



GENETIC PROGRAMMING MODELING OF THE CRITICAL SIZE OF INCLUSIONS

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Abstract

Spring steel quality has a major impact on spring life. Spring steel quality depends also on the inclusions presence. 7 dynamically tested and broken springs (51CrV4) were analyzed. The dynamic test result is the number of the cycles before spring breakage. We were interested in dependency of the inclusion size and the distance from the surface of the inclusion on the spring tool life. In the paper the genetic programming method was used. In the proposed concept the mathematical models for spring life undergo adaptation. The results show that the proposed concept can be used in practice.

Key words: genetic programming, inclusion, spring life, modeling

1. INTRODUCTION

Spring life depends on steel and spring producers activities. Each producer part contribute to mechanical behavior of the produced spring (Šuštaršič et al., 2006; Šuštaršič et al., 2008).

The spring life is determined by dynamical testing. There are many different techniques for spring life determination (Šuštaršič et al., 2006; Šuštaršič et al., 2008; Murakami et al., 1989; Murakami, 2002). In general the whole spring assembly or just a sample cutout is used for the spring life analysis. Šuštaršič et al. (2006, 2008) tried to determine the bend fatigue strength of selected spring steel with a resonant pulsator using standard Charpy V-notched specimens. Murakami et al. (1989) tried to predict the upper and the lower limits of fatigue strength from the Vickers hardness of a matrix and the maximum size of inclusions defined by the square root of the projected area of an inclusion. Murakami (2002) also introduces several spring steel quality determination techniques.

In the present paper the dependence between inclusion size, inclusion location and spring life was discussed. The experimental data was collected after spring breakage between dynamic testing.

After the genetic programming method (Kovačič et al., 2007; Kovačič & Šarler, 2009; Koza, 1999) was used to determine the correlation between spring tool life and inclusion size and inclusion location. With the genetically obtained mathematical model the critical inclusion size was determined.

The critical inclusion size information could be easily used for steel plant metallurgical processes design.

2. SPRING LIFE DYNAMIC TESTING

We were using the three-point flexural testing device. The spring life dynamic testing is schematically presented in figure 1. The tested material was 51CrV4. The chemical composition of the tested material is collected in the table 1. Test frequency was 40 cycles/min, test force (F) between

3.3 kN and 50 kN, spring sink (f) from 16 mm to 225 mm. It is easily to conclude that the load was pulsative and the bottom and top surface were tensile and compressed, respectively.

Table 1. 51CrV4 spring steel chemical composition.

C	Si	Mn	P	S	Cr	Mo	Ni	Al	Cu	Nb	Ti	V	Sn	Ca	B
0,51	0,34	0,96	0,014	0,003	1,07	0,06	0,08	0,012	0,13	0,001	0,004	0,17	0,01	0,0009	0,0002

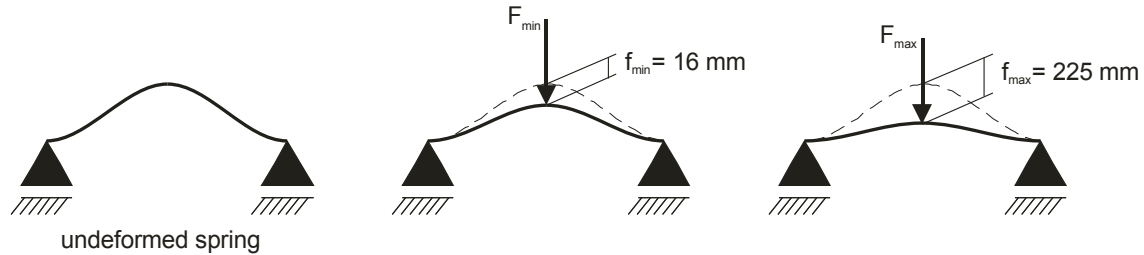


Fig. 1. Spring life dynamic testing.

