

Representing Shapes by Fitting Data using an Evolutionary Approach

Muhammad Sarfraz

King Fahd University of Petroleum and Minerals, sarfraz@kfupm.edu.sa

ABSTRACT

An evolutionary approach has been introduced for representing shapes by optimal curve fitting to planar data raised from the outlines of the two dimensional shapes. The algorithm designed, consists of various phases towards the solution of the problem. The spline model used is a rational cubic spline. It is a C1 model possessing shape parameters in its description in such a way that one parameter is sitting between each two consecutive control points. These shape parameters provide interval tension control and have been utilized to obtain an optimal curve fit to data raised from the outlines of the planar shapes. Detecting corners, from amongst the data points, is one of the important phases in the design algorithm. It helps in many ways including keeping permanent genes in the chromosomes, capturing a pleasant looking spline fitting data. In case of too large data, it provides a data reduction concept. The chromosomes have been constructed by considering the candidates of the locations of knots, together with shape parameters, as genes. The knots to the corresponding corner points have been kept fixed to minimize the computation cost. The best model among the candidates is searched by using Akaike's Information Criterion (AIC). The method automatically determines the appropriate number and location of knots together with optimal vector of shape parameter values.

Keywords: Visualization, data, genetic algorithm, spline, approximation.

1. INTRODUCTION

In the scientific world, data arises from various sources. It may come from some experiment, from a function, or from any other phenomena. Data fitting and visualization with splines is one of the important technologies in the area of computer graphics and scientific visualization. Various authors, in the last decade, have contributed in this direction. For brevity, the reader is referred to [6, 8-12].

If we have to make a good model from measurement data, having a complicated underlying data, it is difficult to approximate it by a single polynomial. In this case, a spline [4] is one of the most appropriate class of approximating functions. The key to using a spline is the determination of good knots [6, 8]. To obtain good approximation, one needs to place the knots as precisely as possible. In such cases, we have to deal with knots as variables. Then the problem becomes a continuous nonlinear and multivariate optimization problem with many local optima.

The underlying evolutionary scheme, in this paper, is based upon a family of spline, which has some extra

features in terms of shape parameters in its description. These shape parameters, sitting between each two consecutive control points, have the capability to control the curve between the control points. They help the curve to get tight or loose depending upon the need of the user. It is desired, using the Genetic Algorithm (GA) approach [5], to optimize the shape parameters so that an optimal spline fit is gained to the target data raised from the outlines of the two dimensional shapes.

In addition, some definiteness is also incorporated in the successive solutions in terms of finding appropriate knots in the spline solution. That is, the knots, corresponding to the corner points [2-3], will be kept fixed in the whole genetic process to make the algorithm evolutionary. Detecting the corner points is one of the important phases of the algorithm. It will help to incorporate some determinism in the search space of solutions of knots.

Given a well-defined search space in which each solution is represented by a bit string, called a chromosome, a GA [5] is applied with its three genetic search operators (selection, crossover and mutation) to transform a

population of chromosomes with the objective of improving the quality of the chromosomes.

The individual bits of a chromosome are called genes, which will be representing the knots and the shape parameters in our case. Before the search starts, a set of chromosomes is randomly chosen from the search space to form the initial population. The three genetic search operations are then applied one after the other to obtain a new generation of chromosomes in which the expected quality over all the chromosomes is better than that of the previous generation. The process is repeated until stopping criterion is met. Finally, the best chromosome of the last generation is reported as a final solution.

This work is a collection of various phases in the process of data visualization. It considers data arose from any phenomena, and a parametric form of B-Spline is used to achieve best approximation curve representation. In order to aid the GA, a corner detection algorithm has also been used to add some determinism and make the algorithm evolutionary. The achievement of corner points is of great importance. It helps to minimize the time for the visualization of the data as the number of iterations, in this case, reduce during the running of GA.

The organization of the paper is as follows. Section 2 gives a brief description of the rational spline method. The idea of corner detection is explained in Section 3. The curve fitting technique is discussed in Sections 4. The practical results are demonstrated in Section 5 and the paper is concluded in Section 6.

