

## FEATURES EXTRACTION FROM HUMAN CHROMOSOMES

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The C-Matrix is a feature extraction method suitable for one or two dimensional signals. This paper describes the concept of C-Filter as well as applications of the C-Matrix and C-Filtering to the classifying and filtering of artificial and natural textures. Some experimental results are reported.

Introduction

The main point of a generic algorithm for shape recognition lies upon features extraction. We are presenting a general character algorithm which doesn't take into account any "a priori" knowledge on the input type and therefore can be adapted for various images as -for example- the chromosomes.

The criteria from which we initiated the compilation of such algorithm are linked to human perception experimental results,<sup>1</sup> more precisely to the study of ocular motion during figure exploration and reading

We summarized the phases through which passes our algorithm as follow:

Pattern → C-matrix → Contour extraction →  
Fragment extraction → Features.

Regarding the first step, i.e. the C-matrix, we refer the interested reader to bibliography<sup>2</sup>. We intend to present in this work the successive steps and precisely the contour and fragments extraction.

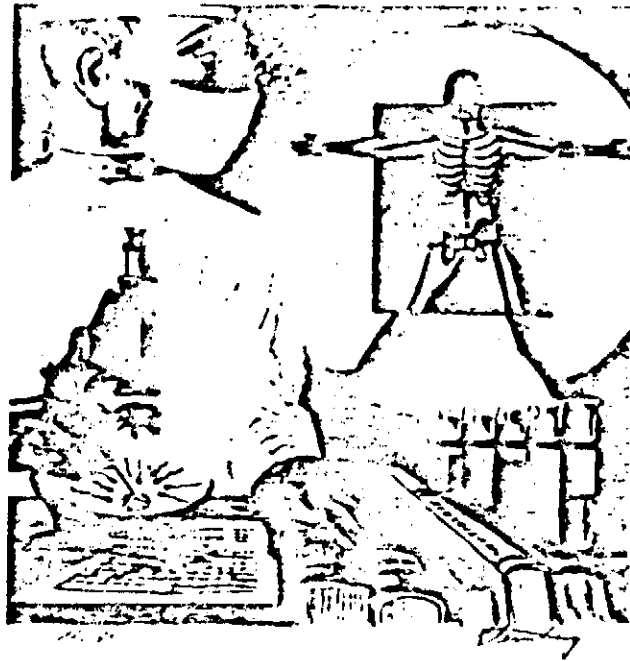
Contour extraction

The purpose of segmentation is to partition the image space into meaningful regions. The definition of a "meaningful region" is a function of the problem being considered. For example, in a image derived from viewing a three-dimensional scene, the objective of segmentation might be to identify regions corresponding to objects in the scene.

In visual images, the method used most often for establishing region characteristics are differences in gray level content between neighbouring regions or, briefly, using contour extraction technique.

We define here the contour as the mono-dimensional interface between the object and the background or, with symbols:

let  $S$  be the object-region on the background-region  $\bar{S}$ , we define contour of  $S$  the set  $S'$ :  $S' = \{x \in S / y \in \bar{S} \text{ four-connected to } x\}$  (1)



# PROCEEDINGS

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We propose a method that is based on detecting transition between neighbouring regions or, in other words the shape of the function  $z=f(x,y)$  in the transition zone between the regions.

As we have shown, in our previous work, from the C-matrix we are able to extract the shape of a one or two-argument function. We are also able to extract the distance between maximum and minimum gray value of the function in the shape zone, or simply the minimum index row, say  $h$ , of the elements in the last non-zero column.

Now we are able to summarize our method.

- 1) To realize the C-matrix of the input image
- 2) to extract from it the value of  $h/2$  and the highest value of the dynamic in the row  $h/2$ , say  $\bar{d}$
- 3) to apply the C-Filter method<sup>2</sup> to the input image, with a window of linear size  $h/2$  that satisfy the conditions:
  - a)  $h/2 \leq D/2 + 1$  where  $D$  is the dimension of the shape region
  - b) the dynamic in each window is equal or greater than  $\bar{d}$ .
- 4) to apply the first step to the filtered image obtained at the preceding step.

An interesting experiments with this algorithm has been effected onto fig.1 image. The grey tone distribution-obtained by simulating the lighting from the botton to the top of an oval object-causes the appearance of bands with different brightnes to

which obviously correspond on that image as many zone of different contrast. This situation may bear some ambiguities in the definition of the object and, in consequence, in its contour extraction.

In fact, if it's true that a dominant region well contrasted onto an uniformly white background does exist, it is equally true that other significative regions can be isolated and therefore as many contours where the mentioned bright bands are formed. This confirmed what has been said of the subjectivity of contour perception.

