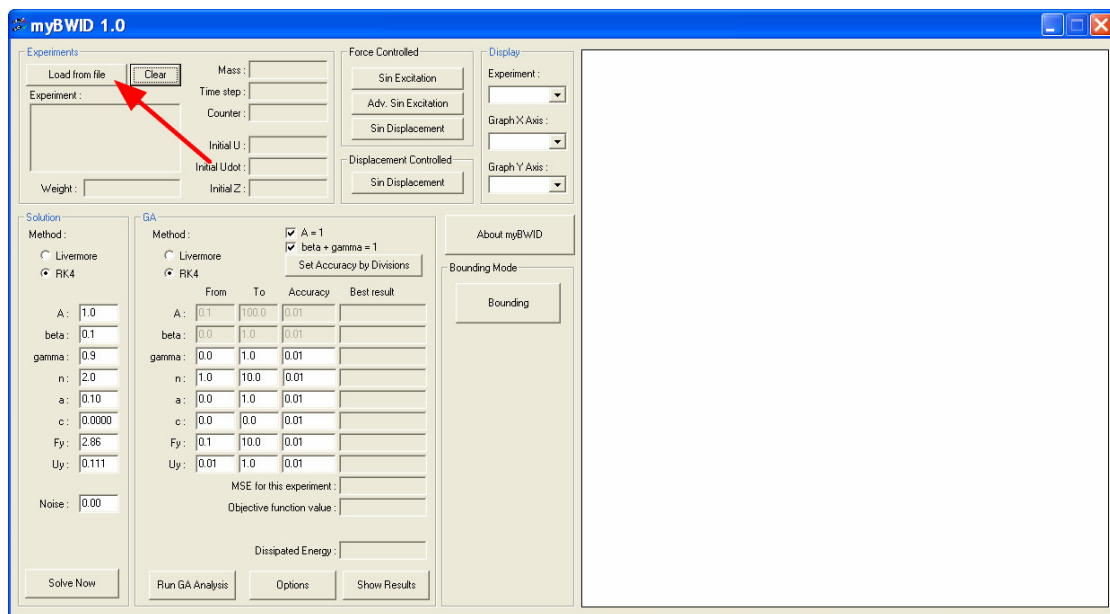
## 3. Example 1: El Centro excitation

### 3.1 General

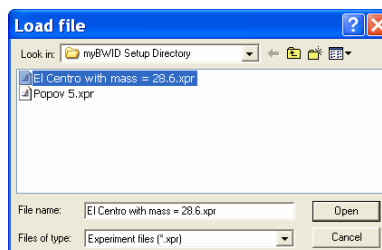
The usage of this program will be described through examples. The first example refers to a SDOF system under the El Centro excitation.

### 3.2 Excitation

The first step is to define the excitation. Click the "Load from file" button at the top left corner:

