

# B-Spline Curve Approximation Using Pareto Envelope-Based Selection Algorithm – PESA

Erkan Ülker

**Abstract**—The most common problems which constitute the subject of research in the field of computer-based modeling are to predict the desired shape of the curve for a set of given points. Many approaches and methods were developed for different types of curve and techniques are used for solution of the problem. In this study similarly, Pareto Envelope-based Selection Algorithm (PESA) is proposed for estimated curves. An Application environment which is collected reverse engineering methods and approaches of the algorithm was improved and the node estimation process of B-spline curves is introduced using PESA.

**Index Terms**—PESA, B-Spline Curve, Approximation, reverse engineering.

## I. INTRODUCTION

Many approaches and method has developed for different curve types in literature and these are used for solution of related problem. Sarfraz (2004) suggested an evolutionary approach for curves represented by optimal curve fit planar data collected from the main lines of the two-dimensional shapes. Iglesias and Galvez (2008) Rational B-spline (RBS) function networks being special type of function networks on curve fitting. A rational cubic spline with shape control parameters is discussed by Habib et al. (2005) perspective in the form of application in the field of computer graphics. Masood et al.(2005) used quadratic B-splines for curve estimate to minimize errors on data points. Yoshimoto et al.(1999) made a study for data fitting with spline target identify the best nodes. Mamic and Bennamoun (2001) suggested a bayesian model to identify automatically node placement in spline modeling. An approach based on genetic algorithm for parameter optimization aiming B-spline curve fitting is proposed by Kumar et al.(2003). The place of genetic algorithm in computer –aided design are deeply examined by Renner and Ekart (2003). An adaptive node settlements algorithm for the prediction of B-spline curve on busy and noisy data is defined by Li et al.(2005). Valenzuela and Pasadas (2010) performed cubic spline estimation by taking actual values of nodes of locations. Problem is solved with simulated annealing (SE). Xiuyang et al. (2001) used Gaussian Mixture Model (GMM) that initial values was improved with k-means algorithm in B-spline curve estimation for finding nodes positions. The use of the pareto Envelope-based selection algorithm( PESA) being one type of genetic algorithm and especially using in stage of multi-objective optimization instead of original genetic algorithm is explained. The solution by properly combining process

steps of he algorithm for especially various reverse engineering method used in B-spline curve estimation is searched in this study. Application environment by concreting of research study and effective presenting is developed and evaluated. Obtained results from taken the algorithm show presenting of effective approach in B-spline curve estimation.

## II. B-SPLINE CURVE KNOT APPROXIMATION

Process step of B-spline curve node estimation are following [Ülker, 2007];

- 1) Firstly, among the available points offered of outside is selected and centripetal nodes from the points are calculated.

$$\bar{u}_0 = 0, \quad \bar{u}_m = 1 \quad (1)$$

$$\bar{u}_i = \bar{u}_{i-1} + \sqrt{|\mathcal{Q}_i - \mathcal{Q}_{i-1}|} / \sqrt{\sum_{j=0}^m |\mathcal{Q}_j - \mathcal{Q}_{j-1}|} \quad (2)$$

where,  $|\mathcal{Q}_i - \mathcal{Q}_{i-1}|$  is euclidian distance.

- 2) In second stage; estimated B-spline knots obtained from centripetal knots are calculated.

$$S(u) = \sum_{q=0}^n c_q N_q^k(u) P_1, u \in [u_{k-1}, u_{n+1}] \quad (3)$$

where,  $u_i$  is Centripetal knots and  $u_j$  is B-spline knots.

