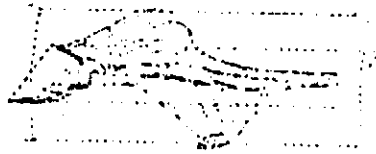
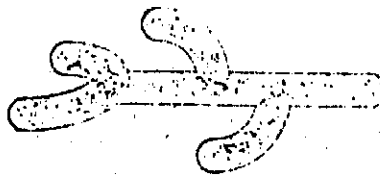


The Third Scandinavian Conference on Image Analysis

Copenhagen, Denmark, July 12-14, 1983
Arranged by The Danish Pattern Recognition Society



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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.

We summarized the phases through which passes our algorithm as follows: Pattern \rightarrow C-Matrix \rightarrow Contour extraction \rightarrow Fragment extraction (curvature analysis, contrast analysis) \rightarrow Features.

Regarding the first step, i.e. the C-Matrix, we refer the interested reader to bibliography (1). We intend to present in this work the successive steps and precisely the contour and fragments extraction.

CONTOUR EXTRACTION

We define here the contour as the monodimensional 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' : $S' = \{x \in S / \exists y \in \bar{S} \text{ four-connected to } x\}$ (1)

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 to the input image, with a window of linear size $h/2$ that satisfy the conditions:

- where D is the dimension of the shape region
- b) the dynamic in each window is equal or greater than d.
- 4) To apply the first step to the filtered image obtained at the preceding step.

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 reaches 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 significative 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:

$$C = \frac{AB}{B} = \frac{B_1 - B}{B}$$

where B₁ and B indicate respectively the Luminance (light intensity per 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) Choise of the scanning window

Let's define the linear dimension of the windows -w₁- and -w₂- 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 w₂ such that the ratio

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

the choise of w₁ allows the fragments extraction of contour of dimension reported to the one global of chromosomes, the condition on w₂ 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 w₂. Once the window has been centered on a generic point R₁, 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 P₁, P₂; whenever there is more than two intersections, the center of the fragment becomes discarded and the analysis goes on.

Let's call (i₁, j₁) and (i₂, j₂) the respective coordinates of P₁ and P₂, 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:

$$d(P_1, P_2) = \left| i_1 - i_2 \right| + \left| j_1 - j_2 \right| \leq \frac{3}{2} w_1$$

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. Here precisely, given the generic point P_c, the two windows w₁ and w₂ become centered in relation to its coordinates, with the condition

in the area w_2-w_1 and w_1 are respectively indicated by D_e and D_i .

The condition which must satisfy the point P_c for being chosen as center of informative fragments is:

$$\left| \begin{matrix} D_e - D_i \\ \vdots \\ \vdots \end{matrix} \right| \gg d^*$$

The condition allows the elimination of these zones in the original image characterized by appreciable variations of the curvature which then are not accentuated in relation to the background of the same image. Fig.1,2,3,4,5.

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 significative 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.1. From the C-matrix (fig.2) we can obtain the parameters $w^*_2=2$ and $d^*_3=3$, through which we extract the limits of fig.3. The centers of the fragments relative to the analysis obtained for the curvature with w_3 are given in fig.4; the successive analysis using contrast with $w_2=5$ and with $d^*_3=3$, enables us to obtain the centers of informatives fragments (fig.5).

CONCLUSION

The features extraction algorithm here introduced has been tested on more that one-hundred images with very interesting and quite satisfactory results. We believe it is interesting to notice that in our algorithm the window dimension and the dynamic are not chosen in a 'ad hoc' way.

ine experimental results obtained applying our algorithm to banded human chromosomes are under investigation.

So we hope that is possible, in the next future, to realize a classification algorithm for human banded chromosomes.

REFERENCES

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- 2) A.Gisolfi, S.Vitulano: 'A method for classifying and filtering textures' in Prog. in Cybernetic and System Research, vol.11 Hemisphere Pub., Washington, 1980.