2. THE SPLINE MODEL

Modeling by splines [4] has got a lot of popularity in various applied field of studies, specifically including Computer Graphics and Visualization. This work is also based upon a rational spline model as an important component of the whole process. The idea of curve design, for any given data set, has been attempted to give an optimal solution in terms of a spline. Using this method, one can generate the curve segments for any given number of data points. Joining these segments, we can generate the desired Design Curve. The curve thus obtained will be C^1 . The procedure for curve design is as follows.

Let $F_i \in R^m, i \in Z$, be data points given at the distinct knots $t_i \in R, i \in Z$, with interval spacing

$h_i := t_{i+1} - t_i > 0$. Also, let $D_i \in R^m, i \in Z$, denote the first derivative values defined at the knots. Then the generalized form of the rational cubic, in the form a

parametric C^1 piecewise piecewise rational cubic Hermite function $P: R \rightarrow R^m$, is defined by

$$P|_{(t_i, t_{i+1})}(t) := \frac{(1 - \theta_i)^3 F_i + \theta_i (1 - \theta_i)^2 r_i V_i + \theta_i^2 (1 - \theta_i) r_i W_i + \theta_i^3 F_{i+1}}{(1 - \theta_i)^3 + r_i \theta_i (1 - \theta_i)^2 + r_i \theta_i^2 (1 - \theta_i) + \theta_i^3} \quad (1)$$

where

$$\theta_i \equiv \theta_i(t) = \theta|_{(t_i, t_{i+1})}(t) := (t - t_i) / h_i, \quad (2)$$

and

$$V_i := F_i + \frac{1}{r_i} h_i D_i, \quad W_i := F_{i+1} - \frac{1}{r_i} h_i D_{i+1}. \quad (3)$$

This form is economical for computational purposes. We have made use of a rational Bernstein-Bezier representation, where the control points $\{F_i, V_i, W_i, F_{i+1}\}$ are determined by imposing the following Hermite interpolation conditions:

$$P(t_i) = F_i \text{ and } P^{(1)}(t_i) = D_i, \quad i \in Z. \quad (4)$$

In most of the applications, the tangent information are not provided. We define a distance-based choice for tangent vectors D_i at F_i as follows:

For open curve:

$$\begin{aligned} D_0 &= 2(F_1 - F_0) - F_2 - F_0 / 2, \\ D_i &= a_i(F_i - F_{i-1}) + (1 - a_i)(F_{i+1} - F_i), \\ &\quad i = 1, \dots, n-1, \\ D_n &= 2(F_n - F_{n-1}) - F_n - F_{n-2} / 2. \end{aligned}$$

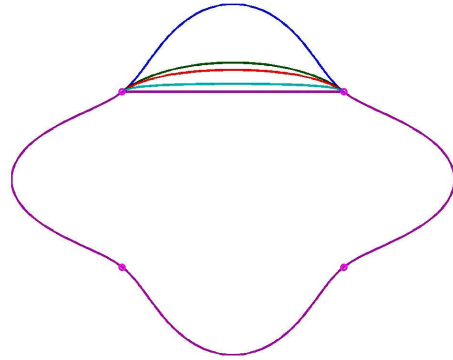


Fig. 1. Spline with Local interval tension for various increasing values.

For closed curve:

$$F_{-1} = F_{n-1}, F_{n+1} = F_1,$$

$$D_i = a_i(F_i - F_{i-1}) + (1 - a_i)(F_{i+1} - F_i), i = 0, \dots, n,$$

where

$$a_i = \frac{|F_{i+1} - F_i|}{|F_{i+1} - F_i| + |F_i - F_{i-1}|}, i = 0, \dots, n.$$

This choice of tangents provides nice and pleasing results.

We observe the following properties of the interpolant defined by Eqn. (1)

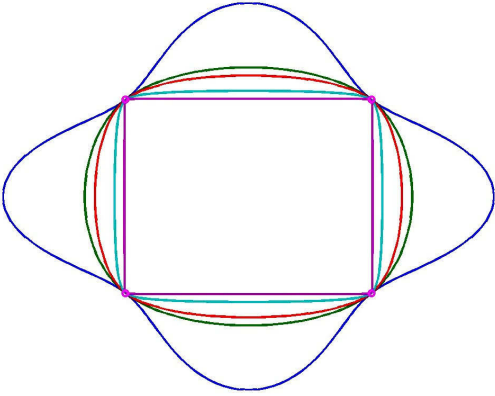


Fig. 2. Spline with global tension for various increasing values.