- 3) B-spline control points (P) should be calculated. Control points using matrix operations can be reached.  $Q=P \times R$  is taken into consideration. For this purpose, to obtain P matrix via expressed matrix order tried to be achieved. Firstly, R matrix is obtained. The Matrix obtains through the use of blend functions according to the N.
- 4) As a result obtaining of R matrix, over  $Q=P \times R$ , matrix operations can be applied to leave alone P matrix. Accordingly, after inverse R matrix, it is replaced in  $Q=P \times R^{-1}$  operation and P matrix s obtained.
- 5) After P matrix obtained, production of estimated B-spline curve is performed.

$$S(u) = \sum_{i=0}^n P_i N_{i,p}(u) \quad (4)$$

- 6) After estimated B-spline curve, evolution of estimation accuracy must be made. For this purpose, error determination by utilizing points datum offered outside

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and estimated curve points must be made. This approach referred sum of euclidean errors is expressed as follows:

$$\text{Error} = \|S_r - F_i\| \quad (5)$$

If obtained error value is closer to zero, points is better estimated. For this purpose, 1-6 steps are repeated depending on the choice of stopping criteria (erro value or iteration number).

### III. THE USE OF PESA FOR CURVE APPROXIMATION

As mentioned previously, approach which is used based on genetic algorithm which is one of the popular artificial intelligence techniques and PESA being type of genetic algorithm is used. Genetic algorithm based approaches, structures of chromosome which stage solution of the problem will be used must be definition. Considering approach generally, defined population and solution of problem according to information of generation is carried out. How is defined chromosome used in B-spline curve approximation is important. After chromosome structures expressed binary order is randomly created, required data can be selected from 1 corresponding to chromosome. Mean that bit 0 of the binary is not selected. Another important issue is that bit number of defined each chromosome is equal to total number of available data points. The approach is expressed in Fig. 1.

Another important issue according to this approach is that pass from first and last points of the curve must be. For this requirement, each chromosome randomly generated must be operated with logical operation "OR" with 1...000...1. To show process step of B-spline node estimation followed by genetic algorithm technique is important to better understand process step in stage using PESA. Node estimation with genetic algorithm is given in Fig. 2.

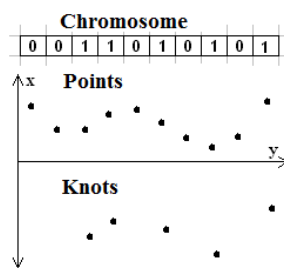


Fig. 1. Definition of chromosome at B-spline knot approximation

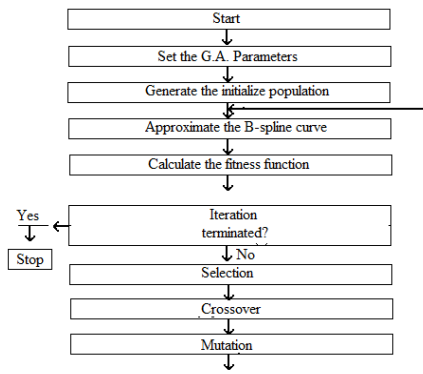


Fig. 2. B-spline knot approximation with genetic algorithm

Information criterion of Akaike is preferred to show the success of the solution and evaluate calculated fitness function.

$$AIC_1 = N \log_e (\varepsilon[S(u)]) + 2(2n + k) \quad (6)$$

$$\varepsilon[S(u)]_1 = \sum (S(u_i) - F_i)^2 \quad (7)$$

where F is estimated curve points. F is all of available data points and k is order of curve. Estimated curve points is obtained from curve function of B-spline.

$$S(u) = \sum_{q=0}^n c_q N_q^k(u) P_1, u \in [u_{k-1}, u_{n+1}] \quad (8)$$

$$N_j^1(u) = \{1 \text{ if } u \in (u, u_{j-1}) \mid 0 \text{ else}\}$$

$$N_j^k(u) = ((u - u_j) / (u_{j+k-1} - u_j))^{*N_j^{k-1}(u)} + ((u_{j+k} - u) / (u_{j+k} - u_{j+1}))^{*N_{j+1}^{k-1}(u)} \quad (9)$$

Specified processing steps are fulfilled according to AIC value obtained from equation (6) and (7) or to the border of a particular generation.

