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A Survey of suboptimal polygonal approximation methods

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Abstract

Polygonal approximation detects a set of feature points on the boundary of a shape that constitute the vertices of the shape. In particular, shape representation by polygonal approximation has become a popular technique due to its easiness, locality and compression. This paper presents a survey of methods that detects a set of dominant points that constitute the boundary of a 2D digital planar curve with an iterative procedure and a comparison of the polygonal approximation algorithms on various shapes with varying number of dominant points is made along with the demerits of each of the techniques.

Keywords: Polygonal approximation, Dominant point detection, Iterative merge.

Introduction

According to human perception information regarding the shape of a curve is concentrated at corners. Its detection is important for the contour methods of shape analysis. Such points are commonly known as dominant points. Dominant points are usually identified as points with extreme local curvature. Polygonal approximation seeks to find a polygon that best fits a digital curve and such polygon may be based on connecting the detected dominant points. The polygonal approximation is used in important applications to recognize planar objects for (e.g. Goyal et al. [1]), for the recognition of numerals on number plate of a car (e.g. Grumbach et al. [2]), for the representation of geographic information (e.g. Semyonov [3]), for electroculographic biosignal processing, for shape understanding [4] and image analysis (with the help of a set of feature points [5]) and for image matching algorithms [6, 7, 8].

There are many approaches developed for detection of dominant points. Such algorithms can be classified into three main groups namely, sequential approach, split-and-merge approach and heuristic-search approach. For sequential approach, Sklansky and Gonzales [9] proposed scan-along procedure. Sequential approaches are simple and fast, but the results are dependent upon the starting point. Ray and Ray [10] proposed a method that uses two criteria functions namely, the ratio of the arc length of the line segment and the ratio of the distance from a point to the line segment to the length of the line segment. Yin [11] proposed polygonal approximation technique using ant colony search algorithm. Heuristic search algorithms are computationally expensive. This paper presents a study of suboptimal closed curve approximation techniques along with an insight of drawbacks. Section 2 narrates how the suboptimal technique obtains initial set of points. Then the subsequent sections present brief study of polygonal approximation techniques that uses iterative merging. In the penultimate section, the evaluation measures and a comparison of the algorithms on popular shapes is presented. Finally, in the last section, conclusion is drawn.

Break point detection

Break points are detected using Freeman's chain-code [12]. These break points become the initial set of dominant points. Calculation of error associated with each dominant point is discussed in this section. A digital curve can be defined as set C such that.

$$C = \{ p_i(x_i\ y_i) \ /\ i = 1.2,\dots , n\} \qquad (1)$$

Where n is the number of points and p_i is the ith point with coordinate (x_i ,y_i). The Figure.1 shows a polygon of break points for the popular shape chromosome. We can determine these break points easily by assigning Freeman's chain code [12] to the curve. For that an integer value c_i varying from 0 to 7 is assigned to each curve point (p_i) according to the direction of the next point. The Figure 2 shows the value of Freeman's chain code

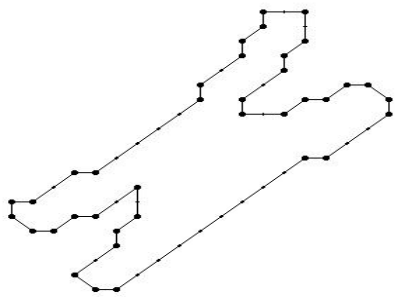

Figure 1. High curvature points for chromosome shape

for all possible directions, where $(¼)\pi c_i$ is the angle between x-axis and the vector c_i. Any point p_i is a break point if its chain code (ci) is not equal to the chain code of previous point (p_{i-1}).

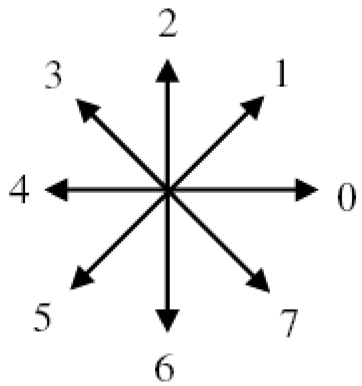

Figure 2 Freeman's chain code

That is if $c_i \neq c_{i-1}$ then point p_i is a break point. The break points are taken as initial set of dominant points and these are called as dominant points from here on. After obtaining the set of points from chain code assignment these points become initial set of dominant points. Different researchers use different criterion metric to detect good as well as high curvature points on the digital planar curve from the set of initial curvature points.