- (a) For $r = 3$, the rational cubic reduces to a cubic (Hermite Cubic) spline.
- (b) The spline curve always passes through F_i and F_{i+1} .
- (c) If $r_i \rightarrow \infty$, then the curve exhibits the interval tension behavior to the curve and is pulled towards the straight line joining the points F_i and F_{i+1} . That is, the curve approaches to the linear interpolant.
- (d) If $r \rightarrow 0$, then the spline curve gets loosened.

The demonstration of the spline scheme has been made in Fig. 1 and Fig. 2. Fig. 1 shows local tension behavior between two data points for corresponding shape parameter values as 1, 3, 5, 10, and 100. Similarly, Fig. 2 displays global tension behavior between all data

points for corresponding shape parameter values as 1, 3, 5, 10, and 100. Some more examples would be experimented at the end of the paper when a complete algorithm demonstration is made for automated selected values by the evolutionary algorithm.

3. CORNER DETECTION

The corner points are those points which partition the data into various pieces. Corner detection is normally related to detection of high curvature points in planar curves. A number of approaches have been proposed by researchers [2-3]. This paper proposes the simple technique based on the curvature analysis [3]. The corner points are searched on the basis of computation of high curvatures at each data point. The details of this procedure are as follows.

We approximate the curvature $C^k(i)$ at each contour point $P_i = (x_i, y_i)$ as follows:

$$C^k(i) = \frac{a_{ik} \cdot b_{ik}}{|a_{ik}| |b_{ik}|}$$

where

$$a_{ik} = (x_i + x_{i+k}, y_i - y_{i+k}),$$

$$b_{ik} = (x_i + x_{i-k}, y_i - y_{i-k}).$$

A threshold value T for $C^k(i)$ is set in such a way that a point F_i is a corner point if:

- $C^k(i)$ takes local maxima.
- $C^k(i) > T$.

The value of k depends on several factors, such as the closeness of the data points. Without threshold value, the algorithm is too sensitive to small variations of $C^k(i)$.

The demonstration of the corner detection scheme has been made in Fig. 3. A data of 451 points, for the outline of Times Roman digit "5", has been tested. One can see that 9 corner points have been detected. Some more examples would be experimented at the end of the paper when a complete algorithm demonstration is made.

4. CURVE FITTING

In order to use GAs in optimization problems, some parameters of interest in the system to be optimized have to be chosen. These parameters are called design

variables. In this work the following parameters have been used:

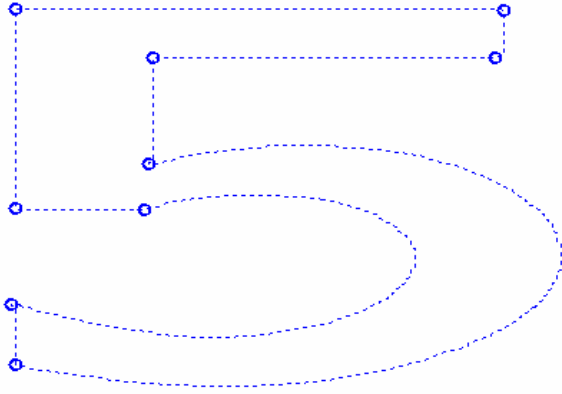


Fig. 3. Detection of corner points on the outline data of digit "5".

- the positions of the spline curve control vertices (corner points together with other initially selected points in this case), and
- the shape parameters r_1, r_2, \dots, r_{n-1} .

Then, they are represented by some set of strings coded in binary or other codes.

All initially selected data points correspond to single genes in the bit string of a chromosome. In this formulation if a gene is equal to 1, we put a knot at the corresponding data point. These knots determine the control points needed to approximate the underlying curve outline. Since we are applying Splines with shape parameters, therefore, the shape parameters associated with the pair of control points are also to be optimized, which makes the problem consisting of two search spaces at the same time. One search space is related to the optimization of the interior knots, while the other one to the positive weights associated with the calculated pair of control points. The weights consist of genes consisting of numbers, which can be positive real or integers. For example,

10 45 67 98 34 99

represents a valid gene in our case. The dual space search makes our algorithm a "Nested Genetic Algorithm".