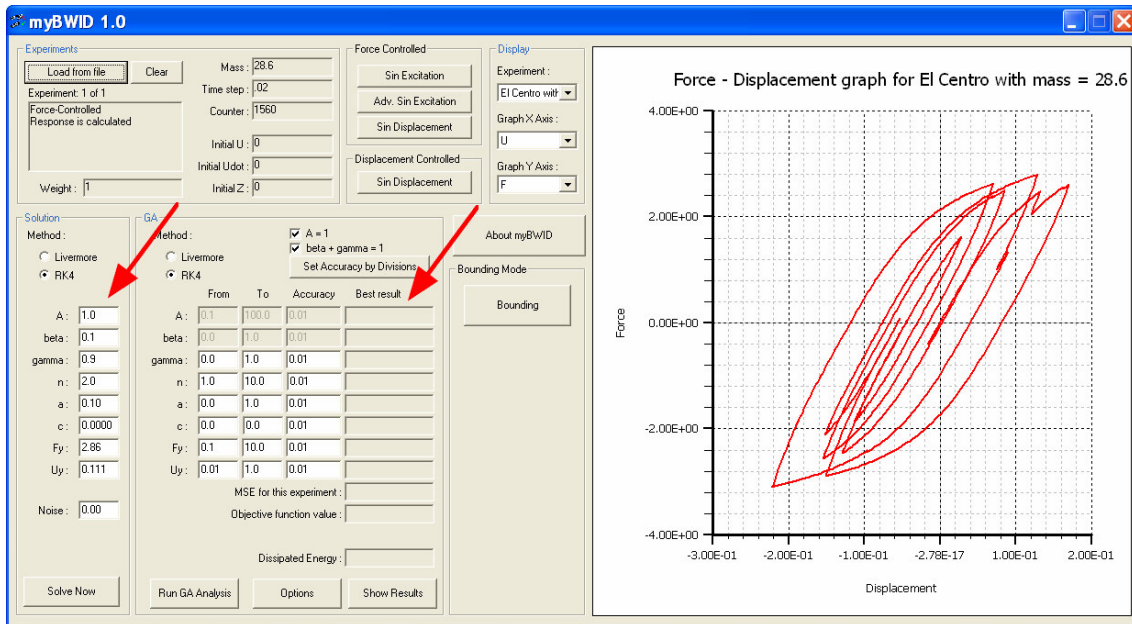


Select the "El Centro with mass = 28.6.xpr" file from the main directory of the program:



As soon as you load the file, the program will evaluate the response of the model. Consistent unit system is used. The "true" model parameters are provided by the frame entitled "Solution" on the left. When identification is under way, the model

parameters corresponding to the current best result are summarized within the "GA" frame, under the "Best result" label.

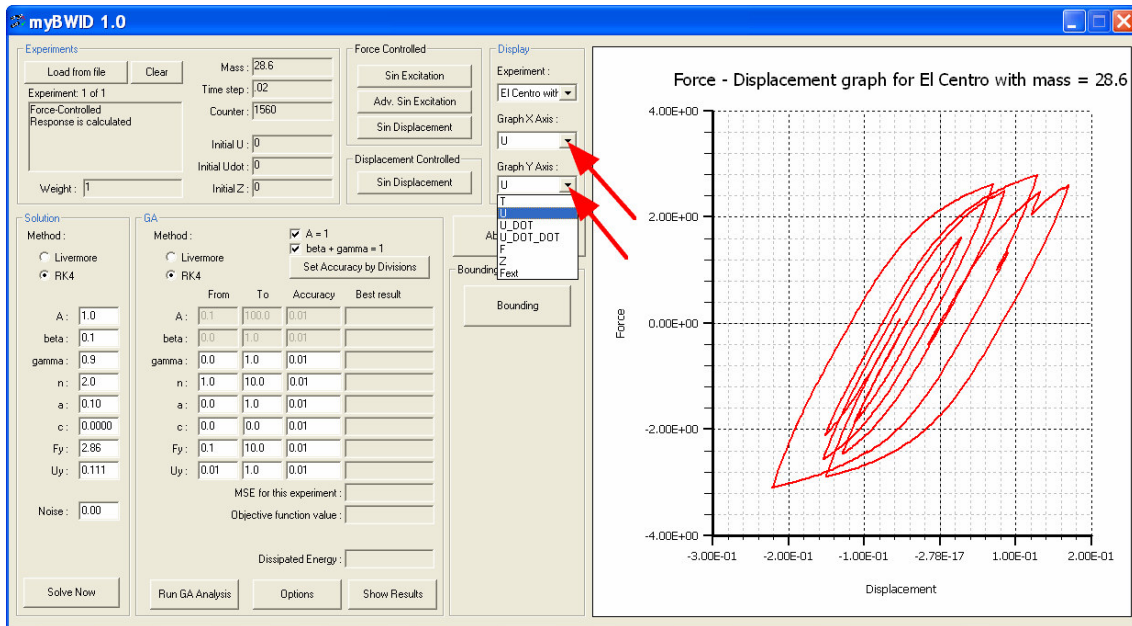


### 3.3 Graph

The program automatically draws the response of both the "true" and "identified" model in a picture box on the right of the main window. The graph of "true" response of the model is drawn using a thick red line. The response of the current best result of identification is drawn using a thin blue line.

