ADAPTIVE CONTOUR ESTIMATION WITH GENETIC ALGORITHMS

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ABSTRACT

We introduce a fully adaptive active contour which is based on elliptic Fourier contour description and on the minimum description length (MDL) principle. The proposed technique estimates the order of the contour description (number of Fourier coefficients), and the contour itself. The search is performed by means of a genetic algorithm (GA). Preliminary results are presented for simple synthetic images with a specified pixel distribution, which testify the performance of the proposed scheme. These results are the first step towards a fully unsupervised contour estimation.

1. INTRODUCTION AND PREVIOUS WORK

Contour estimation is one of the most important, interesting, and challenging problems in image processing and computer vision. Originating from the seminal work of Kass, Witkin, and Terzopoulos [15], *snake*-type approaches (in which we may include deformable contours, active contours, dynamic contours, and deformable templates) constitute one of the most successful approaches.

In the original version [15], snakes work by minimizing an *energy* function composed of an (internal) elastic-type term which increases with the contour deformations, and an (external) attraction potential linking the contour with the image. The goal is a compromise between contour *smoothness* and adequacy to the observed data. In recent years, several improvements, modifications, and reformulations have overcome limitations of the traditional model such as sensitivity to initialization, *myopia* (i.e., insensitivity to distant features), and inability to reparametrize itself during the deformation process (see [4], [5], [3], [17], [18], [20], [23], and references therein).

Deformable templates, though related to snake-type approaches, use shape descriptions with small numbers of parameters; the deformation energy term is usually unnecessary (see [6], [13], [24] and references therein).

From a Bayesian estimation angle, deformable models are interpretable as *maximum a posteriori (MAP)* estimators; the internal energy and the external potential terms are associated with the *a priori* probability function and the likelihood function, respectively; for details, see [9], [13], [24], [25]. The Bayesian estimation perspective has the advantage of giving meaning to all the involved entities; e.g., the form of the energy term that links the contour with the image contents, i.e. the likelihood function (in Bayesian terms) can be derived from knowledge about the observation model rather than simply from common sense arguments [7], [9]. The main difficulties in this approach are the choice of the parameters involved in the definition of the *a priori* probability function and solving the very difficult optimization problem involved.

In this paper, we introduce a new adaptive contour estimation technique based on Fourier contour description and on the *minimum description length* (MDL) principle [21], [22]. In the proposed criterion, the contour shapes are described by as few parameters as possible. Basically, it is a template matching approach with adaptive parametrization. To solve it we use a genetic search strategy[10][11] (see [1][2][3] for genetic optimization on segmentation and edge detection). Some specific genetic operators were implemented in order to improve the algorithm convergence.

2. PROPOSED TECHNIQUE

Fourier Representation

Let a closed curve (i.e., a closed contour) on the image plane be represented by a periodic vector function $v(t) = [x(t) \ y(t)]^T$, of period 2π, i.e., of unit fundamental angular frequency. The complex Fourier series description of the closed curve is defined as

$$v(t) = \begin{bmatrix} x(t) \\ y(t) \end{bmatrix} = \sum_{k=-\infty}^{\infty} \begin{bmatrix} c_k \\ d_k \end{bmatrix} e^{jkt}, \quad t \in [0, 2\pi[\quad (1)$$

where

$$\begin{bmatrix} c_k \\ d_k \end{bmatrix} = \frac{1}{2\pi} \int_0^{2\pi} \begin{bmatrix} x(t) \\ y(t) \end{bmatrix} e^{-jkt} \qquad (2)$$

are the complex Fourier coefficients [14], [24]. The discrete version of this representation is obtained by considering a discretization of a period of the curve v(t) into N points {v_i, i = 0,1,...,N-1}. The discrete complex Fourier series representation is

$$v_i = \begin{bmatrix} x(i2\pi/(N-1)) \\ y(i2\pi/(N-1)) \end{bmatrix} = \sum_{k=o}^{N-1} \begin{bmatrix} e_k \\ f_k \end{bmatrix} e^{jki2\pi/N} \qquad (3)$$

with

$$\begin{bmatrix} e_k \\ f_k \end{bmatrix} \equiv g_k = \frac{1}{N} \sum_{i=0}^{N-1} \begin{bmatrix} x(2\pi \cdot i/(N-1) \\ y(2\pi \cdot i/(N-1) \end{bmatrix} e^{-j \cdot k \cdot i \cdot 2 \cdot \pi/N} \qquad (4)$$

By truncating series (3) to K terms (with K < N), a smoothed version of the curve is obtained. We denote the vector of 2K complex coefficients by

$$\theta_{(K)} = \begin{bmatrix} e_0, f_0, e_1, f_1, ..., e_{K-1}, f_{K-1} \end{bmatrix} \qquad (5)$$

The true unobserved contour is assumed to be smooth, i.e., it can be exactly described by some $\theta_{(K)}$.