The gene strings representing the knots and shape parameters form the initial population. Once the population has been defined, a fitness function or

objective function that measures the behavior of each individual in its environment has to be defined. This function provides a direct indication of the performance of each individual to solve the optimization problem subjected to the imposed constraints from the environment. With the population ranked according to the fitness, a group of chromosomes are selected from the population.

The method used for selection in our algorithm is the Roulette-wheel selection. The crossover used is the simple double point cross over both for the bit string chromosomes and the chromosomes representing shape parameters between the control points. The probability of crossover has been taken as 0.7 for both.

The mutation used for the population consisting of bit strings is just flipping the bits randomly. For the shape parameter population, it is evident that we can not use the same scheme, therefore the following strategy has been adopted:

- 1) For each gene in the chromosome repeat
- 2) Generate a random number uniform in the interval $[0,1]$. If the value is less than or equal to the probability of mutation, then go to step 3. Otherwise, go to step 5.
- 3) Generate a random integer number uniform in the interval zero and the gene length L . Go to the gene having the index same as the generated number.
- 4) Generate another random integer number and replace the previously selected number with it.
- 5) Move to the next gene.

The probability of mutation M is taken to be 0.001 for bit string chromosomes and 0.01 for number chromosomes.

In addition to the conventional genetic control parameters (crossover and mutation), another control parameter knot ratio R has also been used. Akaike's Information Criterion (AIC) [1] is used as a fitness measure. By using AIC we can choose the best model among the candidate models automatically. The AIC is based on the the following measurement:

$$Q_2 = \sum_{j=1}^N w_j \left\{ \left\{ Sx_j(t) - x_j(t) \right\}^2 + \left\{ Sy_j(t) - y_j(t) \right\}^2 \right\} \quad (5)$$

where N is the number of data points. It should be noted that the smaller value of Eqn. (5) gives better fitness. The

$S_x(t)$ and $S_y(t)$ are the x and y components respectively of the approximated spline $S(t)$ over the data F and w_j is the weight of data, taken to be 1 for all data points in our case. The subscript of Q means the dimension of the data.

We also propose a parameter which we have named as decimation. This parameter enables the data to be selected interval wise without losing the contour of the input data as well as the corner points determined by the corner detection algorithm. This has been used in order to decrease the gene length of the chromosomes.

In the context of genetic algorithm, a Roulette wheel selection and a double point crossover has been used. The probability of crossover C is taken to be 0.7 and the probability of mutation M is taken to be 0.001, while $0 \leq R < 0.5$ has been used. In case of the data in Fig. 1a, a decimation of 4 has been used while in case of the data in Fig. 2a, it has been kept as 2.

The summary of the algorithm is as follows:

1. Input the data to be fitted.
2. Input the control parameters.
3. Find corner points using corner detection algorithm
4. Create initial populations, for knots and shape parameters, by using random numbers.
5. For each individual in the knot population make the bits corresponding to the significant points as 1.
6. For each individual compute data fitting and obtain the fitness value.
7. If total number of generations exhausted, stop the computation, otherwise go to step 8.
8. Do selection by using the fitness values.
9. Do crossover and make the individuals of the next generation.
10. Do mutation and go back to step 5.

5. DEMONSTRATION

This section is meant to demonstrate the scheme tested on two data sets. These data sets have been taken by detecting the boundary of the images, in Fig. 4 and Fig. 6, after scanning. The Sobel edge detector [7] has been used to compute the boundary data shown in Fig. 5(a) and Fig. 7(a) respectively.

The Fig. 5(a) is composed of 1524 planar data points, after which were reduced to 381 points after applying a

decimation of 4. The corner detection algorithm detected 17 corner points (see Fig. 5(b)). Fig. 5(c) is simply a cubic spline fit to the corner points. The evolutionary algorithm was run for 120 generations with a population size of 100. The algorithm converged at 40th generation (see Fig. 5(d)).

