A Method for Dominant Point Detection

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Abstract

In this paper, an algorithm for dominant point detection is proposed. It uses the concept of break points to determine an asymmetric region of support of each point on the curves. The curvature is then estimated by the cosine values to assess the degree of possibility of a point being a dominant point. Finally, The dominant points are located by finding the local curvature extreme among the determined asymmetric region of support.

Keywords. Dominant point detection, polygonal approximation, curvature, region of support.

1. Introduction

Attneave [2] pointed out that information on a curve is concentrated at the dominant points with curvature extreme. Over the years, many dominant point detection algorithms have been developed. Two categories of algorithms for detecting dominant points are: (1) polygonal approximation approaches and (2) corner detection approaches.

Sklansky and Gonzalez [12] sequentially partitioned the curve by cone-intersection. Wall and Danielsson [14] segmented the curve at the points which its area deviation per length unit exceeds a preset value, sequentially. Ramer [7] split the curve into two smaller curves at the point with maximum deviation until the maximum deviation is less than a preset threshold, recursively. Ansari and Delp [1] detected the points with maximal curvature by

Gaussian smoothing method as starting points for the following split-and-merge procedure. Kankanhalli [6] started by specifying four dominant points and their support regions to recursively extract the other dominant points. Ray and Ray [9] proposed the concept of rank of a point and followed a split-and-merge procedure to approximate the curves. Dunham [4] determined the optimal approximated polygon by the dynamic programming technique. Yin [17] approximated polygons by employing the genetic algorithm to find the optimal or near-optimal solution.

Rosenfeld and Johnston [10] extracted the vertices with local maximum and minimum cosine values as corners. Rosenfeld and Weszka [11] improved it by averaging the cosine values as the estimated curvatures. Wu and Wang [16] detected the dominant points by the curvature-based polygonal approximation method. Wang et al. [15] proposed the bending value to detect corners.

In early algorithms, the region of support is set to the same for all of the points on the curve. A large region of support will smooth out fine features and a small one will generate too many dummy dominant points. Therefore, it is difficult to select a common region of support for a multi-scaled curve.

Teh and Chin [13] pointed out that the detection of dominant points primary on the precise determinant of region of support. They used chord length and distance to determine the region of support for each

point independently.

Ray and Ray [8] indicated that an asymmetric region of support is more reasonable and more natural than a symmetric region of support. That is, the left support and the right support for the point of the interest are not the same. Once the left support and the right support have been determined, the k-l-cosine value is computed as the estimated curvature.

Cornic [3] addressed that, as for the Teh and Chin algorithm, the Ray and Ray algorithm is not robust in presence of noise. Evaluating the significant of point by the other points of the curve is proposed. He used the chain code properties of digital straight line to compute two vectors of significance. The dominant points are then detected by a logical unction. However, the computation is complex in determining left support and right support. In addition, it is difficult to select a best logical function (strategy) on the dominant point identification step.

In this paper, we focus on developing a simple method to determine an asymmetric region of support. The break point detection procedure is applied to find the candidates of dominant points on the curve. The left and right regions of support are then determined in the same time. The experimental results show that the method is efficient and effective in detecting dominant points. In section 2, we will illustrate the dominant point detection methods as well as the proposed algorithm. Section 3 will present the experimental results of the new strategy. Some concluding remarks are then given in section 4.

2. Dominant Point Detection

The points with local maximum curvature are considered as the dominant points. For a continuous curve, curvature of a point is defined as the rate of change of slope as a function of arc length. That is,

the curvature $\kappa=d\theta/ds$. However, the above definition does not hold for a digital curve, due to that there exist no mathematical definition for the digital curve. Therefore, most of the existing algorithms focus on curvature estimation by use of the information of the neighbors. The presented method intends to determine the region of support for each point quickly.

A digital closed curve C can be defined as the set consisting of n consecutive points

$$C = \{P_i(x_i, y_i) | i = 1, 2, ..., n\}, \tag{1}$$

where n is the number of points, P_i is the i th point with coordinate (x_i, y_i), and points P_{i-1} and P_{i+1} are neighbors of point P_i (modulo n).

The Freeman's chain code [5] of C consists of the n chain codes and is denoted as $c_1 c_2 ... c_n$, where $c_i = c_{i\pm n}$ and all indices are modulo n. All integers are modulo n. That is, each of the vectors is assigned to an integer c_i varying from 0 to 7, where $\frac{1}{4}\pi c_i$ is the angle between the x-axis and the vector, for i=1, 2, …, n (see Fig. 1).
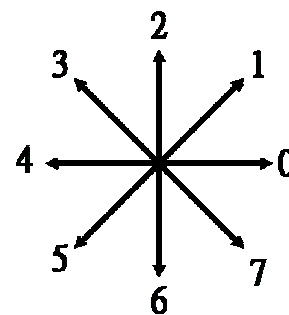

Fig. 1. Freeman's chain codes.