FIGURES

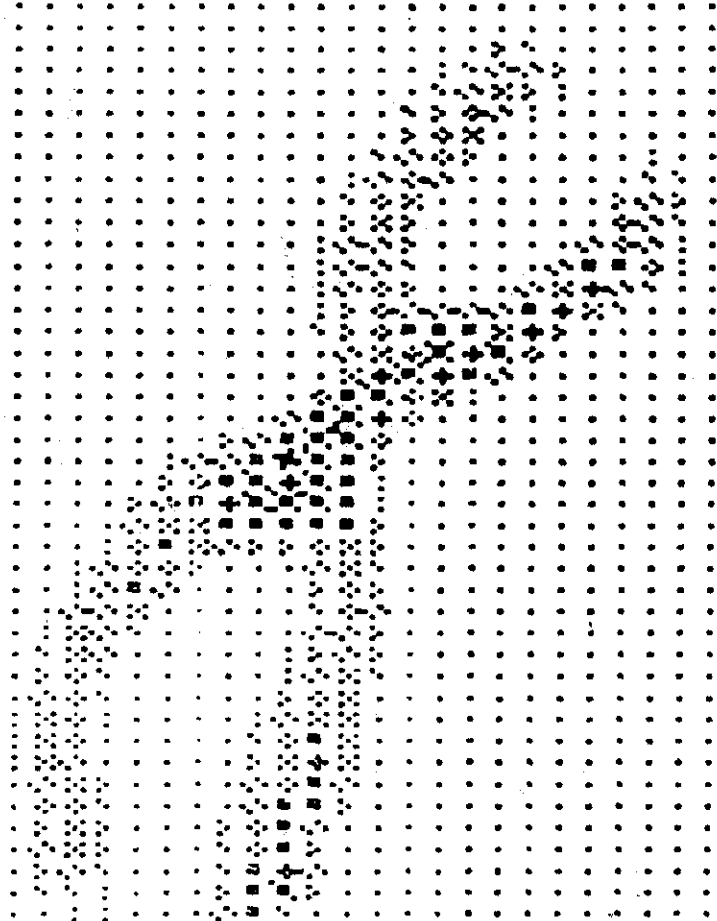


Fig.1

2	1185	42	68	110	87	29	27	12	4	2	9	10
3	1000	34	31	54	93	59	97	63	25	17	34	9
4	819	35	34	47	71	44	145	82	50	86	55	
5	665	23	34	40	71	38	181	82	70	48	86	
6	544	20	27	25	62	34	201	94	81	61	77	
7	433	16	25	25	55	22	196	106	95	77	89	
8	337	13	22	17	51	19	188	108	109	95	101	
9	262	9	11	15	39	15	167	105	114	115	113	
10	202	6	6	8	33	13	145	85	116	137	125	
11	149	6	6	6	25	8	128	61	115	150	137	
12	102	6	6	4	21	7	103	44	111	151	149	
13	61	5	5	4	18	6	98	26	105	136	145	
14	20	4	5	4	15	4	77	21	95	136	137	
15	5	4	1	3	15	1	63	19	81	136	137	

FIG.2

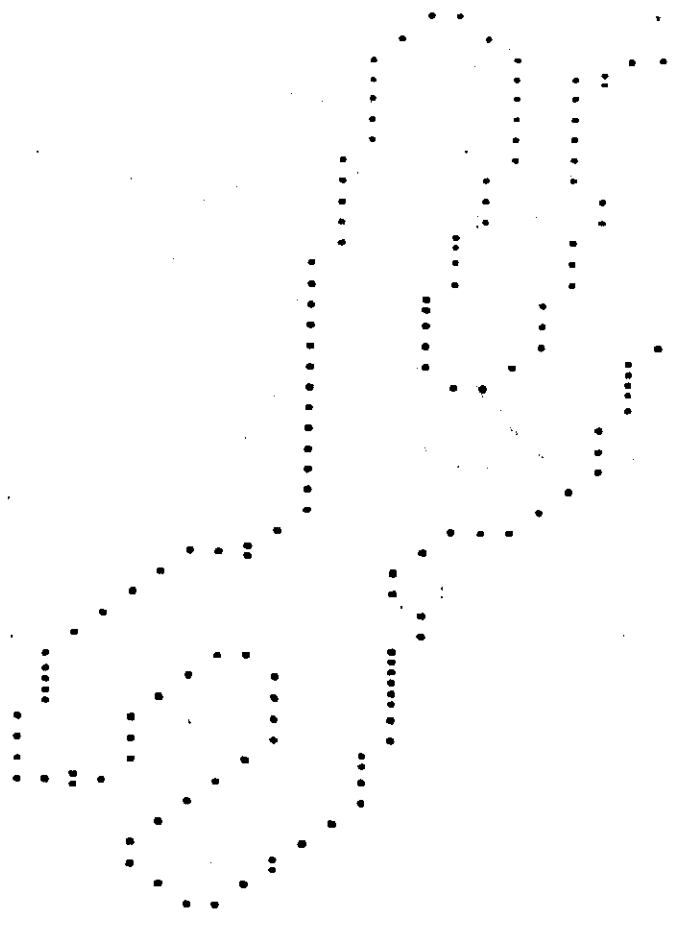


Fig.3

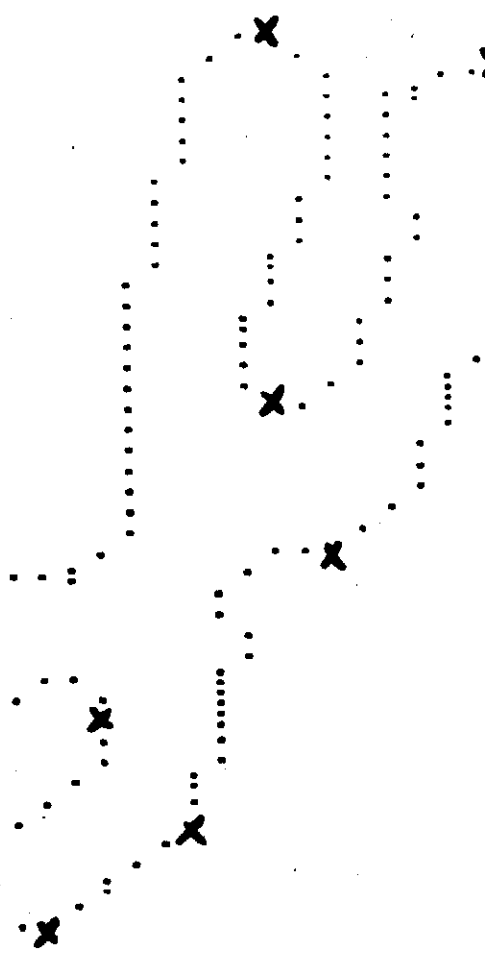


FIG.4



FIG.5