You can select the quantity that corresponds to the X and Y axes by using the drop-down lists in the "Display" frame:





### 3.4 Objective Function

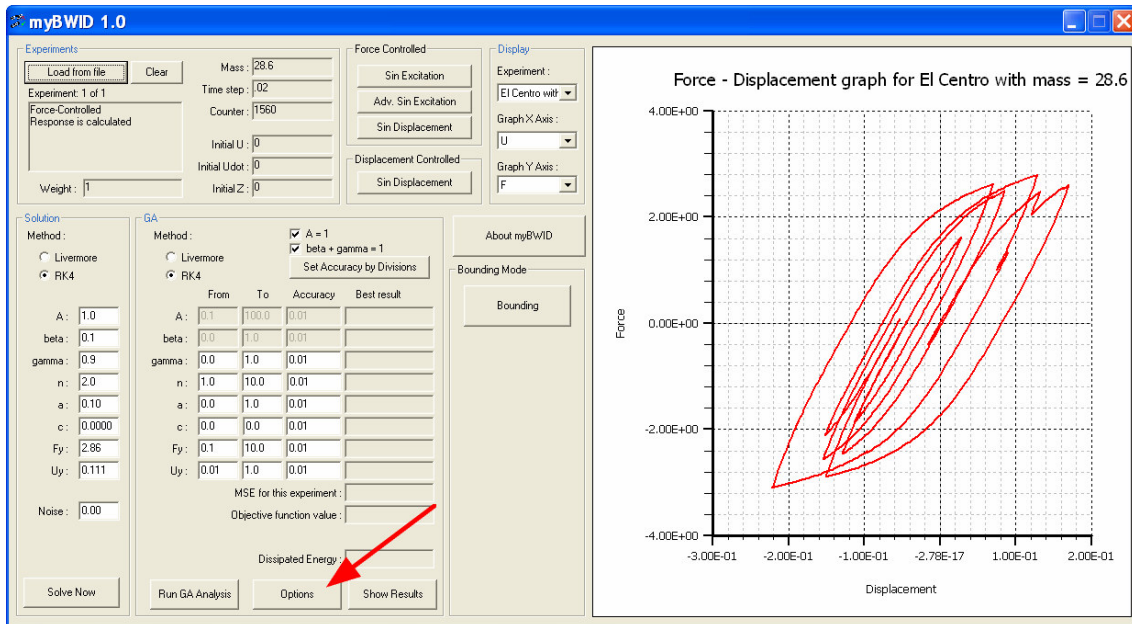
The normalized Mean Squared Error (MSE) of the predicted time history  $\hat{y}(t|\mathbf{p})$  as compared to the reference time history  $y(t)$  is used as objective function. When cast in discrete form, it can be expressed as:

$$OF(\mathbf{p}) = \frac{\sum_{i=1}^N (y(t_i) - \hat{y}(t_i|\mathbf{p}))^2}{N \cdot \sigma_y^2} \quad (1)$$

where,  $\mathbf{p}$  is the parameter vector,  $\sigma_y^2$  the variance of the reference time history and  $N$  the number of points used. The time history of the displacement and external force is used for force- and displacement-controlled experiments, respectively.