It is reasonable to exclude those linear points, since the points on straight line cannot be considered as the dominant points [16]. The survived points are candidates of dominant points and denoted as the break points. The linear points can be removed by

tracking the chain codes. The following rule is applied to identify those linear points.

Rule 1. If $c_{i-1}=c_i$, then the point P_i is a linear point. Otherwise, it is a break point.

An example of chain-coded curve is shown in Fig. 2. The points P_2 and P_3 are linear points ($c_1=c_2=c_3=0$), and the points P_1 and P_4 are break points ($c_{22}=2\neq0=c_1$ and $c_3=0\neq7=c_4$). By tracking the chain codes of the curve, the break points can be located. They are marked as "○" in Fig. 2.
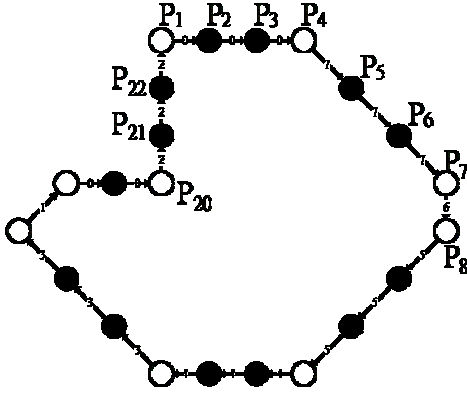

Fig. 2. Break point detection by the relationship between points P_i and the chain codes c_i on the curve. Chain codes: 0007776555444333100222. (○) break point; (●) linear point.

It will reduce the computation time both in determination of support region and curvature estimation, if only the set of break points are considered as the possible dominant points. In fact, once the break points have been identified, the left support as well as the right support for each point can be determined quickly. The considering region of support is asymmetric as in Ray and Ray [8]. That is, the length of the right region of support and that of the left region of support should be determined independently. An intuitive approach is to use the information of break points while determining the region of support. The determination of support can be done by use of its previous and next break points as the left and right supports, respectively. The points between previous break point and the next break point consist the region of support for the point of interest. For example, the points P_4 and P_8 are the left and right supporting points of the point P_7, respectively (see Fig. 2). The region of support for the point P_7 is defined as the set of points P_4 to P_8.

Suppose that there are m break points on the curve and the i th break point B_i is the b_i th point on the curve. The lengths of left and right regions of support for B_i are denoted as l_i and k_i, respectively. The region of support of each break point can be determined by the following rules

Rule 2. For the break point B_i, the left arm terminated at B_{i-1} and the right arm terminated at B_{i+1}. The length of left region of support $l_i=b_i-b_{i-1}$, while the length of right region of support $k_i=b_{i+1}-b_i$. The length of region of support $r_i=b_{i+1}-b_{i-1}+1$. The region of support for the break point B_i consists of the set

$$\{P_{b_{i-1}},...,P_{b_i},...,P_{b_{i+1}}\}.$$

The k-l-cosine value is used to estimate curvature of each break point. For the break point B_i, it is defined as

$$\cos_{ikl} = \frac{\bar{a}_{ik} \bullet \bar{b}_{ik}}{\left|\bar{a}_{ik}\right| \left|\bar{b}_{ik}\right|}, \tag{2}$$

where $\bar{a}_{ik} = (x_{b_{i+1}} - x_{b_i}, y_{b_{i+1}} - y_{b_i})$ and

$\bar{b}_{ik} = (x_{b_{i-1}} - x_{b_i}, y_{b_{i-1}} - y_{b_i}).$

Once the k-l-cosine values have been determined, the next step is to identify the dominant points. Five conditions of suppressing the break point B_i from the set of candidates of dominant points are given as follows.

Condition A. $cos_{ikl} < \varepsilon$ (3)

Condition B. $cos_{ikl} < cos_{jkl}$, for $j=i-1$ or $i+1$ (4)

Condition C. $cos_{ikl} = cos_{i-1,kl}$ and $r_i < r_{i-1}$ (5)

Condition D. $cos_{ikl} = cos_{i+1,kl}$ and $r_i < r_{i+1}$ (6)

Condition E. $cos_{ikl} = cos_{i+1,kl}$ and $r_i = r_{i+1}$ (7)

It is necessary to suppress those break points whose curvature less than a preset threshold ε (Condition A). Condition B indicates that a dominant point should have local maximum curvature. For two neighboring break points, the point with smaller length region of support is removed (Conditions C and D). Further, if two consecutive points has the same curvature and the same length region of support, discard the later one (Condition E). The survived break points with local maximum over its region of support are denoted as the dominant points. Therefore, we can locate of dominant points by the following rule.