Let's see now which results can be obtained with the application of this algorithm.

It can be deduced that

$$\frac{\Delta y_{\max}}{\Delta x_{\min}} = \frac{9}{4}$$

from the C-matrix, fig.2, associated with the above mentioned image. Then, we need to choose the linear dimensions of the window  $w^x$  such that the following condition is satisfied:

$$w^x \leq \frac{D}{2} + 1 \rightarrow w^x \leq \frac{\Delta x_{\min}}{2} + 1 = \frac{4}{2} + 1 = 3$$

If we analyze now the curve of the cardinality relative to the elements on the second row of the C-matrix, we find maximum in relation to the dynamics equal 0,1,2,3. The application of the algorithm, choosing as parameters  $w^x=3$  and  $d^y=0$ , produces the contour of the entire oval region, fig.3. Other results obtained by maintaining the dimensions of the window, but varying the dynamical condition-giving than successive ly the values 1,2,3, are reported in fig.4,5,6.

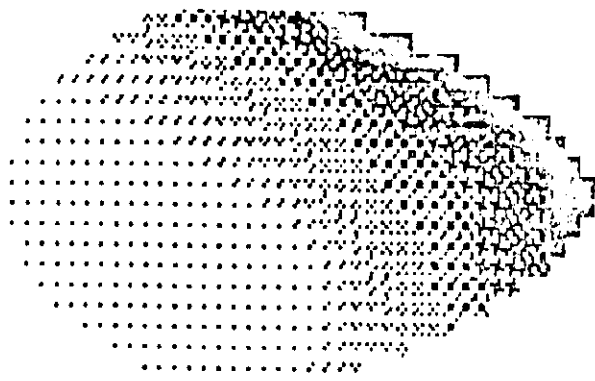


Fig. 1

C-matrix :

WG	0	1	2	3	4	5	6	7	8	9
2	1237	169	85	42	15	2	4	3		
3	1812	182	115	91	47	12	24	9		
4	2355	182	68	96	73	32	32	30	8	14
5	2855	132	41	75	58	38	46	43	17	29
6	3335	152	26	71	45	29	45	35	24	38
7	338	122	11	76	43	22	37	32	16	38
8	175	262	27	82	47	18	38	23	8	35
9	98	195	22	87	35	8	37	24		22
10	42	171	7	181	37	16	38	28		17

Fig. 2

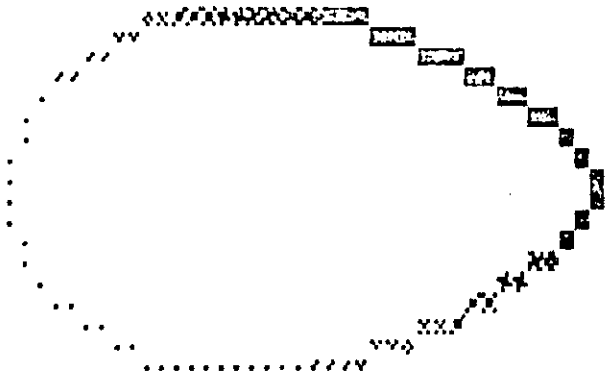


Fig. 3



Fig. 4

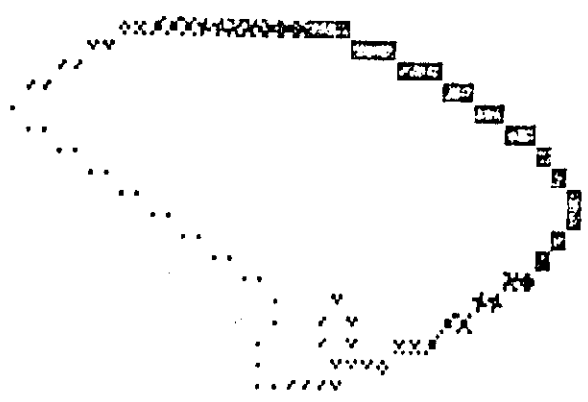


Fig. 5

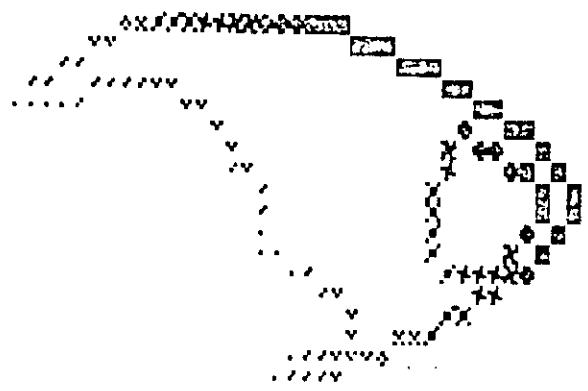


Fig. 6

### Fragments extraction

The selection of the higher informative content of the image zone articulates upon two essential phases:

- a) the fragment extraction relative to the zone of contour in which is reached an accentuated curvature and
- b) the elimination of the selected fragments which do not correspond on the original image to zones with enough contrast.