### 3.5 GA Analysis

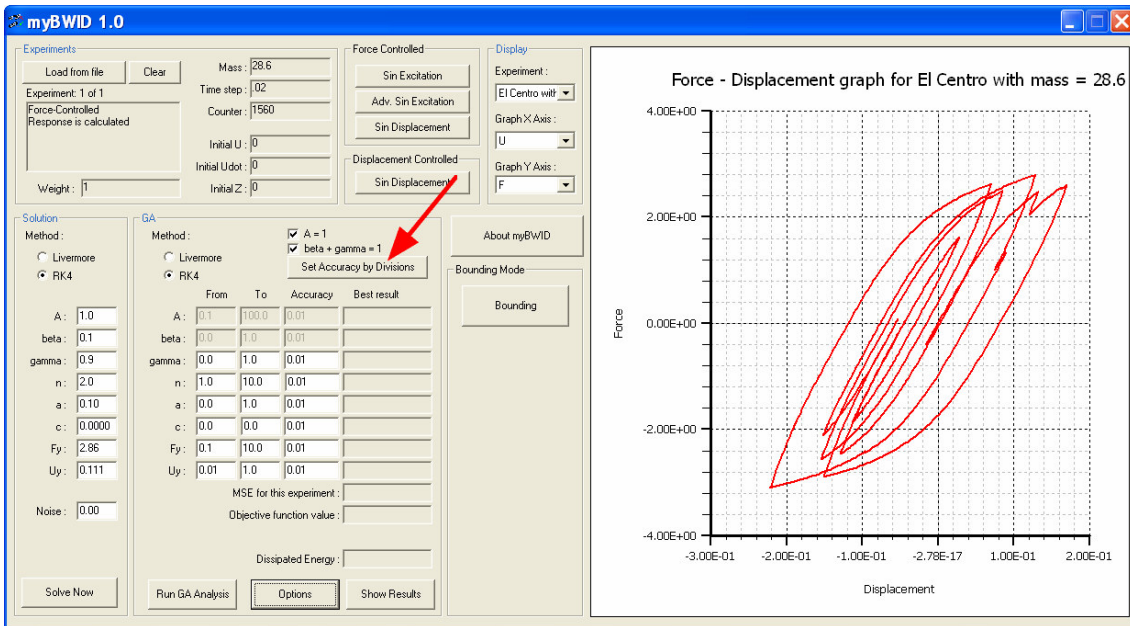
In order to perform a GA analysis, click the "Options" button:



Make the appropriate selections in the options form:

The default GA options include the usage of Sawtooth GA [5] with mean population size equal to 25, amplitude of variation equal to 20 and period 5 generations. In addition, a hill climber is employed when the GA analysis has concluded.

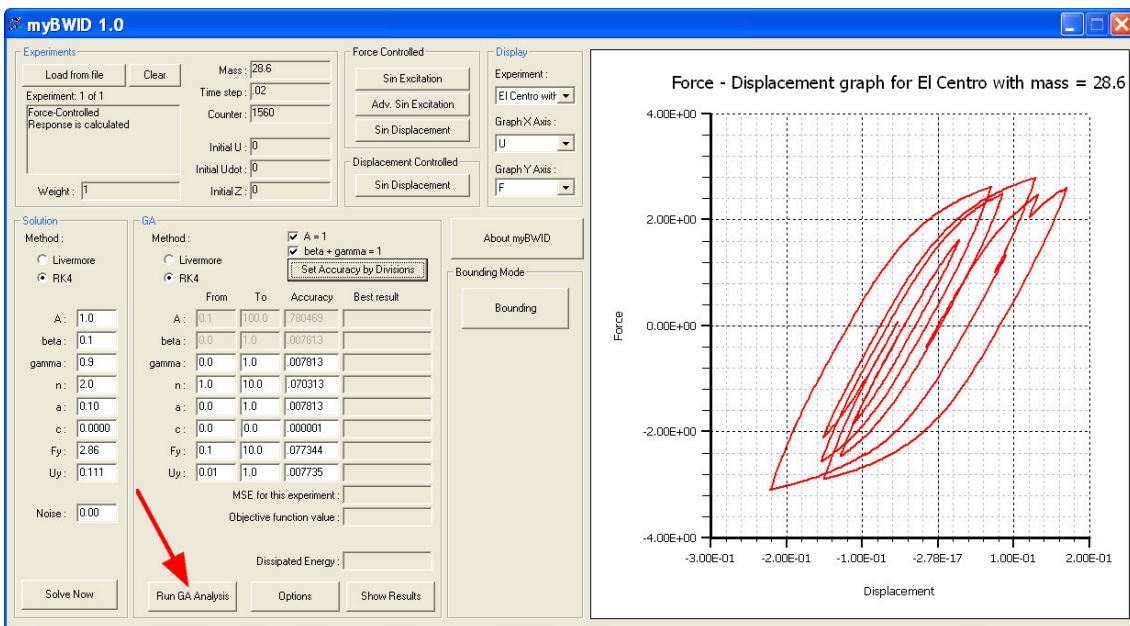
Click the "Set accuracy by divisions" button in the main form:



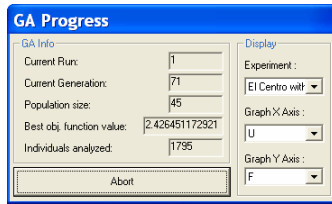
Select the number of divisions that will be applied to the current parameter ranges, as defined within the "GA" frame. This governs the length of the chromosome. Using 128 ( $=2^7$ ) divisions per parameter results in a chromosome length equal to 7 times the number of parameters to be identified.

By default, the lower and upper boundary of the viscous damping coefficient is equal. This means that the viscous damping coefficient will not be identified.

Hit the "Run GA Analysis" button:



Select "0" as the seed for the random number generator. A progress form appears:



The response of best identified result is displayed in blue in the main window. Hit "Abort" once to abort GA analysis and invoke the hill climber directly. Hit "Abort" again to abort the hill climbing analysis.

Hit "Show Results" in the "GA" frame to open the output file of the last analysis executed:

```

myGA.out - Notepad
File Edit Format View Help
=====
myGA analysis started at: 19/3/2008 6:38:54 µµ
Options:
Seed used: -6200
Maximum runs: 1
  Elitism between runs: Yes
  Elite individuals: 1
For each run:
  Population size variation: Saw-Tooth
  Mean value N: 25
  Period T: 5
  Amplitude D: 20
  Maximum generations: 3000
  Convergence criterion: No
GA:
  Selection method: Biased Roulette Wheel
  Niching: No
  Crossover method: Single Point
  Probability: .7
  Children per crossover: One
  Jump mutation: No
  Creep mutation: No
  Elitism between generations: Yes
  Elite individuals: 1
Objective function value check: Yes
  Target objective function value: 0
  Stop when best objective function value is LOWER than or EQUAL to target
Best individual endurance check: No
Output file is appended whenever the best individual changes
Objective function value rounding: No

Total chromosome length (bits): 35
Variables:
  Variable 1:
    Title: A
    Type: Real
    Locked value: 1
  Variable 2:
    Title: beta
    Type: Real
    Locked value: .1

```

### 3.6 Bounding Analysis

A new hybrid identification scheme that is based on bounding of parameters was presented recently [1]. The algorithm is implemented within the program. A brief description of the algorithm is presented below; for more information refer to the published paper or contact the authors.

According to the method presented in [1], identification is performed in stages. Initially, very wide feasible ranges of parameters are specified which are guaranteed to include the optimum values.

Next,  $M_r$  short independent GA analyses are performed. These consist of Sawtooth GA [5] followed by Greedy Ascent Hill Climbing (GAHC) [6]. These analyses can be performed in parallel within a computer network, thus reducing drastically the computational time. The results are gathered, sorted and the worst  $M_t$  ones are truncated (ignored).