The Likelihood Function

Given an N-point contour defined by a K-order discrete complex Fourier series, the observed image I is modeled by the likelihood function $p(I|\theta_{(K)}, \phi)$, where ϕ is the vector of parameters of the observation mechanism. Although this is an often overlooked aspect, great care has to be put on the derivation of the likelihood function. For specific applications (e.g., finding organ boundaries in medical images), all the available knowledge about the image acquisition process should be included [7], [9]. Not doing so may result in disastrous results, specially on very low quality images (see [7]). This approach naturally leads to region based strategies which, unlike gradient based ones, are robust in the presence of noisy or low contrast images [7], [9], [12], [23].

We now make the following assumptions:

Conditional independence: given the true (unobserved) contour, the image pixels are independently distributed.

Inside and outside regions homogeneity: The conditional probability function of each pixel depends only on whether it belongs to the inside or outside region of the contour; i.e., all the pixels inside (resp. outside) have a common distribution characterized by a

parameter vector ϕ_{in} (resp. by ϕ_{out}), with $\phi = [\phi_{in}, \phi_{out}]$.

Accordingly,

$$p(I|\theta_{(K)}) = \left(\prod_{(i,j) \in \mathcal{I}(\theta_{(K)})} p_{in}(I_{(i,j)}) \right) \left(\prod_{(i,j) \in \mathcal{O}(\theta_{(K)})} p_{out}(I_{(i,j)}) \right)$$

where $\mathcal{I}(\theta_{(K)})$ and $\mathcal{O}(\theta_{(K)})$ are the inside and outside regions of the contour defined by $\theta_{(k)}$, respectively; likewise, $p_{in}(I|\theta_{(K)})$ and $p_{out}(I|\theta_{(K)})$ are the pixel-wise conditional probabilities, of the inner and outer regions, respectively.

The Estimation Criterion

If K was known, maximum likelihood (ML) estimates could in principle be obtained by maximizing with respect to $\theta_{(K)}$. However, since K is unknown, there is a model order problem which can be stated as :

- for each K, there is a parameter space of dimension K;
- the spaces are nested, that is, for each $\theta_{(K)} \in \Theta_{(K)}$, there is some $\theta'_{(K+1)} \in \Theta_{(K+1)}$ such that[1]

$$p(I|\theta_{(K)}) = p(I|\theta'_{(K+1)}) \qquad (6)$$

- consequently, K can not be estimated directly by maximizing the likelihood function since $p(I|\hat{\theta}_{(K)})$, where $\hat{\theta}_{(K)}$ is the ML estimate of $\theta_{(K)}$ given K, is a non-decreasing function of K [20].

To overcome this difficulty, we adopt Rissanen's MDL principle (see [21] or [22] for details) where

$$\hat{\theta}_{(K)} = \arg \min \left\{ -\log p(I|\theta_{(k)}) + 2K \log N \right\} \qquad (7)$$

with $\hat{\theta}_{(K)}$ standing for the joint estimates of K and $\theta_{(k)}$. The $2K$ log$N$ term results from the fact that a K-order parametrization involves $2K$ complex coefficients, i.e. $4K$ real ones, and the MDL principle penalizes each real coefficient with a (log N)/2 cost [22].

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[1] In our case, $\theta_{(K)} = \begin{bmatrix} e_0, f_0, e_1, f_1, ..., e_{K-1}, f_{K-1} \end{bmatrix}$ and $\theta'_{(K+1)} = \begin{bmatrix} e_0, f_0, e_1, f_1, ..., e_{K-1}, f_{K-1}, 0, 0 \end{bmatrix}$ describe the same contour.

From a Bayesian point of view, (7) can be interpreted as a MAP estimator,

$$\hat{\theta}_{(K)} = \arg\ \max\left\{p(\theta_{(K)}|I)\right\}$$

$$= \arg\ \max\left\{\log p(I|\theta_{(K)}) + \log p(\theta_{(K)})\right\}$$

with the prior $p(\theta_{(K)}) \propto \exp\left\{-2K\log N\right\}$. Since K is the number of terms in the Fourier description of the contour, this is basically a smoothing prior (as in regularization) expressed in the Fourier domain; this has the advantage of avoiding the shrinkage associated with smoothing priors directly expressed on the contour coordinates [24].

