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GENETIC BASED APPROACH TO PREDICTING THE ELONGATION OF DRAWN ALLOY

Gusel, L.; Rudolf, R. & Brezocnik, M.
University of Maribor, Faculty of Mechanical Engineering, Smetanova 17, 2000 Maribor, Slovenia
E-Mail: leo.gusel@um.si

Abstract
This paper describes a genetic based approach for the modelling of elongation in cold drawn copper alloy. Genetic programming is one of the most general genetic based methods and was used in our research. It is an automated evolutionary computation method for creating a working computer programme from a problem's high-level statement. Genetic programming does this by breeding a population of computer programmes genetically using the principles of Darwinian's natural selection and biologically inspired operations. In our research, material was formed by drawing using different process parameters and then determining elongation of the specimens. On the basis of a training data set, various different genetic models for the elongation distribution were developed during simulated evolution. The accuracies of the best models were proved by a testing data set and comparison between the genetic and regression models was carried out.
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Key Words: Genetic Programming, Prediction, Metal Forming, Elongation, Copper Alloy

1. INTRODUCTION

Many modelling methods for predicting different dependent variables have been developed to reduce the costs of the experiments. Traditional methods often employed to solve real complex problems tend to inhibit elaborate explorations of the search space. In most conventional deterministic modelling methods, such as regression analysis, a prediction model is determined in advance. Because of the pre-specified shape and size of the model, the obtained model is often incapable of capturing complex relationships between influencing parameters. It is important that the independent input variables influence on the dependent output variables and, consequently, on the product quality which has been already been examined in the early stages of a metal forming process.

Evolutionary computation (EC) is generating considerable interest for solving real engineering problems. They are proving robust in delivering global optimal solutions and helping to resolve those limitations encountered in traditional methods. EC harnesses the power of natural selection to turn computers into optimization tools. This is very applicable to different problems in the manufacturing industry. One of most important EC methods is genetic programming (GP) which is, similarly to a genetic algorithm, an evolutionary computation method for imitating the biological evolution of living organisms.

In [1] two models have been developed for roughness modelling: a regression model and a model based on neural networks, with better fitness of the neural model. In [2] Barkallah et al. proposed a three-dimensional statistical approach for determining the manufacturing tolerances based on the components of the small displacements tensors which were considered as random variables. It was found out that the difference between simulation and experiments was reasonably small. Several other researches have been carried out using statistical analysis [3, 4]. In [5] forming process have been investigated experimentally and modelled using generalized GMDH-type which is a group method of data handling neural networks. It was also demonstrated that singular value decomposition can be effectively used to find the vector of coefficients of quadratic sub-expressions embodied in such GMDH-type networks. Special algorithm learning based neural network integrating feature selection and classification was presented in [6] and genetic algorithms with neural networks for modelling of different processes parameters were described in [7]. A technique developed using hybridization of kernel principal component analysis (KPCA) based nonlinear regression and GAs to estimate the optimum values of the three parameters such that the estimated surface roughness is as low as possible was presented by Wibowo and Desa in [8].

Very general attempts to bridge the gap between theory and practice by exploring characteristics of real world problems and by surveying recent evolutionary computation applications for solving real problems in the manufacturing industry were described in [9, 10]. The survey outlines the current status and trends of EC applications in manufacturing industry. Malik et al. [11] have proposed the evolutionary search concept of particle swarm optimization (PSO) and gradient based training of artificial neural network (ANN) to optimize inter connecting synaptic weights, hence to develop a predictive model for estimating the drilling induced damage in CFRP laminates. Using well balanced search (exploration and exploitation) property of hybrid PSO-ANN, the developed predictive model shows satisfactory performance. The model incorporates more input variables at large number of levels, therefore is more generic in nature. In [12] two procedures for the identification of material parameters, a genetic algorithm and a gradient-based algorithm were presented. A hybrid algorithm was also used in such a way that the result of the genetic algorithm was considered as the initial values for the gradient-based algorithm. The objective of this approach was to improve the performance of the gradient-based algorithm, which is strongly dependent on the initial set of results. With this method it was shown that by performing a fine parameter optimization, it has been possible to fit most of the macroscopic effects observed in the material, using the constitutive models.