Considering the remaining  $M_r - M_t$  solutions, weight coefficients are assigned as follows:

$$w_k = \frac{\max_k(OF_k)}{OF_k} \quad (2)$$

where,  $OF_k$  is the objective function value of the  $k^{th}$  solution. According to the above formulation, the worst solution is assigned a weight of unity. The weighted mean value of parameter  $i$  is calculated as follows:

$$m_i = \frac{\sum_{k=1}^{M_r-M_t} (w_k \cdot p_{ik})}{\sum_{k=1}^{M_r-M_t} (w_k)} \quad (3)$$

where,  $p_{ik}$  is the value of parameter  $i$  of the  $k^{th}$  solution. The descriptive weighted standard deviation is expressed as:

$$s_i = \sqrt{\frac{\sum_{k=1}^{M_r-M_t} (w_k \cdot (p_{ik} - m_i)^2)}{\sum_{k=1}^{M_r-M_t} (w_k)}} \quad (4)$$

The new trial upper and lower bounds of parameter  $i$  are defined symmetrically around the weighted mean value  $m_i$  as follows:

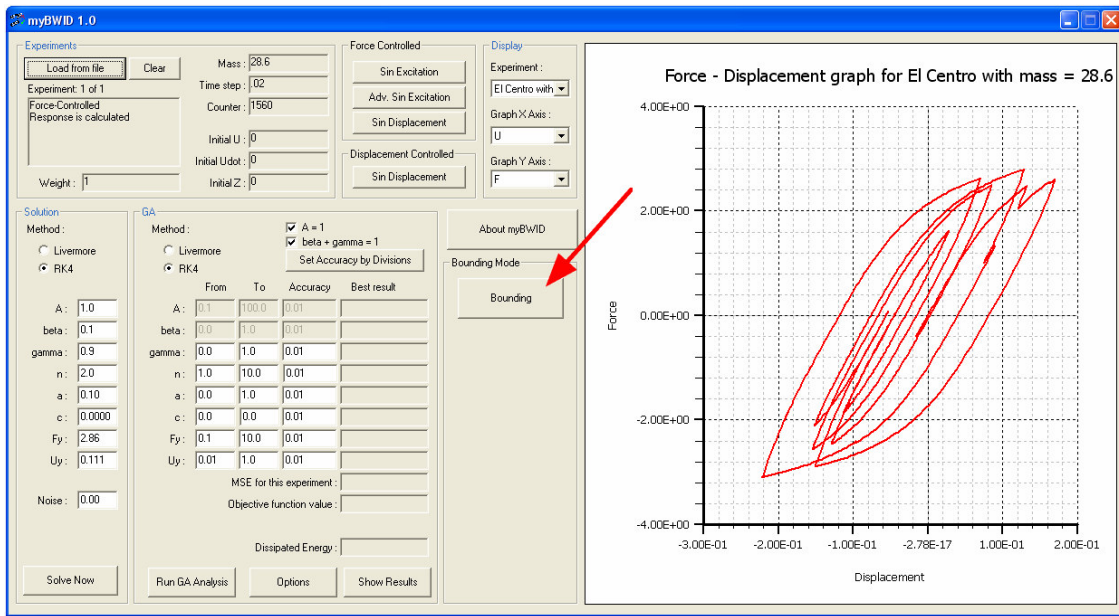
$$\begin{aligned} \bar{u}_{i,j+1} &= m_i + q \cdot s_i \\ \bar{l}_{i,j+1} &= m_i - q \cdot s_i \end{aligned} \quad (5)$$

where,  $q$  is a real coefficient which represents the semi-width of the new trial range in terms of standard deviations. Finally, the feasible domain of parameter  $i$  in the next optimization step is defined as the intersection of the current range with the trial range:

$$[l_{i,j+1}, u_{i,j+1}] = [l_{ij}, u_{ij}] \cap [\bar{l}_{i,j+1}, \bar{u}_{i,j+1}] \quad (6)$$

This process is repeated until the ratio of the current feasible range to the initial feasible range reaches a specific value ( $10^{-4}$  by default) for all model parameters. At this point, the upper and lower bounds of all parameters almost coincide. This consists a very convenient termination criterion.

