

ON MODELING GENETIC PATTERN SEARCH FOR BLOCK MOTION ESTIMATION

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ABSTRACT

Pattern search algorithms, such as diamond search, hexagonal search and their variations, have been widely adopted by the block matching motion estimations in the modern video encoding systems. Recently we propose a weighting function (WF) to model the number of search points of a pattern search. Yet, WF fails to properly describe the behavior of the genetic pattern search algorithms due to some over-simplifications in their models. Therefore, we propose a refined weighting function (RWF) to more accurately describe both genetic and non-genetic pattern searches. In addition, we propose a new search algorithm, namely, the momentum directed genetic rhombus pattern search (MD-GRPS). It can accelerate the previous genetic rhombus pattern search by 8% on the average and this concept can be applied to the other genetic pattern searches.

Index Terms—Refined weighting function, Genetic pattern search, Block motion estimation, Video coding.

1. INTRODUCTION

The modern video coding systems [1][2] adopt block motion estimation (BME) to remove inter-frame redundancy of image sequences. Despite the success of BME in compression, it requires a huge amount of computing power particularly for sophisticated coding algorithms that include multiple reference frames and variable size motion estimations. Therefore, researchers have been developing fast algorithms to reduce computation without sacrificing the coding efficiency. Among all BME algorithms, the pattern search algorithms, such as diamond search [3], hexagonal search [4] and their enhanced versions [5][6], are the most popular due to their simplicity and effectiveness. Moreover, because real image sequences may have different amount of motion activities in different parts of a long sequence the so-called adaptive schemes [7][8][9] that switch between two or more search patterns were also proposed.

In [8], we use the notion of weighting function (WF) to predict the efficiency of a pattern search algorithm. The WF is defined as the *minimum* number of search steps that a specific pattern search algorithm can achieve when the

matching error surface is monotonic. Therefore, its values depend on the search pattern used. Given the probability distribution of the motion vectors (MVs) of a video sequence, we can predict the performance (search points) of a BME algorithm by using its WF when it is applied to this particular video sequence.

In [8] and [10], we combine the genetic optimization method with pattern search to further reduce computation. The so-called *genetic pattern search* algorithm is thus devised. It matches the ideal minimum WF and indeed it shows substantial performance improvement. However, the afore-mentioned WF is not adequate in characterizing the behavior of the genetic pattern searches because WF does not represent the *average* performance (search points). This difference is due to the fact that, even when the matching error surface is monotonic, the genetic pattern search picks up the search direction randomly but the classical pattern searches move along the steepest descent path on the matching error surface towards the best matching point. The purpose of this paper is to construct a more accurate model (essentially, a better WF) for the genetic pattern search. In this process, we also devise a new type of genetic pattern search that further reduces the computation.

The remaining parts of this paper are organized as follows. Section 2 analyzes and models the behavior of a genetic pattern search. Based on this analysis, a new search algorithm is proposed in Section 3. Section 4 shows the experimental results of the proposed algorithm in comparison with some classical and genetic pattern searches. Finally, a brief summary is given in Section 5.

2. ANALYSIS ON GENETIC PATTERN SEARCH

Because WF does not well convey the randomness nature of the genetic pattern search, here we propose a refined weighting function (RWF). We assume the matching error (distortion) surface is *unimodal* and *monotonic*. In other words, let the optimal point be the origin, and $\mathbf{u}=(x_1, y_1)$ and $\mathbf{v}=(x_2, y_2)$ be two points in the domain. The distortion at \mathbf{u} , $D(\mathbf{u})$, is smaller than $D(\mathbf{v})$, if $|x_1| < |x_2|$ and $|y_1| \leq |y_2|$ or if $|x_1| \leq |x_2|$ and $|y_1| < |y_2|$. The RWF, $RWF(x,y)$ is defined to be the *average number* of search points (SPs) needed by a search algorithm, when the best matching point is located at (0,0) and the starting point is (x,y). As an example, we will

construct the RWF for the genetic rhombus pattern search (GRPS) in [10]. The flow chart of GRPS is in Fig. 1 and its search patterns are shown in Fig. 2. In the search process, only one (black dot, for example) out of the four (grey and black) points in Fig. 2(a) is randomly chosen as the next check point. And the search ends when all four (black) points in Fig. 2(b) have been checked and all of them have larger matching errors than that of the center (white) point.