Only a few papers are dealing with the much more general genetic programming method, such as researches described in [13, 14], in which the authors have successfully used the genetic programming method for obtaining genetic models for several material properties and also stress and strain distributions in formed material. The obtained genetic models were very accurate and quite simple in form. For adequate predictions of the results or properties in forming and cutting processes also other evolutionary or conventional methods (like Particle Swarm Optimization, Finite Element Method, Response Surface Method, Multiple Linear Regression etc.) were successfully applied [15-18].

A Nonlinear model for R-R interval variation using genetic programming approach was proposed in [19]. In the GP method which is relatively new, the structure subject for adaptation is the population of hierarchically-organised computer programmes. This method is most often used for complex system modelling, but it can also be used effectively for the modelling of a relatively simple system, such as the systems described in our paper.

In this paper we propose an evolutionary computation approach for the modelling of elongation in formed material. Elongation is important in components which absorb energy by deforming plastically, and in manufacturing where it measures how much bending and shaping a material can withstand without breaking. Experimental data obtained during the cold drawing processes of copper alloy under different conditions serves as an environment which, during simulated evolution, models for the elongation have to be adapted to. Different values for effective strains and coefficients of friction were used as independent input variables, while elongation was a dependent output variable.

Then, GP programme was developed and used for the evolutionary development of the models for elongation prediction, on the basis of a training data set. The size and form of the models were left to the evolutionary process. Finally, the prediction accuracy of the model was proved using the testing data set.

2. METHOD USED

Genetic programming is probably the most general evolutionary computation method in which the structures subject to adaptation are those hierarchically organised computer programmes whose size and form change dynamically during simulated evolution. The space for solutions in the GP method is the huge space of all possible computer programmes consisting of components describing the problem area studied.

The aim of GP is to find out the computer programme that best solves the problem. Possible solutions in GP are all those possible computer programmes that can be composed in a recursive manner from a set of function genes *F* and a set of terminal genes *T*. Function genes are arithmetical functions, Boolean functions, relation functions, etc., while terminal genes are numerical constants, logical constants, variables, etc. [20]. The initial population for genetic programming is obtained by the creation of random computer programmes consisting of available function genes from set *F* and available terminal genes from set *T*.

Each programme represents a random point in the searching space. The next step is the calculation of fitness for each computer program. Fitness is a guideline for modifying those structures undergoing adaptation. Computer programmes change in GP, in particular during genetic operations regarding reproduction and crossover. The reproduction operation gives a higher probability of selection to more successful organisms. They are copied unchanged into the next generation. The crossover operation ensures the exchange of genetic material between computer programmes while the mutation operation increases the genetic diversity of a population.

After finishing the first cycle, which includes creation of the initial population, calculation of fitness for each individual of the population, and genetic modification of the contents of the computer programmes and formation of a new population, an iterative repetition of fitness calculation and genetic modification follows.

After a certain number of generations the computer programmes are usually much better adapted to the environment. The evolution is terminated when the termination criterion is fulfilled. This can be a prescribed number of generations or sufficient quality of the solution. Since evolution is a non-deterministic process, it does not end with a successful solution after each run (i.e., civilization). In order to obtain a successful solution, the problem must be processed over several independent runs. The number of runs required for the satisfactory solution depends on the difficulty of the problem.

3. EXPERIMENTAL WORK

The aim of the experimental work was to determine the influence of the effective strain ε and coefficient of friction μ during cold drawing on the change of elongation (A_5) of cold drawn copper alloy CuCrZr. This is a special copper alloy with 0.71 % Cr, 0.05 % Zr and 0.018 % Ni. It has high electrical and thermal conductivity, with excellent mechanical and physical properties at elevated temperatures.