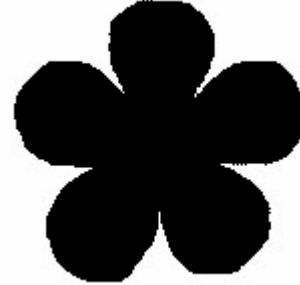
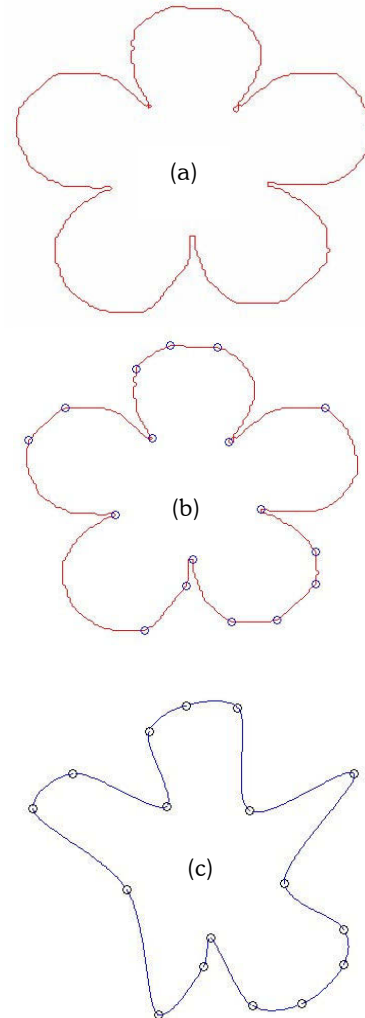


Fig. 4. A bitmapped flower image.



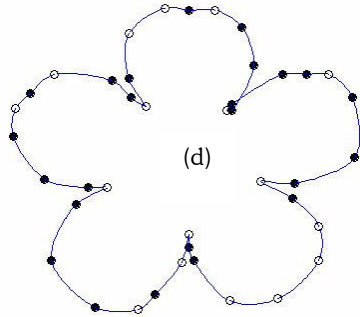


Fig. 5. (a) The outline data of the flower image shown in Fig. 4, (b) After detecting the corner points as “circles”, (c) Spline approximated to the corner points before running GA, (d) Spline fit at 40th generation, it converges (the extra points were obtained as “bullets”).

Fig. 7(a) is composed of 1620 planar data points, which were reduced to 406 points after applying a decimation of 4. The corner detection algorithm detected 9 corner points (see Fig. 7(b)). The evolutionary algorithm was run for 120 generations with a population size of 100. Fig. 7(c) is simply a cubic spline fit to the corner points. The evolutionary algorithm was run for 120 generations with a population size of 100. The algorithm converged at 50th generation (see Fig. 7(d)).



Fig. 6. An Arabic alphabet “Hamza”.

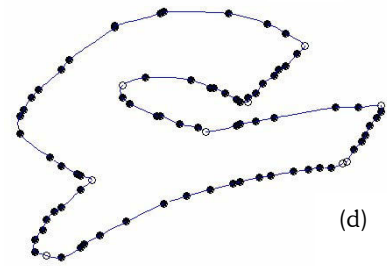
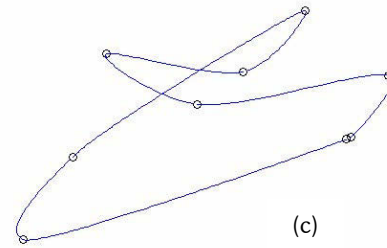
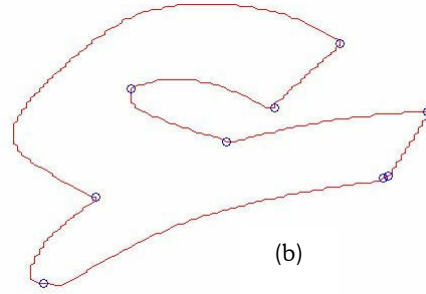
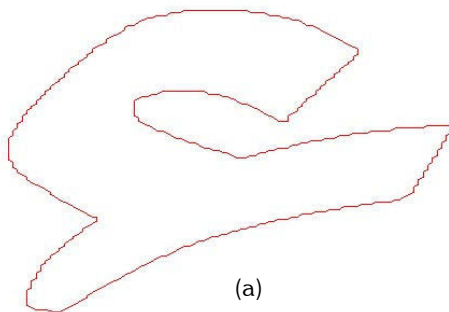


Fig. 7. (a) The outline data of a bitmapped image, (b) After detecting the corner points “circles”, (c) Spline approximated to the corner points before running GA, (d) Spline fit at 50th generation it converges (the extra points were obtained as “bullets”).

