Proceedings of the IASTED International Conference
ADVANCES IN COMPUTER SCIENCE AND TECHNOLOGY
November 22-24, 2004, St. Thomas, US Virgin Islands

RETINA IMAGES PROCESSING USING GENETIC ALGORITHM AND MAXIMUM LIKELIHOOD METHOD

Vitoantonio Bevilacqua, Giuseppe Mastronardi, Andrea Colaninno, Annarita D'Addabbo
D.E.E., Politecnico di Bari
Via E. Orabona, 4 70125 Bari – Italy
bevilacqua@poliba.it

ABSTRACT
In this work we examine the applicability of an evolutionary algorithm combined with a maximum likelihood method to assist a physician in performing a diagnosis of some retina's pathologies. The main objective of this work is to automatically implement the process of matching different images of the same retina to study the evolution of some pathologies. In particular, we combined a previous handling constraints genetic algorithm to localise and recognise digits in a licence plate [1] with a new technique to optimise the process of overlapping different images acquired at different time, considering that the images differ from each other due to different acquisitions, different illuminations, and to different step of pathology.

KEY WORDS: genetic algorithm, expectation maximisation algorithm, handling constraints, retina's images.

1. Introduction

During the last decade several search groups direct one's efforts to automatic acquisition of information in medicine. To reduce costs, time and human intervention, it seems reasonable to invest resources in development of particular technology for data acquisition and processing.
In particular, medical image processing plays a key role in the study of a large number of pathologies, where it is used to carry out diagnosis or to perform tracking of clinical events. In this last application field, since information gained from two images acquired in the clinical track is usually of a complementary nature, proper integration of useful data obtained from the separate images is often desired. A first step in this integration process is to bring the modalities involved into registration. In literature, several works concerning medical image registration are found using different methods, classified as extrinsic, i.e. based on foreign objects introduced into the image space, or intrinsic, i.e. based only on the image information [2]. Intrinsic registration can be based on a limited set of identified salient points called landmarks, on the alignment of segmented binary structures, or directly onto measures computed from the image grey values. Currently, intrinsic methods using the full image information content are regarded as the most interesting and flexible, because they can be applied in almost any medical application area. As concerns these techniques, literature reports on several paradigms being used: cross-correlation of images, minimisation of variance of intensity ratio, histogram clustering and minimization of its dispersion, and so on. Moreover some hybrid approaches, exploiting two different registration methods subsequently applied to analysed images, are presented in literature. In [3], a first registration step is pursued by using anatomical landmarks, then the intensity difference image is minimized. In [4], after that a pre-registration method is applied, the final registration is performed by locally finding the optimal shift minimising the squared intensity differences.
In the present work we propose an hybrid registration technique, exploiting geometric and spectral information, that is applied to the study of the evolution of a retina's pathology. Algorithm starting point are two bitmap images representing two different views of the same retina. The basic idea, which this work is based on, is that, initially, it is necessary to find the best overlapping of the two images, and then, when it is reached, to find the regions in which these two images differ. The algorithm we have implemented works in two different steps, in the first one the best overlapping of the two different images has been regarded of a handling constraints optimisation problem, and the best solution is searched for, using only geometric information. So image analysis is based on minimisation method that turns problem into optimisation one's and makes interesting the use of Genocop III, a genetic algorithm specialised into optimisation problems with non-linear constraints spaces [5][6][7]. In the second phase an improvement of the previous overlapping has been realised taking into account not only geometric information but also that the amounts of change and no change in the difference image give a significant hint about the shift between the two original images. This second step is realized by applying the algorithm of Expectation-Maximization (EM).

2. Genetic Algorithm

The Genocop (for GEnetic algorithm for Numerical Optimization of COnstrained Problems) system assumes linear constraints only and a feasible starting point (or feasible population). A closed set of operator maintains the feasibility of solutions. [5]
Genocop III incorporates the original Genocop system, but also extends it by maintaining two separate populations, where a development in one population influences evaluations of individuals in the other population. The first population consists of so-called search points from S, which satisfies linear constraints of the problem (as in the original Genocop system). The feasibility (in the sense of linear constraints) of these points is maintained, as before, by specialized operators. The second population consists of so-called reference points from *F*; these points are fully feasible, i.e., they satisfy all constraints. Reference points R, being feasible, are evaluated directly by the objective function (i.e., *eval*(*R*) = *f*(*R*)). On the other hand, unfeasible search points are "repaired" for evaluation and the repair process works as follows. Assume, there is a search point S, not fully feasible. In such a case the system selects *R*, one of the reference points (better individuals have better chances to be selected), and creates random points *T* from a segment between S and R by generating random numbers from the range [0;1] , T = a·S + (1 – a)· R . Once a feasible T is found, eval(S) = eval(T) = f(T). Once a feasible T is found, eval(S) = eval(T) = f(T). Additionally, if f(T) is better than f(R), then the point T replaces R as a new reference point. Also, T replaces S with some probability of replacement p_r.
The Genocop III avoids many disadvantages of other systems. It introduces few additional parameters (the population size of reference points, probability of replacement) only. It always returns a feasible solution. Making references from the search points searches a feasible search space F. The neighbourhoods of better reference points are explored more often. Some reference points are moved into the population of search points, where they undergo transformation by specialised operators (which preserve linear constraints). [6]
Individuals' chromosomes in Genocop have floating point representation. Despite our individuals are integer, we round value after operation so that operators have always effect. Experiments and results showed how dynamic operators are frequently decisive. [7]
In particular, Genocop Gaussian mutation operation is obtained by central limit theorem, as sum of 12 variables with uniform distribution in [–1, +1]. Result is well closed to normal distribution. The factor (1+t/T) at evolution, t, out of T total evolutions, makes dynamic operator.