#### A. Pareto Envelope-Based Selection Algorithm

Pareto Envelope-Based Selection Algorithm (PESA) proposed by Corne et.al. is type of genetic algorithm [Corne et al., 2000].

Process steps of PESA is basically as follows:

- 1) Generate all of the chromosome of initial population (Internal population: IP) and evaluate. On the other hand, create external population: EP as empty set.
- 2) Add individual not suppressed in IP to EP.
- 3) Stop running if chosen termination criterion is reached (fitness values, error, .. generation etc.) and accept chromosome set in EP as result. Otherwise, delete current contents of IP and fulfil to produce new candidate solution by IP processing follows:  
 Select two parent in EP by probability value, produce a child using crossover and perform mutation. According to probability, select a parent and perform mutation to produce a child.
- 4) Return step 2.

In this study, random chromosome (accordingly point number) up to population size is generated at B-spline knot approximation. Selection and use of nodes used are fulfilled using equation (1)-(5), flow monitoring in Fig. 1 and reverse engineering calculation. Error value obtained continuously is monitored, generation number reached or accordingly obtained fitness value criterion by utilizing from equations (6) and (7), processes are repeatedly fulfilled to find optimum solution.

To express this approach at more concrete form, evaluate of efficiency of approach is important issue in this study. Therefore, application environment realized B-spline knot approximation utilizing PESA is developed.

#### IV. REALIZATION OF B-SPLINE CURVE ESTIMATION USING PESA IN PRACTICE

A software using C# programming language to realize B-spline curve knot approximation with PESA is developed by utilizing Visual Studio 2010 platform. Developed software by using given parameters and values realized B-spline curve approximation by using PESA. To analyze use characteristics of developed application environment

provides examination of developed software for solution of the problem. Developed software has easy use and it is fast. Entry interface providing necessary all adjustment and processes is displayed when software firstly run. Entry interface is shown in Fig. 3. Parameter of PESA algorithm and to show shape parameter is on the left in this software. In the middle area of the software is shown best B-spline curve. Obtained error and fitness value are shown on the right in the software.

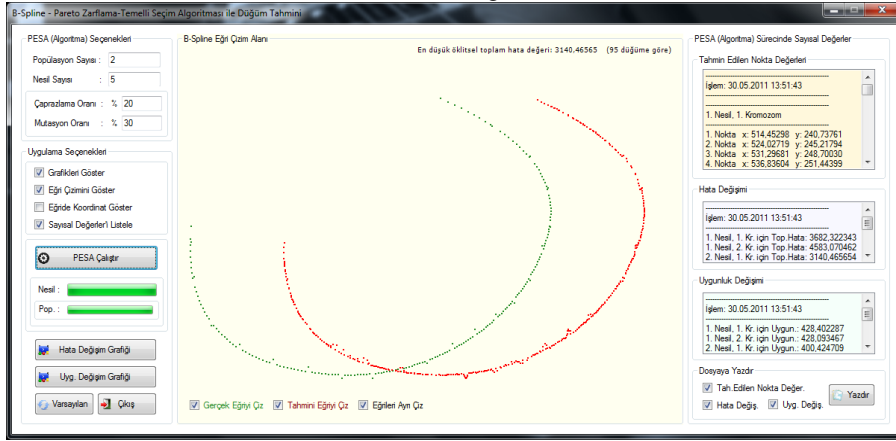


Fig. 3. Software-Entry Interface (in Turkish Language).