6. CONCLUDING REMARKS

This paper has introduced a technique to represent two dimensional shapes by data fitting using genetic algorithm and spline idea. The scheme presented is effective in the determination of the appropriate number of knots and their locations simultaneously for as large data as available. Moreover, the determination of shape parameters also help to get a reasonable approximation. The genetic algorithm is partly aided by the corner detection for the determination of corner points. These corner points are important in capturing the shape of the data.

Some of the suggested future work directions may be as follows. Instead of rational splines, one can think of using the Non-rational splines to be used, incorporating the optimization of weights. This might help to reduce the computation cost to a significant amount. This work

is in progress with the author and expected to be sent for publication as a subsequent paper.

Use of Parallelism is another idea to be introduced for faster visualization of the data. In this case, the algorithm needed to be redesigned. It is expected that the load of computation will be concentrated in steps 5 and 6 of the algorithm in Section 4. We can apply parallel computing here to save computational time. The authors are currently looking for a practical implementation of such a parallel algorithm.

Acknowledgement: The author is thankful to the anonymous referees for their constructive and helpful comments in the construction of the paper. The author also acknowledges the support of King Fahd University of Petroleum and Minerals in the development of this work.

7. REFERENCES

- [1] Akaike, H., A new look at the statistical model identification. *IEEE Trans. Automatic Control*, 19(6), (1974), 716-723.
- [2] Chetverikov, D., and Szabo, Z., A simple and efficient algorithm for detection of high curvature points in planar curves. *Proc. 23rd Workshop of the Australian Pattern Recognition Group*, (1999), 175-184.
- [3] Davis, L., Shape Matching using Relaxation Techniques, *IEEE Trans. PAMI*, Vol. 1, (1979), 60-72.
- [4] Farin, G. E. *Curves and Surfaces for Computer Aided Geometric Design*, Academic Press, New York, (1994).
- [5] Goldberg, D. E., *Genetic Algorithms in Search, Optimization and Machine Learning*. Addison Wesley, (1989).
- [6] Harada, T., Yoshimoto, F., and Aoyama, Y., Data Fitting using a genetic algorithm with real number genes. *Proc. of the IASTED International Conference on Computer Graphics and Imaging*, (2000), 131-138.
- [7] Jain, R., Kasturi, R., Schunck, B. G., *Machine Vision*, McGraw-Hill, (1995).
- [8] Moriyama, M., Yoshimoto, F. and Harada, T., A method of plane data fitting with a genetic algorithm. *Proc. of the IASTED International Conference on Computer Graphics and Imaging*, (1998), 21-31.
- [9] Sarfraz, M., Optimal Curve Fitting to Digital Data, *International Journal of WSCG*, Vol 11(1), (2003), 128-135.
- [10] Sarfraz, M., and Razzak, M. F. A., A Web Based System to Capture Outlines of Arabic Fonts, *International Journal of Information Sciences*, Elsevier Science Inc., Vol. 150(3-4), (2003), 177-193.
- [11] Sarfraz, M. and Khan, M. A., An Automatic Outline Fitting Algorithm for Arabic Characters, *Lecture Notes in Computer Science 2669: Computational Science and Its Applications*, Eds.: V. Kumar, M. L. Gavrilova, C. J. K. Tan, and P. L' Ecuyer, Springer-Verlag, (2003), 589-598, ISSN 0302-9743.
- [12] Sarfraz, M, and Raza, A, Visualization of Data using Genetic Algorithm, *Soft Computing and Industry: Recent Applications*, Eds.: R. Roy, M. Koppen, S. Ovaska, T. Furuhashi, and F. Hoffmann, ISBN: 1-85233-539-4, Springer, (2002), 535 - 544.