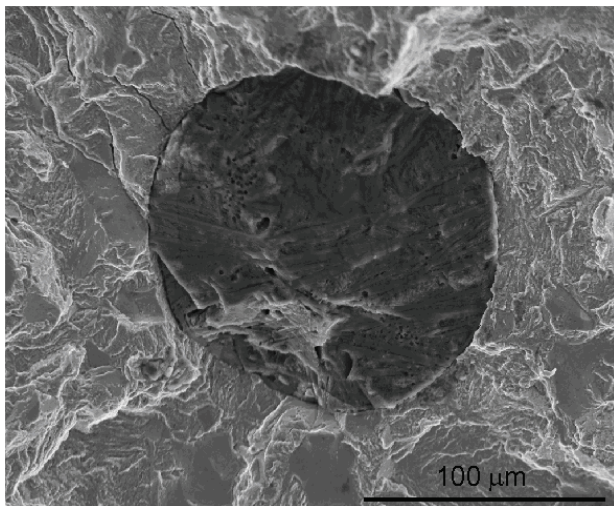


Fig. 2. The inclusion found at the breakage surface of the spring number 2 (table 3).

Table 2. The inclusion (spring number 2) chemical composition.

O	Mg	Al	Si	S	Ca	Ti	Fe	Zn
43,42	3,26	19,77	2,91	1,08	24,47	0,20	4,69	0,21

Table 3. The spring life dynamic testing data.

Spring number	Inclusion size [mm]	Inclusion depth [mm]	Spring life [cycles]
1	0.33	3.75	53667
2	0.16	1.34	96484
3	0.22	0.91	60157
4	0.26	3.87	62437
5	0.44	3.71	57454
6	0.38	3.09	53200
7	0.2	1.19	53062

After the spring breakage the inclusion size of and the depth of the inclusion found at the breakage surface (distance from the bottom spring surface) were measured. The inclusion and spring life data is collected in the table 3. The inclusion found at the

spring number 2 breakage surface (table 3) and its chemical composition is presented in the figure 2 and table 2, respectively.

3. SPRING LIFE MODELING BY GENETIC PROGRAMMING

Genetic programming is probably the most general evolutionary optimization method (Kovačič et. al, 2007; Kovačič & Šarler, 2009; Koza, 1999). The organisms that undergo adaptation are in fact mathematical expressions (models) for spring life prediction consisting of the available function genes (i.e., basic arithmetical functions) and terminal genes (i.e., independent input parameters, and random floating-point constants). In our case the models consist of: function genes of addition (+), subtraction (-), multiplication (*) and division (/), terminal genes of inclusion size (S) and inclusion depth (D).

Random computer programs of various forms and lengths are generated by means of selected genes at the beginning of simulated evolution. Afterwards, the varying of computer programs during several iterations, known as generations, by means of genetic operations is performed. For the progress of the population only the reproduction and crossover are sufficient. After completion of varying of computer programs a new generation is obtained that is evaluated and compared with the experimental data, too. One of the randomly generated mathematical models $\left(\frac{4}{0.333} + D\right) \frac{S}{5.1}$ is



schematically represented in figure 3 as a program tree with included function genes (*, +, /) and terminal genes (S, D, and a real number constants 4, 0.333 and 5.1).

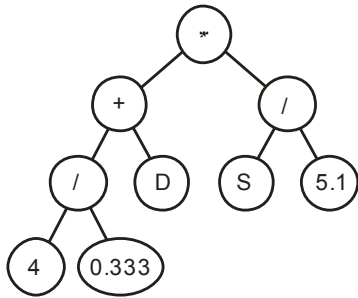


Fig. 3. Randomly generated mathematical model for the spring life represented in form of a program tree

Figure 4 shows the crossover of two computer programs on function genes. The crossover point is randomly chosen either on function genes or terminal genes. Two new child computer programs result from two parental computer programs. Two parental computer programs are Parent 1 and Parent 2. They are in fact mathematical expressions usually written as:

$$\left(\frac{4}{0.333} + D\right) \frac{S}{5.1} \text{ and } \frac{S}{5.1}$$

are created: $(S + D) \cdot \frac{S}{5.1}$ and $\frac{4}{0.333}$.