The problems which arise from the analysis of curvature are: the non-applicability of euclidean measure techniques due to the discrete domain of the signal, and the difficulty in correlating the local measure of the curvature with the global curve of the entire contour.

If we consider the case of chromosomes, the small variations in curvature which, could be observed on the contour, are not significant when compared with the wider variations relative to the centromeric zone and arms. In reference to it, we could retain the local measure of the curvature in some way correlated to the distance at which is observed the entire shape under examination.

To improve the meaning of the extracted fragments, we carry out a further selection based on contrast. Among the various measures of the contrast in use, we have chosen the one adopted in psychology :

$$C = \frac{\Delta B}{C} = \frac{E_0 - B}{B}$$

where  $B_0$  and  $B$  indicate respectively the luminance (light intensity for superficial units) of the object and of its immediate surrounding. With this definition, the contrast can be either positive or negative depending on whether the object is more or less bright on the background; it is therefore important to specify the area and the shape of the object.

We can pass now to the description of the phases which contribute to such extractions.

#### 1) choice of the scanning window

Let's define the linear dimension of the windows  $w_1$  and  $w_2$  used for the curvature analysis and relative to contrast of extracted fragments.

If  $w^*$  is the window used for contour extraction, we have

$$w_1 = \begin{cases} w^* & \text{if } w^* \text{ is odd} \\ w^* + 1 & \text{otherwise} \end{cases}$$

and  $w_2$  such that the ratio

$$\frac{w_2^2 - w_1^2}{w_1^2} \quad \text{tends towards } 1$$

the choice of  $w_1$  allows the fragments extraction of contour of dimension reported to the one global of chromosomes, the condition on  $w_2$  is essential for the contrast estimation of concentric areas of nearly equal dimensions.

#### 2) Selection of the curvature points.

The set of the points which define the curve relative to the contour of the chromosome is scanned sequentially with the window  $w_2$ . Once the window has been centered on a generic point,  $R_1$ , we consider the

two points of the mentioned curve which will intersect laterally the edge of the window. Since the extracted contour constitute a closed curve, we must necessarily find at least two points of intersection, say  $P_1, P_2$ ; whenever there is more than two intersections, the center of the fragment becomes discarded and the analysis goes on.

Let's call  $(i_1, j_1)$  and  $(i_2, j_2)$  the respective coordinates of  $P_1$  and  $P_2$ , if the result satisfies the following condition, the point  $P_c$ -center of the scanning window-under examination is memorized as the center of a fragment of good curvature:

$$d(P_1, P_2) = |i_1 - i_2| + |j_1 - j_2| \leq 3/2 w_1$$

otherwise, the fragment-and therefore  $P_c$ -are rejected and the analysis proceeds to the next points.

### 3) Selected zone of contrast.

Each one of the extracted points at the preceding step is selected in terms of the corresponding contrast on the original image. More precisely, given the generic point  $P_c$ , the two windows  $w_1$  and  $w_2$  become centered in relation to its coordinates, with the condition that  $w_1$  shall be always at the center of  $w_2$ . The dynamics existing in the area  $w_2 - w_1$  and  $w_1$  are respectively indicated by  $D_e$  and  $D_1$ . The condition which must satisfy the point  $P_c$  for being chosen as center of informative fragments is:

$$|D_e - D_1| \geq d'$$

The condition allows the elimination of these zones in the original image characte

rized by appreciable variations of the curvature which then are not accentuated in relation to the background of the same image. Fig.7,8,9,10.

### Application to chromosome analysis

The application of algorithms in order to identify chromosomes could considerably reduce the investigation and make the work more objective. Because of our recent significant results we think to apply algorithms to banded chromosomes.

Chromosomes coloured by band technique allow a more accurate identification because they are characterized in their whole length by differently coloured areas which are constant for each pair chromosomes.

From many experimental results that we obtained applying the algorithms, we present here one example with a brief description of the parameters involved.

Extraction of chromosomes features in fig.7. From the C-matrix (fig.7') we can obtain the parameters  $w^x=2$  and  $d^x=3$ , through which we extracted the limits of fig.8. The center of the fragments relative to the analysis obtained for the curvature with  $w_1=3$  are given in fig.10; the successive analysis using contrast with  $w_2=5$  and with  $d^x=3$ , enables us to obtain the centers of informative fragments.