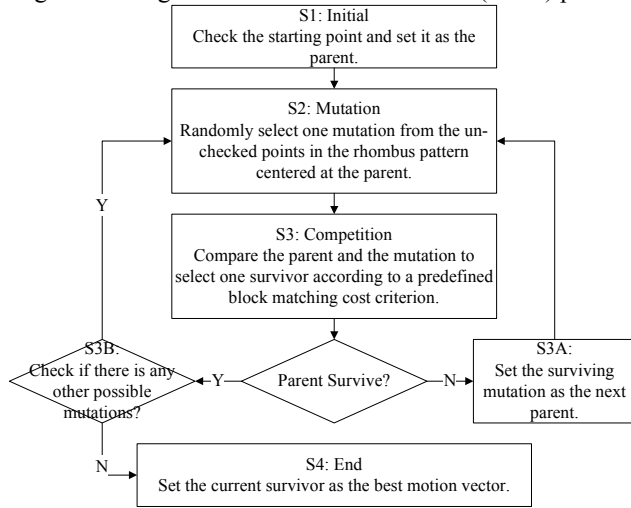


Fig. 1 GRPS flow chart

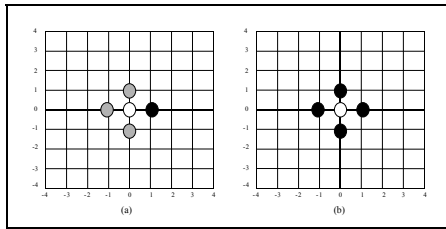


Fig. 2 GRPS search pattern

Under the unimodal and monotonic matching error surface assumption, the number of mutations with matching error smaller than that of the current point is decided by the relative position of the current point to the best matched point as shown in Fig. 3. Specifically, there are two types of starting search point cases (S1 and S2) and two types of intermediate search point cases (M1 and M2) for GRPS, as shown in Fig. 4. Herein, points A, B, C and D are the search candidates (mutations), and point E denotes the best matching point. In Fig. 4(a), only one out of the 4 points centered at S1 may have a smaller matching error than S1 when point E has the same X or Y coordinate as S1. Otherwise, it is the Fig. 4(b) case, in which 2 out of the 4 points centered at S2 may have smaller errors. Similarly, in Fig. 4(c), only one out of the 3 points centered at M1 may have smaller matching error when point E has the same X or Y coordinate as M1. Otherwise, in the case of Fig. 4(d), 2 out of the 3 points centered at M2 may have smaller errors.

Fig. 5 shows all possible search sequences starting from S2. Eqn.(1) gives the average number of SPs (W_{S2}) moving from S2 one step towards the final destination, which is $5/3$. We assume that the probability of selecting any candidate point is equal. Similarly, the average SPs moving from S1, M1 and M2 (W_{S1} , W_{M1} and W_{M2}) are $5/2$, 2 and $4/3$, respectively.

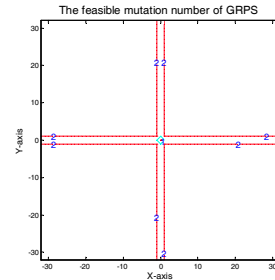


Fig. 3 The contour plot of the number of small-error mutations in the search area (GRPS), wherein the origin denotes the best matched point.

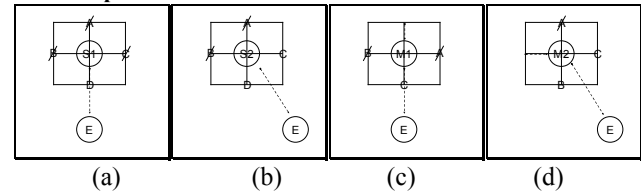


Fig. 4 Four typical cases of starting search points and intermediate search points.

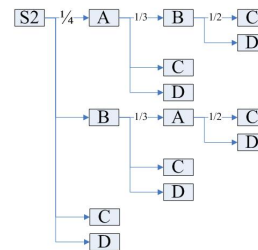


Fig. 5 All possible search order for S2

Let the coordinate of the starting point be (x,y) and the best matching point be $(0,0)$. The average SPs moving from (x,y) to $(0,0)$ is $RWF_{GRPS}(x,y)$. Fig. 6 shows the algorithm of calculating RWF for GRPS according to the previous analysis. The contour plot of $RWF_{GRPS}(x,y)$ is shown in Fig. 7(a). In comparison, Fig. 7(b) shows the real average search points when it is applied to the sequence '2X MD96' in Table I. The outer ring of Fig. 7(b) is empty because these points never become the best matching points. Because we have a good starting point predictor, a typical best matching point is fairly close to the starting point. Likewise, the RWF for the other genetic pattern searches can be constructed.