Copper alloy rods were formed by cold drawing under different conditions. The drawing speed was v = 20 m/min and the drawing die angle was δ = 28°. Copper alloy rods were drawn on drawing machine from an initial diameter of D = 20 mm to six different diameters (i.e., six different effective strains). Three different lubricants with different coefficients of friction (μ = 0.07, μ = 0.11 and μ = 0.16) were used for the drawing process. In order to evaluate the elongation, standard specimens for tensile tests were prepared from locations in the middles of the drawn rods. In this way we obtained 18 different experimental specimens.

Elongation of all specimens was determined by providing three tensile tests for each specimen in order to provide reliable results. The average measured values for elongation are presented in Table I. Experimental data serve as an environment to which, during simulated evolution, models for elongation have to adapt.

Table I: Experimental results for elongation.

Nr.	Effective strain ε	Coefficient of friction μ	Elongation A_5 [%]
initial spec.	/	/	19.0
1	0.10	0.07	18.5
2	0.21	0.07	18.1
3	0.32	0.07	17.8
4	0.44	0.07	17.6
5	0.57	0.07	17.6
6	0.71	0.07	17.5
7	0.10	0.11	18.3
8	0.32	0.11	17.9
9	0.71	0.11	17.4
10	0.10	0.16	18.1
11	0.44	0.16	17.4
12	0.71	0.16	17.1
13	0.21	0.11	18.0
14	0.44	0.11	17.7
15	0.57	0.11	17.3
16	0.21	0.16	17.9
17	0.32	0.16	17.7
18	0.57	0.16	17.3

4. GENETIC PROGRAMMING MODELLING OF ELONGATION

In the GP method the initial random population *P(t)* consists of randomly generated organisms which are, in fact, mathematical models. The variable *t* represents the generation time. Each organism in the initial population consists of the available function genes *F* and the terminal genes *T*. In this research terminal genes were in fact independent variables: strain and coefficient of friction. Random floating-point numbers within the range [-10, 10] were added to the set of terminals to increase the genetic diversities of the organisms. Function genes *F* were basic arithmetical functions of addition, subtraction, multiplication, division, and the natural exponential function.

4.1 Evolutionary parameters

The absolute deviation $R(i, t)$ of individual model *i* (organism) in generation time *t* for the GP approach, was introduced as the standard raw fitness measurement [20]:

$$R(i,t) = \sum_{j=1}^{n} \left| E(j) - P(i,j) \right|, \tag{1}$$

In eq. (1) $E(j)$ is the experimental value for measurement *j*, $P(i, j)$ is the predicted value returned by the individual model *i* for measurement *j*, and *n* is the maximum number of measurements. The aim of the optimization task is to find models that eq. (1) would give as having as low an absolute deviation as possible. However, because it is unnecessary that the smallest values of the above equation also means the smallest percentage deviation of this model, the average absolute percentage deviation of all measurements for individual model *i* was defined as [14]:

$$\Delta(i) = \frac{R(i,t)}{|E(j)|\,n} \cdot 100\% \tag{2}$$

Eq. (2) was not used as the fitness measurement for evaluating population, but only to find the best organism in the population after completing the run. In the GP method, reproduction, crossover, and mutation operations were used for altering the population *P*(*t*). Evaluation and altering of the population *P*(*t*) were repeated until termination condition had been fulfilled. The termination condition was the prescribed maximum number of generations to be run. Reproduction, crossover, and mutation were used as genetic operations.

Fig. 1 shows the operation of the crossover. Two randomly selected parts of two parental organisms (in boldface) are interchanged. Thus, two offsprings are created.

a (***b***-2***c***)		***c/b*** (***b***-2***c***)
Parent 1		Child 1
	Crossover →	
c/b + 2		*a* + 2
Parent 2		Child 2

Figure 1: Crossover of two mathematical expressions.

The evolutionary processes were controlled by the following evolutionary parameters: population size was 1000, maximum number of generations to be run was 50, probability of reproduction was 0.1, probability of crossover was 0.8, probability of mutation was 0.1, maximum depth for initial random organisms was 6, maximum depth of mutation was 6, and maximum permissible depth of organisms after crossover was 12.