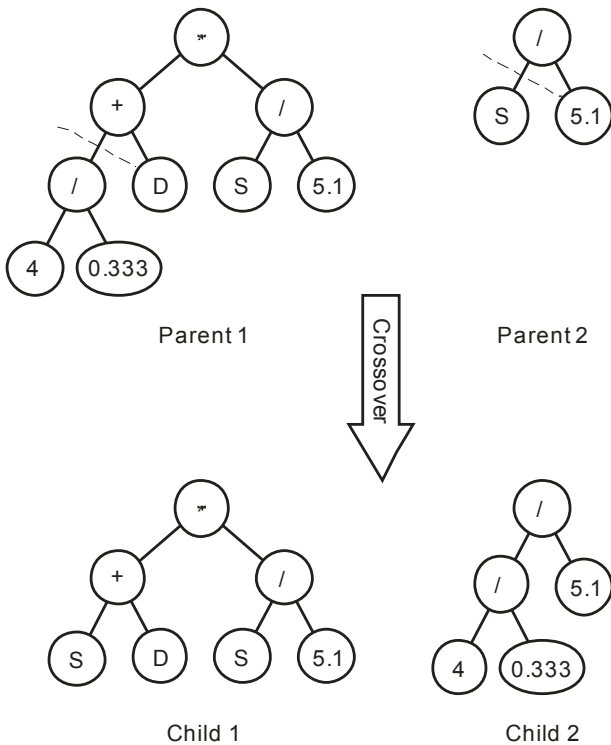


Fig. 4. Crossover operation.

For spring life prediction the fitness measure was defined as:

$$\Delta = \frac{\sum_{i=1}^n \Delta_i}{n}, \tag{1}$$

where n is the size of sample data, Δ_i is a percentage deviation of single sample data. The percentage deviation of single sample data, produced by individual organism, is:

$$\Delta_i = \frac{|E_i - G_i|}{E_i} \cdot 100\%, \tag{2}$$

where E_i and G_i are the actual spring life and the predicted spring life by a model, respectively. The smaller the values of equation (1), the better is adaptation of the model to the experimental data.

The process of changing and evaluating of organisms is repeated until the termination criterion of the process is fulfilled. This was the prescribed maximum number of generations.

For the process of simulated evolutions the following evolutionary parameters were selected: size of population of organisms 500, the greatest number of generation 100, reproduction probability 0.4, crossover probability 0.6, the greatest permissible depth in creation of population 6, the greatest permissible depth after the operation of crossover of two organisms 10 and the smallest permissible depth of organisms in generating new organisms 2. Genetic operations of reproduction and crossover were used. For selection of organisms the tournament method with tournament size 7 was used.

We have developed 100 independent civilizations of mathematical models for spring life prediction. Each civilization has the most successful organism – mathematical model for spring life prediction. The best most successful organism from all of the civilizations is presented here:



$$\left(\frac{8.32555 + 8.40678(8.23089 + D) + \frac{8.23089 + D}{D} + \frac{D}{3.48269 \cdot D - \frac{0.85092}{S}}}{\frac{8.55026}{8.32555 - \frac{D}{S}} - \left[\frac{-29.777904 + \frac{D}{8.32555 - \frac{8.55026}{9.17647 + \frac{8.23089 + D}{D} - \frac{D}{S}} + \frac{2}{S}}{6.66951 + S} \right]} \right) \cdot 27.21465 \cdot S \left(S + D + \frac{-8.55026 + \frac{D}{S} + S}{1 + \frac{1}{S \cdot D}} \right) + S \left(\frac{8.23089 + D}{D} + S + \frac{-8.55026 + 2D + S}{8.32555 - \frac{D}{S}} \right) + \frac{D + \frac{D}{S} + S}{3.48269 \cdot D - \frac{0.85092}{S}} \quad (3)$$

with fitness measure (average percentage deviation) 0.64%.