Rule 3. If one of the Conditions A to E is satisfied, then the break point B_i is removed from the set of candidates of dominant points.

Overall, the proposed method is summarized as follows:

Step 1. Extract break points from Freeman's chain codes by Rule 1.

Step 2. Determine region of support for each break point (k_i and l_i, $i=1, 2, ..., m$) by Rule 2.

Step 3. Compute the estimated curvatures for all of the break points (cos_{ikl}, $i=1, 2, ..., m$) by Eq. (2).

Step 4. Identify the dominant points by Rule 3.

3. Experimental Results

The proposed method has been applied to four commonly used curves in many studies [8]. They are the chromosome curve (Fig. 3(a)), infinity curve (Fig. 4(a)), leaf curve (Fig. 5(a)), and semicircle curve (Fig 6(a)). In the experiment, the curvature threshold ε is set to -0.5. By tracking the chain codes, the break points can be determined, and they are shown in Figs. 3(b), 4(b), 5(b), and 6(b), for the four types of curves, respectively.
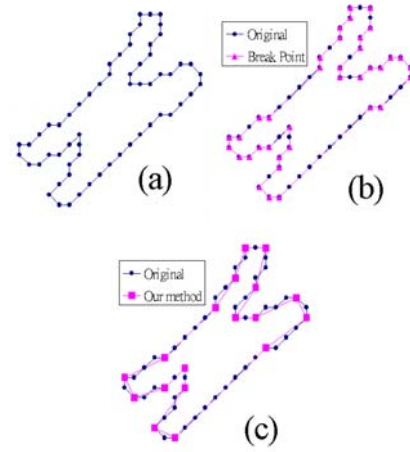

Fig. 3. The chromosome curve: (a) original, (b) break points, and (c) dominant points.
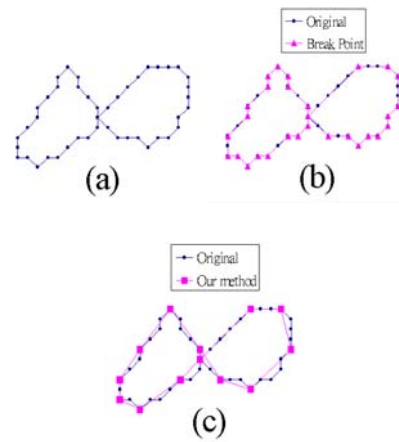

Fig. 4. The infinity curve: (a) original, (b) break points, and (c) dominant points.

In order to assess the performance of the proposed method, six performance evaluation criteria were used in the experiment. Most of them were used by Conic [3]. They are the number of the dominant points, inverse of compression ratio, sum of square error, maximum error, weighted sum of square error, and weighted maximum error.
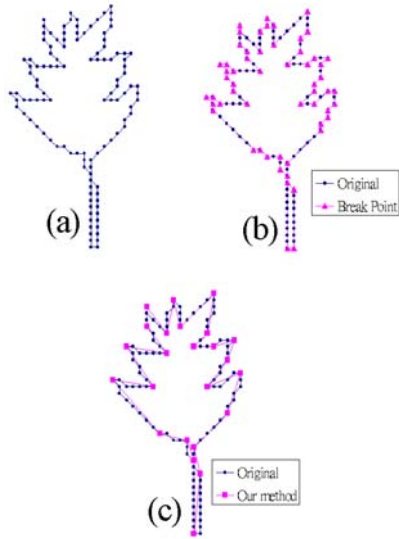

Fig. 5. The leaf curve: (a) original, (b) break points, and (c) dominant points.
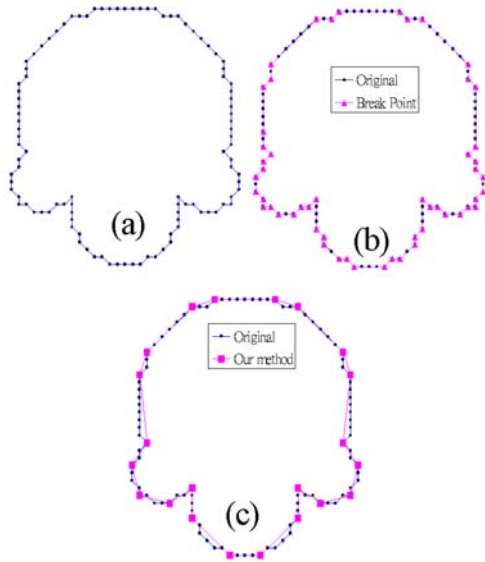

Fig. 6. The semicircle curve: (a) original, (b) break points, and (c) dominant points.

(1) Number of the dominant points (n_d): It is desirable to have the number of dominant points as small as possible.