4.2 Realisation of the evolutionary process

Modelling of elongation was carried out by the special GP system in LISP programming language and was programmed in our laboratory. The GP system ensures repeated development of the individual civilization if necessary. This is very useful when it is necessary to repeat evolution of the civilization with a greater number of generations or when evolution is interrupted for any reason.

Each individual GP run started with the training phase by the training data set shown in Table I (Nr. 1 to Nr. 12). The testing data set (Table I: Nr. 13 to Nr. 18) was not included within the training range. Each run lasted up to generation 30 when it was interrupted temporarily. If an average percentage deviation $\Delta(i)$ of at least one prediction model (organism) in the population was smaller than 5 %, the evolution of the population continued up to generation 50, otherwise it was terminated. After each training phase, the accuracy of predicting the best models was tested using the testing data set.

More than 100 independent runs were executed for the modelling of elongation. The GP models in our research were developed originally as prefix LISP expression, and then converted into an infix notation.

5. RESULTS AND DISCUSSION

GP modelling was executed by two different genes function sets *F* = (+,-,*, /) and *F* = (+,-,*, /, ZEXP). The best (the most accurate) model obtained with genes function set *F* = (+,-,*, /) is quite complicated and is written in LISP as:

(- (% (+ (% μ (- (- (% μ μ) (+ μ 0.798609)) (+ (+ (- (* ε ε) (* μ ε)) μ) μ))) -3.57641) (% (- (+ (+ (% -1.08891 μ) (+ -9.21933 -9.21933)) (- (% (+ ε ε) ε) -4.03358)) (+ ε (* μ 4.53704))) (% (- (* (% ε ε) (% (+ ε (+ ε ε)) (- (% μ μ) (+ μ 0.798609)))) (* (% 5.33162 2.22928) (- 4.02197 μ))) (- (* (- -7.25921 -2.49658) (% ε μ)) (- (% μ (- (% μ μ) (+ μ 0.798609))) (+ μ 0.798609)))))) (+ (+ ε μ) (+ -9.07545 -9.21933)))

The same model written as a mathematical expression:

$$18.294-\varepsilon-\mu-\frac{\left(2.391\mu-9.619+\dfrac{3\varepsilon}{0.201-\mu}\right)\left(-3.576+\dfrac{\mu}{0.201-\varepsilon^2-3\mu+\varepsilon\mu}\right)}{\left(12.405+\varepsilon+4.537\mu+\dfrac{1.088}{\mu}\right)\left(0.798+\mu-\dfrac{4.762\varepsilon}{\mu}+\dfrac{\mu}{\mu-0.201}\right)} \tag{3}$$

The model (3) was generated in generation 49 and has the average percentage deviation of the training data $\Delta(i)$ = 0.21 % and that of the testing data $\Delta(i)$ = 0.20 %. Percentage deviation is in fact the percentage error between a single experimental value and the value predicted by the genetic model. Slightly better accuracy ($\Delta(i)$ = 0.20 %, and that of the testing data $\Delta(i)$ = 0.19 %) of the GP model was obtained when the genes function set which includes the exponent function was used: F = (+,-,*, /, ZEXP):

(+ (* (+ (ZEXP (+ -2.86387 -1.79054)) (ZEXP (% ε ε))) (- (+ (* ε ε) (- 7.96425 ε)) (+ μ (% ε ε)))) (- (* (- ε (- ε (ZEXP (+ -2.86387 (- ε -2.86387))))) (* (- ε (- ε (ZEXP (+ -2.86387 (- ε 1.67353))))) (% ε (+ (+ (% -2.06645 ε) -1.79054) (% ε μ))))) (- ε (* (- (ZEXP μ) 1.50148) μ))))

The upper model in LISP can be written as a mathematical expression:

$$18.997-3.727\varepsilon+\left(e^{\mu}-4.229\right)\mu+\varepsilon^2\left(2.7278-\frac{\mu\cdot 0.0059e^{2\varepsilon}}{\varepsilon\mu+1.154\mu-0.558\varepsilon^2}\right) \tag{4}$$

Fig. 2 shows the percentage deviation curve (Δi) between the best model regarding individual generation and experimental results when using the set of function genes F = {+, -, *, /, ZEXP}. It is obvious that in early generations the best models are not as precise as the models generated in late generations. The relatively slow improvement of the best models in later generations (after generation 29) is due to the unification trends of the population leading to the shortage of new genetic ideas.