To perform Bounding analysis, make sure you have loaded the "El Centro with mass=28.6.xpr" file. Then, hit the "Bounding" button:



The following form appears:

The following settings can be changed:

- *Runs.Start/End* is the number  $M_r$  of independent short GA analyses at the beginning and at the end of identification. A linear progress rule is implemented within the program, as analyzed in [1].
- *Trunc.Start/End* is the number  $M_t$  of results that are truncated (ignored).
- *Gen.Start/End* is the number  $K_T$  of Sawtooth GA periods that are applied for each run.
- *SDev.Start/End* is the  $q$  coefficient which signifies the semi-width of the new trial range in terms of standard deviation.
- *Lg.Start/End* is the gene length in bits per unknown parameter.
- *Ar2* is the termination range ratio. When the range ratio of all model parameters reaches this value, analysis stops.
- *Max number of iterations* is the maximum number of optimization steps that are allowed per analysis. Normally, this should never be triggered.
- *Total Iterations* is the total number of analyses that should be performed. This is very helpful when a statistical sample of the algorithm performance is needed.

The other settings should not be modified.

Press "Ok" to start the bounding analysis. Upon conclusion, all results are automatically put into folders within the root directory of the program.

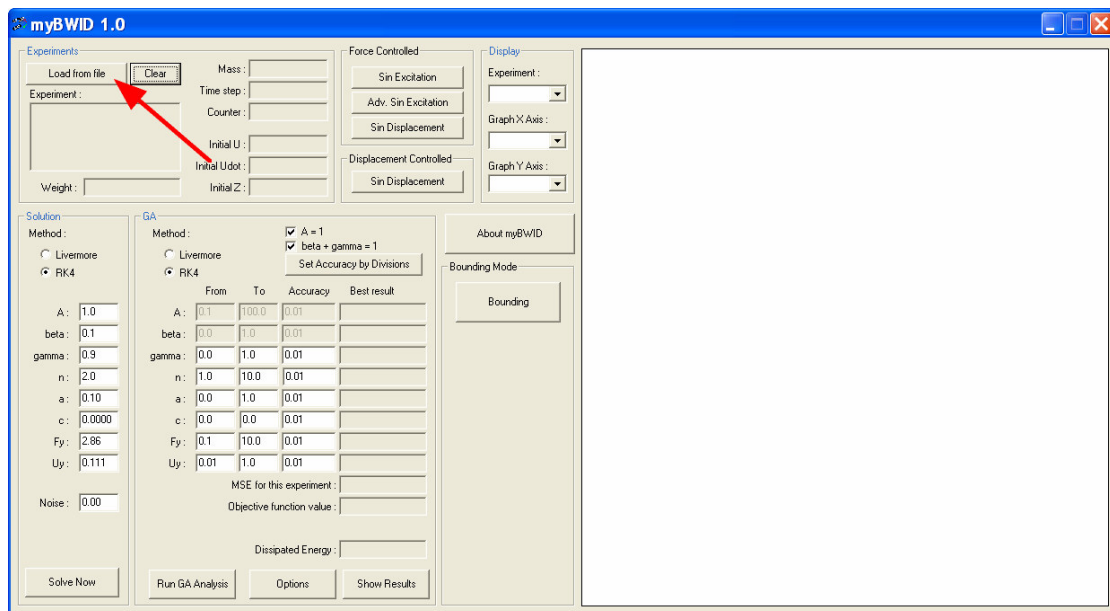
## 4. Example 2: Identification using real data

### 4.1 General

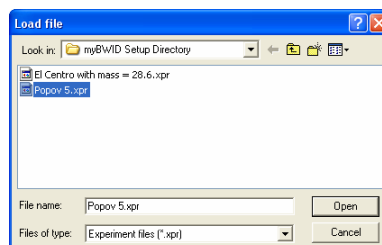
The second example refers to a full-scale bolted-welded steel connection that was tested by Popov and Stephen [7]. A Bouc-Wen model will be identified so that its response closely fits the experimental data.