The calculated spring life and percentage deviations from experimental data is presented in the next table (table 3).

Table 3. The calculated spring life and percentage deviations from experimental data.

Spring number	Inclusion size [mm]	Inclusion depth [mm]	Spring life [cycles]	Predicted spring life [cycles]	Percentage deviation
1	0.33	3.75	53667	53673	0.01%
2	0.16	1.34	96484	95829	0.68%
3	0.22	0.91	60157	59715	0.73%
4	0.26	3.87	62437	62788	0.56%
5	0.44	3.71	57454	57969	0.90%
6	0.38	3.09	53200	53187	0.02%
7	0.2	1.19	53062	53890	1.56%

4. CRITICAL INCLUSION SIZE

According to the best genetically developed spring life model it is easily to calculate the critical size of inclusion on the spring surface. The spring life and inclusion size on the surface dependency is presented in the next figure (figure 5).

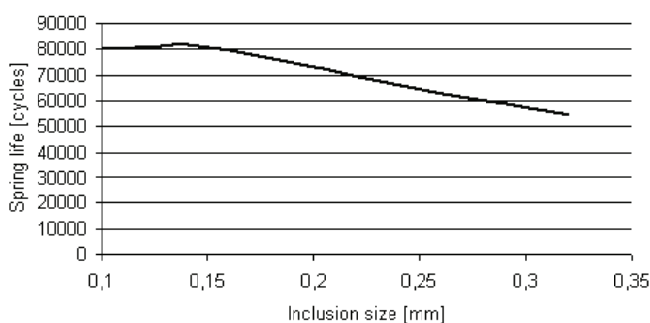


Fig. 5. Spring life and inclusion size on the surface dependency.

The highest calculated spring value is at inclusion size 0.14 mm. After that value spring life rapidly decreases.

5. CONCLUSION

Spring life depends on many properties. One of the most important is inclusions size.

In the research 7 springs were dynamically tested on three-point flexural testing device. The tested material was 51CrV4. Test frequency was 40 cycles/min, test force between 3.3 kN and 50 kN, spring sink from 16 mm to 225 mm.

After the spring breakage the inclusion size and depth (distance from the bottom surface) were measured.

The genetic programming method was used to determine the correlation between spring tool life and inclusion size and inclusion location.

From the 100 runs (civilizations) the best predictive model for spring life was developed with average percentage deviation 0.64%.

According to the best genetically developed spring life model it was easily to calculate the critical size of inclusion on the spring surface. The value is 0.14 mm.

With the help of genetic programming method the decision value was determined. According to known critical inclusion size value the right spring steel and steel plant technology could be easily selected. The results are compared with the similar more experimentally-oriented research [1].

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MODELOWANIE KRYTYCZNEGO ROZMIARU CZĄSTKI WYDZIELEŃ W OPARCIU O PROGRAMOWANIE GENETYCZNE

Streszczenie

Jakość stali sprężynowej decyduje o długości życia sprężyny. Jakość tej stali zależy przede wszystkim od obecności wydzielen. Analizowano 7 sprężyn ze stali 51CrV4 poddanych dynamicznym obciążeniom do zniszczenia. W próbach wyznaczono liczbę cykli obciążenia do zniszczenia sprężyny. Celem pracy było wyznaczenie zależności pomiędzy wielkością cząstek wydzielen i ich odległością od powierzchni a czasem życia sprężyny. Do wyznaczenia tej zależności wykorzystano programowanie genetyczne. W zaproponowanym rozwiązaniu prowadzona jest adaptacja modelu czasu życia sprężyny. Analiza wyników potwierdziła praktyczne zastosowanie opracowanego modelu.

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