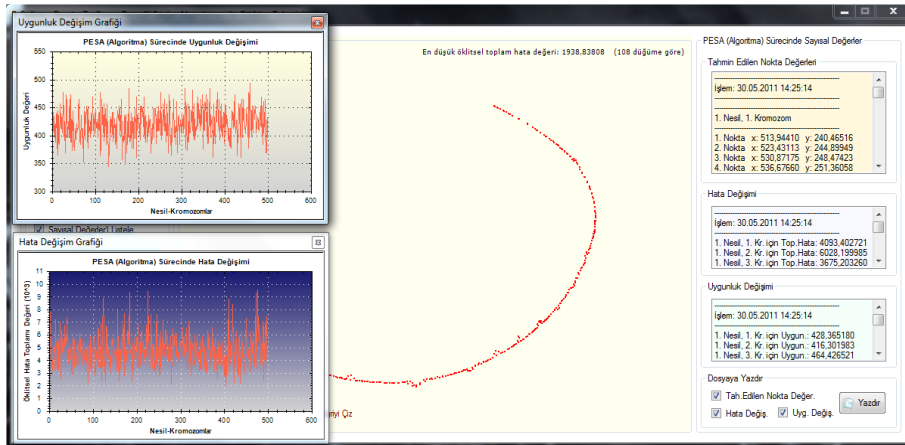


Fig. 4. General view after PESA process

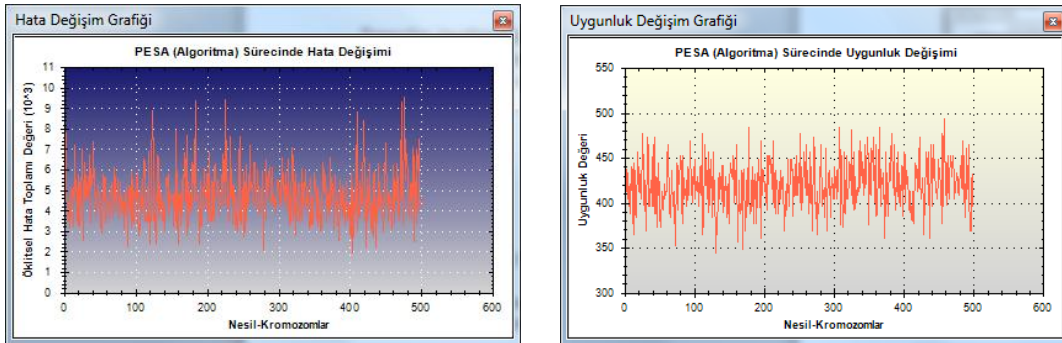


Fig. 5. a) Graphic change of error, b) Graphic change of fitness

To estimate knots of B-spline curve, PESA parameter is set up before running the program. PESA parameters are “Population number”, “Generation Number”, “Crossover rate” and “Mutation rate”. Default values are 10, 50, (%)20, and =(%)30, respectively. Using datum in knot approximation of B-spline curve are taken from TXT file.

When software is running, software reads content of TXT file, it gets necessary data, it starts estimation process. A curve is displayed during the process. At the end of the process, drawing curve obtained with minimum error value is shown in the middle, estimated coordinate number, error values and fitness values are shown in the right, change of

error and fitness values are shown in two different graph.

To show the effectiveness of the software, PESA is worked with default values. After the process, obtained results are shown in Fig. 4.

According to the results, displayed curve has 1938,83808 sum of Euclidean distance(according to  $m=108$  knots). The value is obtained for Generation #41, and Chromosome #4. Error change graph and fitness change graph are shown in Fig. 5.a and Fig. 5.b, respectively.

## V. CONCLUSIONS

In this study, use of Pareto Envelope-Based Selection Algorithm being one type of genetic algorithm is expressed for B-spline curve approximation. At the stage of knot approximation of curve, reverse engineering approach and PESA process step combined. Chromosomes presenting problem of genetic algorithm at curve approximation process are generated to specify random points using and to evaluate success. Use to evaluate performance of PESA using multi-objective optimization problems in curve estimation is provided in this study. Generally, to show effectiveness proposed method, application environment fulfilled node estimation of B-spline curve obtained from data points is developed. Software environment developed using C# programming language according to given data points provided to effectively obtain of points of appropriate B-spline curve and to draw according to result obtaining using PESA.

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