The Genetic Algorithm

Introduction

To deal with the difficult task of solving (7) we used a genetic search strategy [10][11]. Behind the genetic algorithms is the idea of maintaining a population of solutions to a global optimization problem. Each different solution has an associated cost function value, which is used to measure its degree of *fitness*. The evolutionary process occurs over generations, in which the population undergoes 3 distinct stages. During *Reproduction*, the solutions are subjected to a stochastic selection procedure. The probability of survival, i.e., passing to the next generation, is computed according to the fitness measure. This mechanism assures a level of evolutionary pressure, thus providing a way for the population to evolve. *Crossover* combines pairs of solutions, creating new elements with features existing in the population. *Mutation* aims at introducing new information into the population, by randomly altering the contents of a solution.

Specific Genetic Operators

Genetic Algorithms are a tool for a large class of optimization problems because they do not require any problem information apart from a fitness evaluating function. Anyhow, additional information on the problem characteristics can be valuable on the convergence speed of the algorithm.
A new set of mutation operators were added, intended for a fine adjustment of the contour. These are:

- **Translation**: A Gaussian random variable (GRV) with zero mean is added to the first Fourier coefficient, translating the contour.
- **Resizing**: The contour is resized by multiplying the coefficients of $K > 1$ with a GRV with unitary mean.
- **Rotation**: The contour is rotated around its center by an angle given by GRV with zero mean.

During the selection procedure, the survival probability of each solution is scaled according to the formula [16]:

$$f(c) = e^{\frac{\ln(\phi)}{\bar{c} - c_{min}}(c - c_{min})}$$

where c the description length cost of the individual, c_{min} and $\bar{c}$ are the minimal and average description length cost of the population in each iteration. The parameter ϕ is used to adjust the selective pressure of the genetic algorithm.
This is a dynamic fitness scaling which has the advantageous properties of being scale and translation invariant.

3. IMPLEMENTATION AND PRELIMINARY RESULTS

The performance of the proposed technique was tested using synthetic images with and without added noise. The image regions have known mean and variance following a Normal distribution. This information is used by the algorithm.
The MDL criterion can therefore, in this case, be expressed as :

$$\left\langle\hat{\theta}_K\right\rangle = \arg\ \min\left\{-\log\prod_{(i,j)} p(I_{(i,j)}|\theta_{(K)}) + 2K\cdot\log N\right\}$$

where

$$p(I_{(i,j)}|\theta_{(K)}) = \begin{cases} \dfrac{1}{\sqrt{2\pi}\sigma_I}e^{\frac{-(I_{(i,j)}-\mu_I)^2}{2\sigma_I^2}} \\ \dfrac{1}{\sqrt{2\pi}\sigma_O}e^{\frac{-(I_{(i,j)}-\mu_O)^2}{2\sigma_O^2}} \end{cases}$$

This expression can be simplified to

$$\arg\min\left\{\frac{1}{2}\log(2\pi\sigma_I^2)N_{in} + \frac{1}{2}\log(2\pi\sigma_O^2)N_{out}\right.$$

$$+ \sum_{in}\frac{(x_{(i,j)} - \mu_I)^2}{2\sigma_I^2} + \sum_{out}\frac{(x_{(i,j)} - \mu_{OI})^2}{2\sigma_O^2}$$

$$\left. + (1 + 2K)\log N\right\}$$

where N_{in} and N_{out} are the number of pixel in the inner and outer regions.
Figures 1 and 2 show the results after 21600 and 6000 solutions processed, respectively. The first image is a superposition of two ellipses (with perpendicular major axis) which was approximated by a rhombus. Both contours are based on 2nd order descriptors.
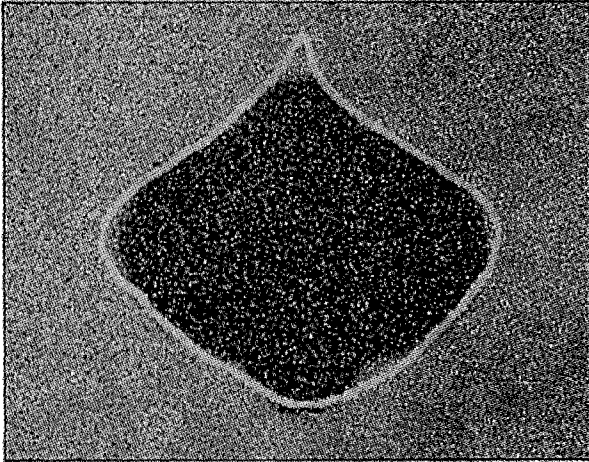
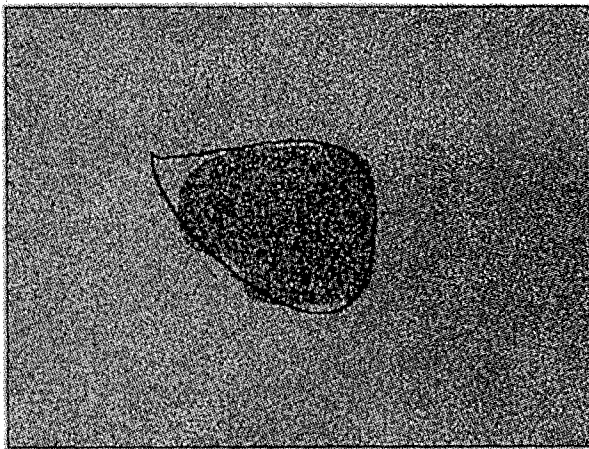*Fig 1: Test image and best contour*