Greedy Iterative point elimination

Pikaz and Dinsten [13] proposed an algorithm for polygonal approximation based on iterative merging. In the conventional approach towards polygonal approximation, the vertices of the polygon are searched for. But it can be done in opposite direction by choosing at each iteration a point that will not be a vertex and eliminating the same based on certain criterion. The points that are left after a stopping criterion is satisfied constitute the vertices of the polygon. They used area of triangle and square of the height of the triangle as measures of collinearity and suppress those points for which the value of co linearity measure is less than a pre-specified value. This algorithm is independent of starting point and may not result in an optimal approximation but it will converge to a solution close to an optimum because of its small incremental nature. Noise tolerance issue need to be addressed.

Critical point detection

Zhu and Chirlian [14] use similar approach for polygonal approximation. Initially, this approach finds the list of pseudo critical points. Then it transfers the contour to polar coordinates because it is easier to handle rotation and scale change in polar coordinates than in rectangular coordinates. Then critical level was assigned to each pseudo critical points I(Pi) on the curve. The algorithm then starts eliminating the least critical points whose level is below than the specified critical value and it updates the critical level of $I(P_{i-1})$ and $I(P_{i+1})$. Then this algorithm iteratively deletes the points on the curve till the required level of approximation is obtained. This algorithm is geometric invariant, but the authors need to address noise tolerance issue as well as visiting points in counter clock wise direction.

Polygon evolution by vertex deletion

Latecki and Lakamper [15] presents a method that yield low quality of polygonal approximation because of the use of unsuitable relevance measure (K) given by

$$K(v) = K(\beta, l_1, l_2) = \frac{\beta l_1 l_2}{l_1 + l_2} \quad (2)$$

The contribution of a vertex is measured by its relevance measure K. This procedure eliminates point with the lowest value of K, and then the relevance measure of neighboring vertex is updated. This procedure recursively eliminates points in the contour in this way until the required level of approximation is reached. The relevance measure (K) only depends on the turn angle (β) and length of neighboring vertices (l_1 and l_2) and do not take care of overall distortion (e.g. ISE) from the actual shape. Noise tolerance issue need to be addressed.

Reverse polygonization

Masood [16] proposes a polygonal approximation technique using reverse polygonization. The break points are detected using freeman's chain code [11]. These break points become the initial set of points. To calculate the contribution associated with each dominant points two neighboring dominant points are joined with a straight line. The maximum perpendicular (squared) distance of all boundary points between successive from the straight line is called as associated error value. The point elimination starts from an initial set of break points and eliminates those points whose squared perpendicular distance is less than a pre-specified value. This algorithm does not address the issue of noise tolerance.

Optimized algorithm

Massod [17] proposes an optimized algorithm where a recursive stabilization technique is applied to move a vertex so that the integral square error of the entire approximation is reduced to the minimal possible. After elimination of the dominant point with the least associated error value, a stabilization technique is applied that moves a dominant point so that the integral square error of the entire approximation is reduced to the minimal possible. The stabilization process is called recursively until no merging is required.

Break point suppression

Camorna et.al [18] Describe a method for polygonal approximation through break point suppression. The set of initial break points is obtained from the initial boundary. The points whose distance from the straight line that joins the next point and previous point is lower than threshold value (d_t) are deleted, because they are collinear points. Termination of the algorithm is based on the decrease in length $\Delta l_{i,j}$ associated with a deleted break point (P_i)

and the maximum error $E_{\infty j}$ obtained in the j^{th} iteration. The authors need to establish noise tolerance issue.