### References

1. Zusne L. "Visual perception of form" Academic Press. N.Y.70
2. A.Gisolfi, S.Vitulano; "C-matrix" to appear Pattern Recognition

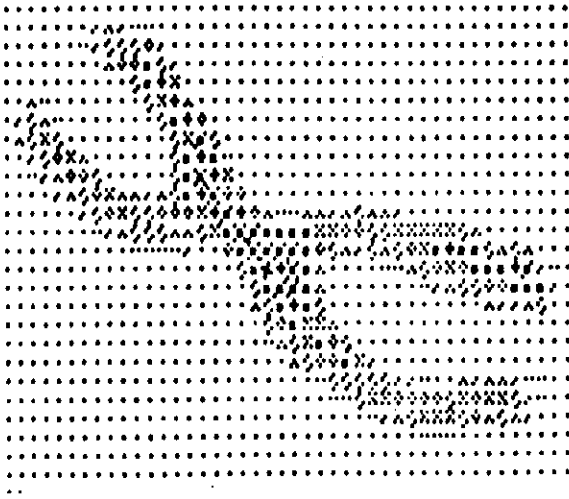


Fig. 7

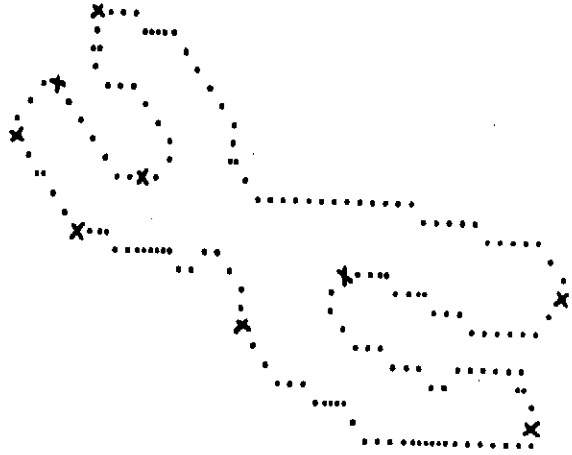


Fig. 9

Matrix :

Row	0	1	2	3	4	5	6	7	8	9
0	1185	42	68	118	87	26	27	12	4	2
1	1622	32	51	52	93	55	57	63	25	27
2	819	35	34	47	71	24	145	82	12	24
3	685	22	24	48	71	24	101	82	78	48
4	544	22	27	33	82	22	203	92	81	81
5	433	11	25	25	55	22	14	105	95	77
6	337	11	22	17	51	19	115	105	109	95
7	257	5	11	15	39	12	117	105	114	115
8	187	5	6	8	31	12	145	15	116	137
9	145	5	6	6	25	8	126	61	115	156
10	107	5	6	6	21	7	183	42	111	151
11	77	5	5	4	18	6	92	24	102	136
12	51	5	5	4	15	4	77	21	95	134
13	26	4	5	3	15	1	62	19	81	136

Fig. 7'

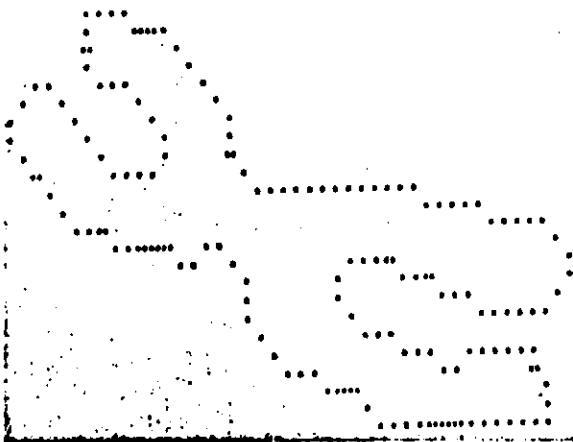


Fig. 8

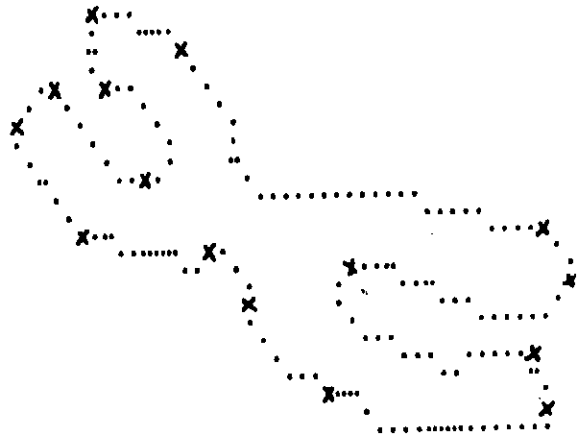


Fig. 10



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