Fig 2: Test image with added Gaussian noise and best contour

The evolution of the MDL cost function for the best element in each generation (of the figure 2 run) is charted on figure 3.
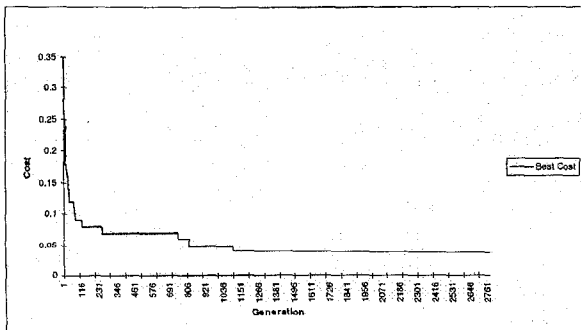

Fig 3: Evolution of the MDL cost

The algorithm was also tested on images having two regions with equal average pixel intensities and different variances. Since the implemented criterion uses Gaussian distributions with specified mean and variance, it is able to identify the boundaries of regions with different variances.

The image on figure 4 was used, resulting in a contour which comes close to the correct one. This type of images cannot be dealt with by traditional *snake*-like contour descriptors. These methods perform a local gradient-based adjustment in the region border, thus requiring different intensities for the inside and the outside regions [7][8][9][23].
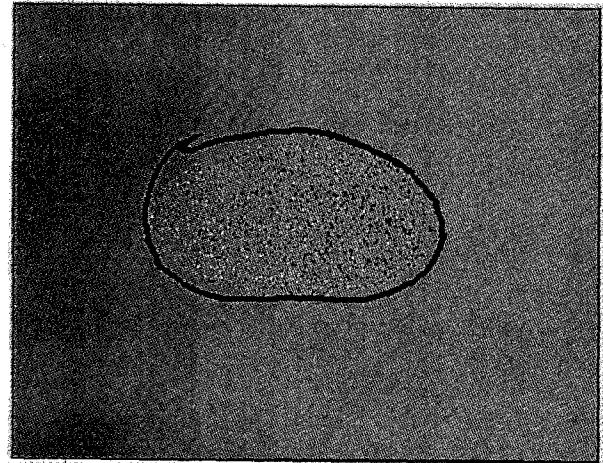

Fig 4: Test image with equal average intensity regions

The contours presented here are some of the results of the preliminary tests for the proposed scheme. The algorithm is able to quickly find the main region, but finer adjustments of the contour are much more time consuming. Since the description length cost function relies entirely on the distributions of the pixel intensities and on the model order (and not, for instances, on the contour smoothness), it is not an efficient guide for the algorithm during the final adjustments. Nonetheless it is worth noting that the MDL approach is to select a model minimizing codelength for encoding both the model and data. This model may not be (and usually is not) the one providing the best fitting contour.

Another main difficulty of the algorithm, lies on the fact that the search space can have many local minima. Although genetic algorithms can be made more suitable than other classes of algorithms when considering local minima, their performance is conditioned to suitable representations. A good representation is often the key to a well behaved search space.
In the problem addressed in this paper, it is clear that, sometimes, small contour adjustment, require large simultaneous changes in the Fourier descriptor space. On the other hand, small changes in the Fourier coefficients may lead to poor solutions.

4. FUTURE WORK

Current undergoing work includes modifications to the algorithm, such as performing mutation directly on the contour, as opposed to just on the Fourier descriptor. After mutating a K-order contour, a new descriptor can be computed. By setting the higher order coefficients to zero, a smoothed version of the contour is obtained. This procedure can be seen as a complex mutation on the Fourier descriptor space, which is not very disruptive in the image space.

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