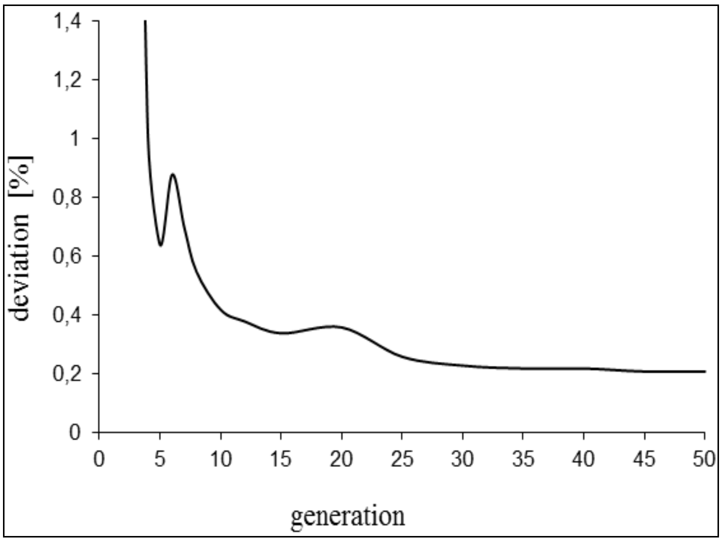

Figure 2: Percentage deviation curve between the best genetic models regarding individual generation and experimental results (F = +, -, *, /, ZEXP).

The total number of genes of the best genetic models (generated with function genes F = {+, -, *, /}) in each generation is presented in Fig. 3. In the first ten generations the total number of genes of best models did not exceed 60. Then, from generations 15 to 17 there was a big leap in the number of genes from 65 to 88 genes. In generation 20 the number of genes decreased but after that the number of genes increased slowly until the generation of 39. Finally, in generation 41, the total number of genes in the best genetic model reached a maximum of 110. The higher number of genes usually means higher complexity of the genetic model.

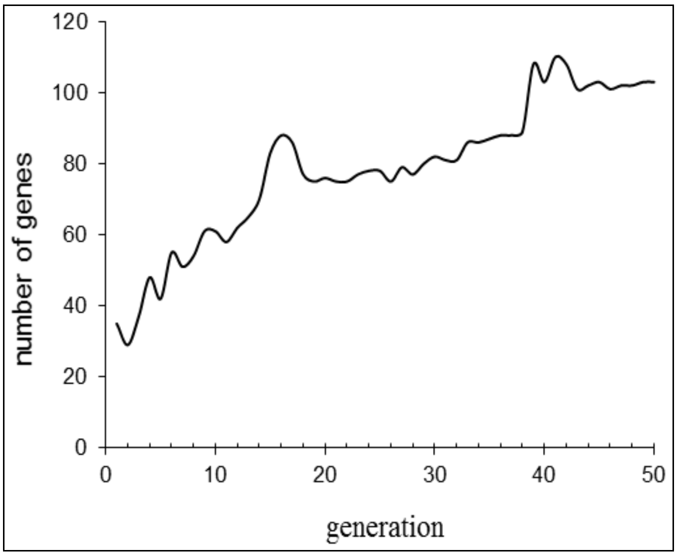

Figure 3: The depth of the best genetic models regarding individual generation.