3. THE PROPOSED SEARCH ALGORITHM

We assume that a doable search method moves at most one unit distance horizontally or vertically per step, as

shown in Fig. 2(a). Then, the minimal number of search points for reaching point (x,y) is 'abs(x)+abs(y)+1'. At the ending stage, to decide the best motion vector generally requires examining at least the center point and its 4 neighboring points as shown in Fig. 2(b). Consequently, the smallest number of search points for motion vector (x,y) can be expressed by (2) and its contour plot is shown by Fig. 8(a).

$$W_{s2} = \left[\begin{array}{l} \frac{1}{4} \times \frac{1}{3} \times \frac{1}{2} \times 3 \times 2 + \\ \frac{1}{4} \times \frac{1}{3} \times 2 \times 2 \\ \frac{1}{4} \times 1 \times 2 \end{array} \right] \times 2 + \frac{5}{3} \quad (1)$$

$$RWF(x,y) = \text{Max}(5, 4 + \text{abs}(x) + \text{abs}(y)) \quad (2)$$

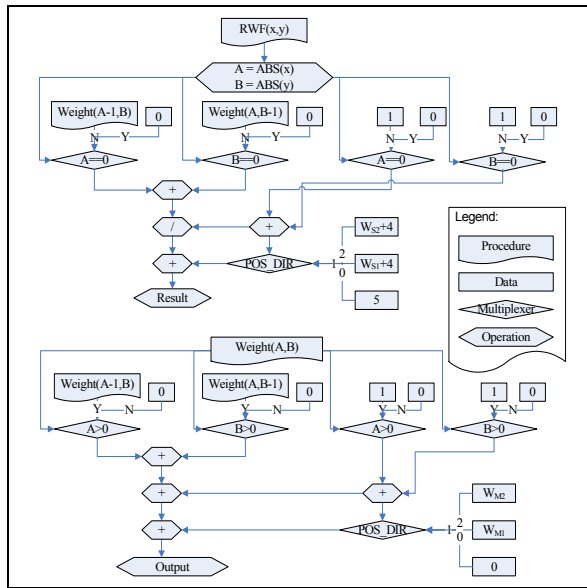


Fig. 6 Construction of RWF

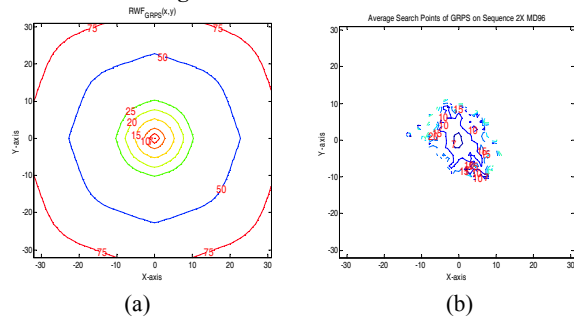


Fig. 7 Comparison between RWF of GRPS and its real average search points on the sequence '2X MD96'.

Comparing Fig. 7(a) to Fig. 8(a), it is obvious that the RWF of GRPS does not match the ideal RWF. How can we devise a search method that matches the ideal RWF?

Observing the ideal RWF carefully, we find a clue: the algorithm should proceed straightly towards the best matching point. Statistically, the successful direction of the previous search likely reappears at the current point. Therefore, instead of randomly select one mutation from the candidate child set, we select the mutation according to its likelihood to be a successful mutation. That is, it tends to move along the same direction of the prior successful searches. On the other hand, it can still change the search directions when the assumption of monotonic matching error surface is not totally valid. The flow chart of the proposed algorithm, namely, the *momentum-directed GRPS* (MD-GRPS), is almost the same as Fig. 2, except that in step 2, the mutations are generated according to the search order shown in Fig. 9. In comparison, when MD-GPRS is applied on the sequence '2X MD96' in Table I, its contour plot of real average search points is shown in Fig. 8(b).

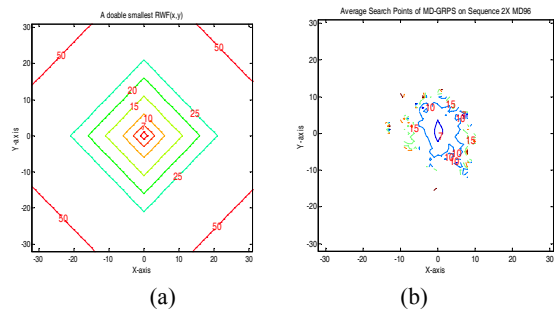


Fig. 8 Comparison between a doable smallest RWF and the real average search points when applying MD-GRPS on the sequence '2X MD96'.

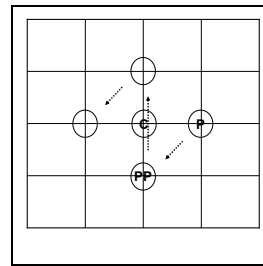


Fig. 9 The search order of mutations in MD-GRPS specified by the positions of the previous successful mutation (P) and the differential successful mutation before that (PP). And C denotes the current parent.