### 4.2 Excitation

Press the "Clear" button to clear all experiments. Then, click the "Load from file" button at the top left corner:



Select the "Popov 5.xpr" file from the main directory of the program:



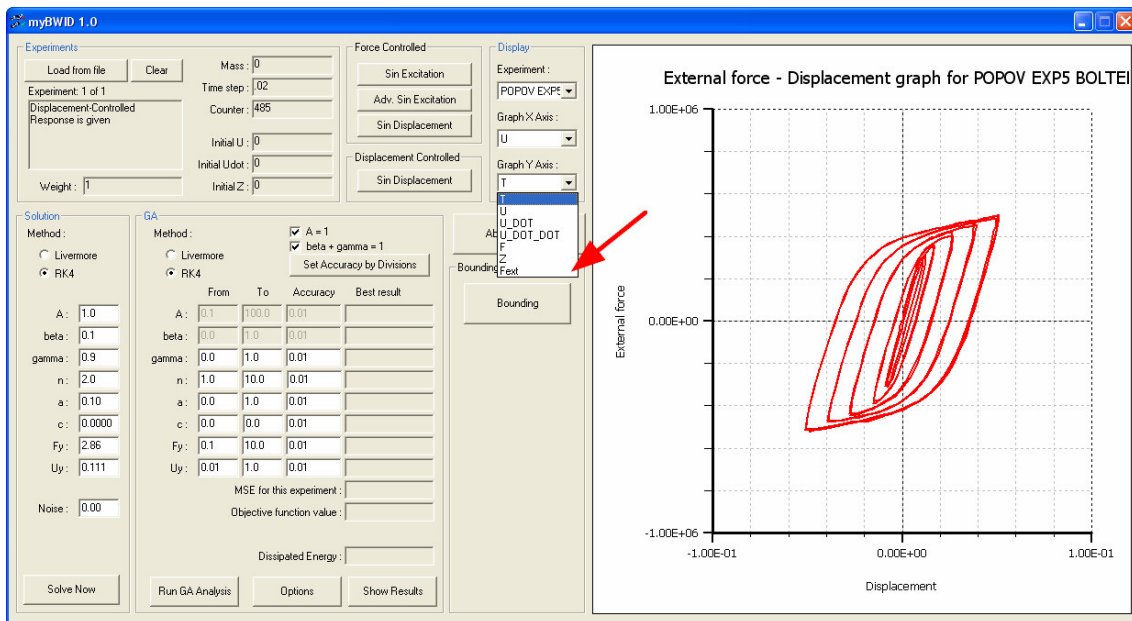
In this case, the response is given by experimental data which are stored in the file. Therefore, the "true" parameter values in the "Solution" frame are inactive.



### 4.3 Graph

The program automatically draws the response of both the “true” and “identified” model in a picture box on the right of the main window. The graph of “true” response of the model is drawn using a thick red line. The response of the current best result of identification is drawn using a thin blue line.

Since this excitation is based on experimental data, only external force and displacement data are available. Select the “Fext” option in the “Graph Y axis” drop-down list to view the hysteretic loops:



### 4.4 Feasible domain

Set the proper feasible domain ranges as follows:

- $F_y$ : from 0 to 1000000
- $u_y$ : from 0.001 to 0.1

These are the initial parameter ranges that were used in [1]. Regarding the other model parameters, the correct initial feasible domains are selected by default.

At this point, you can perform the identification using either a GA variant or the Bounding scheme, as described in the first example. Due to the smaller amount of data, this second example is identified much faster. The use of Bounding scheme with the default settings is recommended.

## References

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- [7] Popov, E.P., Stephen, R.M., *Cyclic Loading of Full-Size Steel Connections*, UCB/EERC-70/03, 1970.