6. REGRESSION ANALYSIS MODELLING RESULTS

Mathematical model for the regression method was used according to [21]:

$$y(x) = b_0 + \sum_{i=1}^{n} b_i x_i + \sum_{i=1}^{n-1} \sum_{j=i+1}^{n} b_{ij} x_{ij} + \sum_{i=1}^{n} \sum_{j=i}^{n} b_{ij} x_{ij}^2 \tag{5}$$

In eq. (5) y is the dependent variable, x_i, x_{ij} are independent variables, while b_0, b_i, b_{ij} are coefficients to be determined by using regression analysis. In our case, the dependent variable was elongation A_5, while effective strain ε and coefficient of friction μ were independent variables. Coefficients b_0, b_i and b_{ij} were determined by using the regression analysis computer programme. By inserting the computed values of coefficients into eq. (5), the regression model for elongation can be presented as:

$$A_5 = 18{,}973 - 3{,}71\ \varepsilon - 1{,}714\ \mu + 2{,}587\ \varepsilon^2 - 9,\ 217\ \mu^2 + 0{,}30\ \varepsilon\mu \tag{6}$$

Eq. (6) represents a mathematical model of the influence of effective strain and the coefficient of friction on elongation for chosen material within the experimental area. It has the average percentage deviation of the training data set $\Delta(i)$ = 0.38 % and that of the testing data set $\Delta(i)$ = 0.34 %.

When regression models are compared to genetic programming models, the first important difference is the complexities of the genetic models. Because of the evolutionary concept, genetic programming models are complex, with high numbers of genes, and the forms of these models can be confusing. Of course, when it comes to the accuracies of different models, GP models show much greater accuracy then regression models. The comparison of accuracy (deviation from the experimental results) of the best genetic and regression models is presented in Fig. 4. Both GP models are more accurate than the regression model.

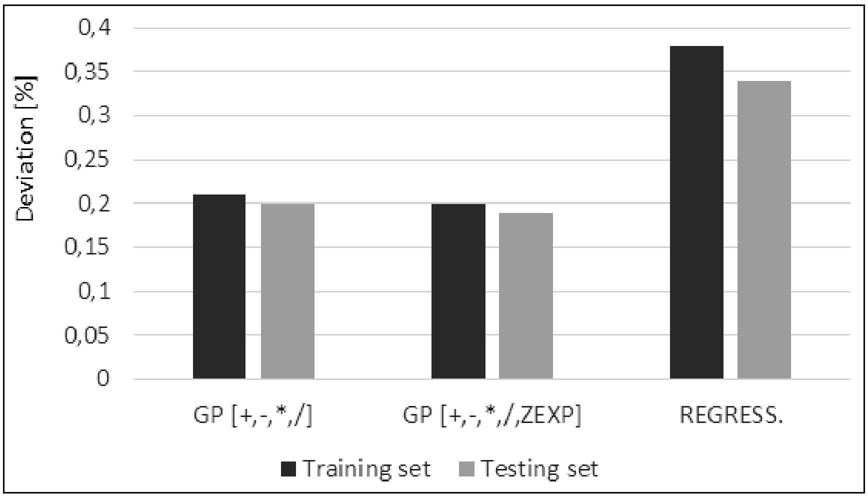

Figure 4: Deviation of the best GP and regression models from the experimental results.

7. CONCLUSIONS

The genetic development of models took place on the basis of experimental data. The experimental data in this research were in fact the environment to which the population of models had to be adapted as much as possible. The models presented are a result of the self-organisation and stochastic processes taking place during simulated evolution, and not of human intelligence. The accuracies of the models developed during the training phase were also confirmed using testing data not included within the training range. Only two genetically developed models out of many successful solutions are presented here.

The accuracies of solutions obtained by GP depend on applied evolutionary parameters and also on the number of measurements and the accuracy of measurement. In general, more measurements supply more information to evolution which improves the structures of models. At the same time, the greater number of measurements causes time-consuming computer processing and the execution of experiments is very expensive and requires much time. Because of the high precision regarding the models developed by the GP approach, with the proposed new concept, the excessive number of experiments/simulations can be avoided, which leads to the reduction of the product development costs.

The research showed that simple and, at the same time, very precise models are often hard to reach because the evolution is a stochastic process and, therefore, rationality in the development of the models is rare. However, in modern computerized production the accuracy of prediction is of vital importance, not the model complexity.

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