4. EXPERIMENTAL RESULTS

To test the proposed algorithm, four sequences with different MV variances (denoted as '1X') are tested under the setting given in Table I. Moreover, to test the extreme cases, we generate four new test sequences consisting of the odd frames of these sequences (denoted as '2X'). They equal to the two times fast forward playback of the originals. These 8 test sequences are coded by an MPEG-4 [SP@L3](#) encoder. All the sequences are in the CIF (352X288) format. Only the first frame is coded as I frame, and all the

remaining frames are coded as P frame. The search range is 16, and the block size is 16x16.

Table I. Test Sequences and Their Settings

Abbreviation	Sequence	Bitrate (K bps)	Frame rate (fps)	Number of frames
MD96	mother and daughter	96	10	300
FM512	foreman	512	30	300
FB1024	football	1024	30	90
ST1024	steven	1024	30	300

Table II. ASP (Average Number of Search Points)

Type	ASP	MD-GRPS	GRPS[8]	PHS[6]	DS[3]	FS
1X	MD96	5.94	5.98	10.02	14.85	1024
	FM512	6.80	7.13	10.57	16.17	1024
	FB1024	10.35	11.89	14.18	22.36	1024
	ST1024	7.24	7.65	11.40	16.96	1024
2X	MD96	6.29	6.40	10.38	15.44	1024
	FM512	8.25	9.07	12.02	18.72	1024
	FB1024	13.27	15.75	17.15	27.39	1024
	ST1024	8.61	9.28	13.00	19.49	1024
Average		8.34	9.14	12.34	18.92	1024

Table III. PSNR (Peak Signal to Noise Ratio)

Type	PSNR	MD-GRPS	GRPS	PHS	DS	FS
1X	MD96	40.05	40.08	39.85	39.99	39.80
	FM512	34.04	34.05	33.92	34.06	34.06
	FB1024	34.92	34.87	34.87	34.93	35.28
	ST1024	29.16	29.39	29.33	29.44	29.48
2X	MD96	38.66	38.66	38.44	38.60	38.41
	FM512	32.36	32.34	32.23	32.38	32.42
	FB1024	33.26	33.22	33.22	33.28	33.44
	ST1024	27.86	27.99	27.88	27.97	28.10
Average		33.79	33.83	33.72	33.83	33.87

Table IV. Performance Comparison

Type	Sequence	MD-GRPS over GRPS		MD-GRPS over PHS		MD-GRPS over DS		MD-GRPS over FS	
		CG	QG	CG	QG	CG	QG	CG	QG
1X	MD96	0.7%	-0.02	68.7%	0.20	1.50	0.06	171.39	0.25
	FM512	4.9%	-0.01	55.4%	0.12	1.38	-0.02	149.59	-0.01
	FB1024	14.9%	0.05	37.0%	0.05	1.16	-0.01	97.94	-0.36
	ST1024	5.7%	-0.23	57.5%	-0.17	1.34	-0.29	140.44	-0.32
2X	MD96	1.7%	0.00	65.0%	0.22	1.45	0.06	161.80	0.25
	FM512	9.9%	0.02	45.7%	0.13	1.27	-0.02	123.12	-0.06
	FB1024	18.7%	0.03	29.2%	0.03	1.06	-0.02	76.17	-0.18
	ST1024	7.8%	-0.13	51.0%	-0.02	1.26	-0.11	117.93	-0.24
Average		8.0%	-0.04	51.2%	0.07	1.30	-0.04	129.80	-0.08

The average number of search points (ASP) and the peak signal to noise ratio (PSNR) for various sequences and search algorithms are listed in Table II and Table III, respectively. FS denotes the full search. The optimal point is the one with the smallest block matching error in the search area. Because we do not use the rate-distortion optimization, the PSNR value of some fast algorithms may outperform that of FS. The initial MV predictor defined by the MPEG-4 standard is the only starting point in all cases. Table IV

shows pair-wise performance comparisons. In Table IV, the computing gain (CG) is defined as the ratio of ASP minus one, and the quality gain (QG) is the PSNR difference. For complicated sequences, MD-GRPS can be up to 19% faster than GRPS and its PSNR quality is about the same. On the average, the ASP of MD-GRPS is 8% faster than that of GRPS, 51% faster than PHS, 1.3 times faster than DS and 130 times faster than FS. And the PSNR of MD-GRPS is about the same as that of all the other search algorithms (+0.07dB~-0.08dB).

5. CONCLUSIONS

In this paper, we propose a refined weighting function (RWF) that models the SPs of a pattern search algorithm. With the help of RWF, we suggest a *momentum-directed genetic rhombus pattern search* (MD-GRPS). Taking the advantage of the correlation of successful search directions between two succeeding searches, the proposed design further improves the performance of the genetic rhombus pattern search (GRPS). This concept, momentum-directed genetic search, can be applied to all the other genetic pattern searches.

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