(2) Inverse of compression ratio (n_d/n): One of the objectives for dominant point detection is to reduce the amount of data. The smaller the inverse of compression ratio is, the more effective in data reduction the method is.

(3) Sum of square error (E_2): This criterion assesses the distortions caused by the approximated curve. The smaller the sum of square error is, the better descriptive ability the method is. It is defined as

$$E_2 = \sum_{i=1}^{n} e_i^2, \tag{8}$$

where e_i is the distance from P_i to the approximated segment.

(4) Maximum error (E_1): This criterion assesses the approximated errors. The smaller the maximum error is, the better fitness the method is. It is defined as

$$E_1 = \max_{i=1}^{n} \{e_i\}. \tag{9}$$

(5) Weighted sum of square error (WE_2): The weighted sum of square error is to compromise the compression ratio and the sum of square error. It is defined as

$$WE_2 = \frac{n_d}{n} \times E_2 \tag{10}$$

(6) Weighted maximum error (WE_1): The weighted maximum error is to compromise the compression ratio and the maximum error. It is defined as

$$WE_1 = \frac{n_d}{n} \times E_1 \tag{11}$$

The objective for detecting dominant points is to minimize all of the six criteria, whereas it seems to be impossible to obtain an optimal solution. The

objective of this paper is not to propose an optimal solution to dominant point detection. Alternatively, it attends to show that the new method is very simple and it can improve the performance of the family of region of support determining algorithms. The experimental results of our method and of the other methods are listed in Table 1. The presented result of the Conic's method is that of the best performance indicated in his paper.

Table 1. Results of the proposed method and of the other methods.

Curve	Method	n_d	n_d/n	E_2	E_1	WE_2	WE_1
Chromosome (n=60)	T & C	15	0.25	7.20	0.71	1.88	0.18
	R & R	18	0.30	4.81	0.65	1.44	0.20
	Cornic	17	0.28	5.54	0.86	1.57	0.24
	Our	18	0.30	3.72	0.60	1.12	0.18
Infinity (n=45)	T & C	13	0.29	5.93	1.00	1.71	0.29
	R & R	15	0.33	4.39	0.72	1.46	0.24
	Cornic	10	0.22	4.30	0.78	0.96	0.17
	Our	13	0.29	5.01	0.73	1.45	0.21
Leaf (n=120)	T & C	29	0.24	14.96	0.99	3.62	0.24
	R & R	32	0.27	14.18	0.99	3.78	0.26
	Cornic	*	*	*	*	*	*
	Our	24	0.20	13.70	0.99	2.74	0.20
Semicircles (n=102)	T & C	22	0.22	20.61	1.00	4.45	0.22
	R & R	27	0.26	11.50	0.88	3.04	0.23
	Cornic	30	0.29	9.19	0.88	2.70	0.26
	Our	22	0.22	12.00	0.88	2.59	0.19

* not provided

For the chromosome curve, Teh & Chin's method detects the minimum number of dominant points, but it has the largest E_2. It is seen that our method has the smallest E_2, E_1, WE_2, and WE_1. That is, our method has the better performance than the other methods. For infinity curve, Cornic's method seems to have the best performance. However, our method has

smaller sum of square error than that of Cornic's method. In addition, our method detect the same number of dominant points to that of Teh & Chin's method, whereas it is superior to Teh & Chin's method since all of the other criteria of our method are smaller than that of Teh & Chin's method. The new method has higher compression ratio than that of Ray & Ray's method, and it has the smaller values of WE_1 and WE_2. The proposed method has the smallest n_d for the leaf curve (Cornic's method doest not provide the result in his paper). Further, it has the best performance on all of the other criteria while comparing to the other methods. That is, the new method can detect a set of the most significant points that has the minimum number of points and it can approximate the original curve very well. Again, the same finding can be seen for the semicircle curve. Especially, it detects a set of symmetric dominant points for the semicircle curve.

The detected dominant points superimposed to the respective original curves are shown in Figs. 3(c), 4(c), 5(c), and 6(c), respectively. Overall, the new method proposes a simple method to determine region of support for each point, and it perform very well while comparing to the other methods.

4. Conclusions

Dominant points are those points that have curvature extreme on the curve and they can suitably describe the curve for both visual perception and recognition. Teh-Chin [13] proposed an adaptive method to determine region of support for each point. Ray and Ray [8] further suggested that an asymmetric region of support is more reasonable and more natural than a symmetric region. Cornic [3] used the information of the other points to determine the support region.

In this paper, the concept of linearity is used to

find a set of break points. The asymmetric region of support for each break point is then determined in the same time. The proposed method is fast and it needs no input parameters. From the experimental results, it is show that the proposed method is efficient and effective in detecting dominant points.

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