Evaluation measure

The evaluation of a polygonal approximation technique may be based on various measures. The two most common measures are the compression ratio (CR), the integral square error (ISE), maximum error (MaxErr) and the figure of merit. The CR is the ratio between number of points of the input curve (n) and the number of detected dominant points (nDP). The ISE is the sum of squared (perpendicular) distance of all curve points from approximating polygon. Sarkar [19] combined these two measures as a ratio producing figure of merit (FOM). [19] Sarkar's FOM is not suitable for comparing approximation results with different number of dominant points[20] Maximum error is the maximum deviation of approximating polygon from the original curve, measured as a squared distance. Figure of merit makes the tradeoff between the compression ratio (CR) and the total distortion (ISE) caused.

$$CR = \frac{n}{nDP} \tag{3}$$

$$ISE = \sum_{i=0}^{n} e_i \tag{4}$$

$$MaxErr = max_{i=1}^{n} \{e_i\} \tag{5}$$

$$FOM = \frac{CR}{ISE} \tag{6}$$

The results of the polygonal approximation algorithms using different methods are displayed in Table 1 for a number of digital planar curves, namely, a chromosome shaped curve, a leaf shaped curve and a curve consisting of a number of semi circles.

Table 1 Comparative result of the popular shapes (chromosome, leaf and semicircle)

Shape	Methods	nDp	CR	MaxErr	ISE	FOM
Chromosome	Zhu and chirlian [14]	18	3.33	0.71	3.44	0.80
	Latecki and Lakamper[15]			1.99	27.0	0.12
	Pikaz and Dinstein [13]			0.51	2.88	1.15
	Carmona et.al [18]			0.51	3.01	1.11
	Masood [16]			0.52	2.88	1.16
	Masood[17]			0.514	2.76	1.18
	Method	16	3.75			
	Zhu and chirlian [14]			0.71	4.68	0.80
	Latecki and Lakamper[15]			1.98	32.0	0.12
	Pikaz and Dinstein [13]			0.51	3.84	0.97
	Carmona et.al [18]			0.51	3.97	0.95
	Masood [16]			0.52	3.84	0.98
	Masood[17]			0.63	3.49	1.07
	Method	15	4.00			
	Zhu and chirlian [14]			0.74	5.56	0.72
	Latecki and Lakamper[15]			1.98	38.5	0.10
	Pikaz and Dinstein [13]			0.63	4.14	0.96
	Carmona et.al [18]			0.63	4.27	0.94
	Masood [16]			0.63	4.14	0.97
	Masood[17]			0.76	3.88	1.03
Leaf	Method	23	4.29			
	Zhu and chirlian [14]			0.89	11.5	0.44
	Latecki and Lakamper[15]			2.83	60.4	0.09
	Pikaz and Dinstein [13]			0.74	11.2	0.38
	Carmona et.al [18]			0.74	10.6	0.49
	Masood [16]			0.74	10.6	0.49
	Masood[17]			0.92	9.40	0.55
	Method	22	5.45			
	Zhu and chirlian [14]			0.89	13.7	0.39
	Latecki and Lakamper[15]			2.83	60.5	0.09
	Pikaz and Dinstein [13]			0.744	11.0	0.49
	Carmona et.al [18]			0.63	4.14	1.31
	Masood [16]			0.76	3.88	1.40
	Masood[17]			0.63	3.97	1.37
Semicircle	Method	30	3.40			
	Zhu and chirlian [14]			0.63	4.30	0.79

Latecki and Lakamper[15]			1.00	4.54	0.75
Pikaz and Dinstein [13]			0.65	3.39	1.00
Carmona et.al [18]			0.49	2.91	1.17
Masood [16]			0.49	2.91	1.17
Masood[17]			0.49	2.64	1.29
	26	3.92			
Zhu and chirlian [14]			0.63	4.91	0.80
Latecki and Lakamper[15]			1.21	13.0	0.30
Pikaz and Dinstein [13]			0.65	5.04	0.77
Carmona et.al [18]			0.63	4.91	0.80
Masood [16]			0.63	4.91	0.80
Masood[17]			0.49	4.05	0.97

Conclusion

In this paper we have presented an overview of polygonal approximation techniques for digital planar curve using iterative merging. The performance measures are discussed. The goodness of a polygonal approximation results always depends on allowable error value. On an average among all the suboptimal techniques Masood [17] algorithm results are better than other algorithms

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