3. The Maximum Likelihood estimation method

In order to support the registration process, the difference image between the two analysed images has been explicitly taken into account. The basic idea is that the amounts of change and no change in the difference image give a significant hint about the shift between the two original images: at the correct registration point there will be a minimum in change percentage. Moreover, it is worth noting that in this way the spectral information is explicitly considered, whereas the genetic algorithm uses only the geometrical one.
The analysis of the difference image and the detection of changes has been carried out by using a fully automatic thresholding technique [8][9]. This approach is based on the idea that the histogram of difference image can be modelled as a mixture density distribution composed of the probability density functions of two classes ω_C and ω_{NC}, respectively associated with changed and unchanged pixels, i.e.

$$p\left(X_{DIFF}\right) = p\left(X_{DIFF}\left|\omega_C\right.\right)P\left(\omega_C\right) + p\left(X_{DIFF}\left|\omega_{NC}\right.\right)P\left(\omega_{NC}\right)$$

Under this assumption, the estimation of each term can be computed by using the EM algorithm [10]. Moreover, assuming that both $p\left(X_{DIFF}\left|\omega_C\right.\right)$ and $p\left(X_{DIFF}\left|\omega_{NC}\right.\right)$ can be modelled by Gaussian distributions and so can be described by their mean and variance, the parameter set to estimate is $\theta = \left\{P\left(\omega_C\right), P\left(\omega_{NC}\right), \mu_C, \mu_{NC}, \sigma_C^2, \sigma_{NC}^2\right\}$. It is possible to prove that the EM iterative equation for estimating the above mentioned parameters for the class ω_C are the following:

$$P^{k+1}\left(\omega_C\right) = \frac{1}{I \times J}\sum_{x \in X_{DIFF}} \frac{P^k\left(\omega_C\right)p^k\left(x\left|\omega_C\right.\right)}{p^k\left(x\right)}$$

$$\mu_C^{k+1} = \frac{\sum_{x \in X_{DIFF}} \frac{P^k\left(\omega_C\right)p^k\left(x\left|\omega_C\right.\right)}{p^k\left(x\right)} \cdot x}{\sum_{x \in X_{DIFF}} \frac{P^k\left(\omega_C\right)p^k\left(x\left|\omega_C\right.\right)}{p^k\left(x\right)}}$$

$$\left(\sigma_C^2\right)^{k+1} = \frac{\sum_{x \in X_{DIFF}} \frac{P^k\left(\omega_C\right)p^k\left(x\left|\omega_C\right.\right)}{p^k\left(x\right)} \cdot \left(x - \mu_C^k\right)^2}{\sum_{x \in X_{DIFF}} \frac{P^k\left(\omega_C\right)p^k\left(x\left|\omega_C\right.\right)}{p^k\left(x\right)}}$$

where I and J indicate the difference image dimensions, *k* and *k*+1 denote the values of parameters at the current and next iterations.
Successively, on the basis of the estimates obtained by EM, the optimum threshold value T_0, between ω_C and ω_{NC}

distributions, can be computed by solving the following equation (fig.1):

$$\frac{P(\omega_C)}{P(\omega_{NC})} = \frac{p(X_{DIFF}|\omega_{NC})}{p(X_{DIFF}|\omega_C)}$$

which, for Gaussian distributions, is equivalent to solve the following equation:

$$T_0^2\left(\sigma_{NC}^2 - \sigma_C^2\right) + 2T_0\left(\mu_{NC}\sigma_C^2 - \mu_C\sigma_{NC}^2\right) +$$
$$+\mu_C^2\sigma_{NC}^2 - \mu_{NC}^2\sigma_C^2 - 2\sigma_C^2\sigma_{NC}^2 \ln\left(\frac{\sigma_{NC}P(\omega_C)}{\sigma_C P(\omega_{NC})}\right) = 0$$

When the optimal threshold value has been estimated, the difference image can be binarised and the corresponding percentages of changed and unchanged pixel can be computed.

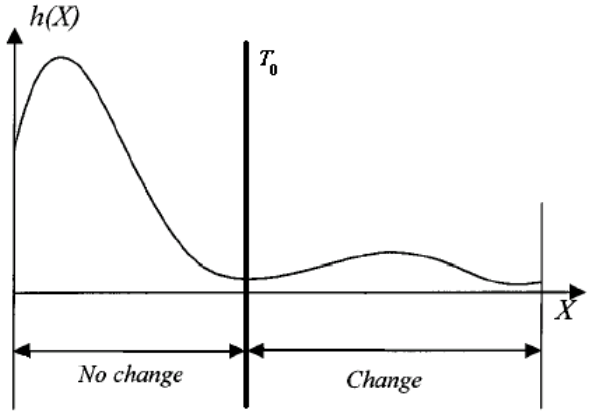

Fig.1 – No change and change distributions with optimal threshold value T_0.

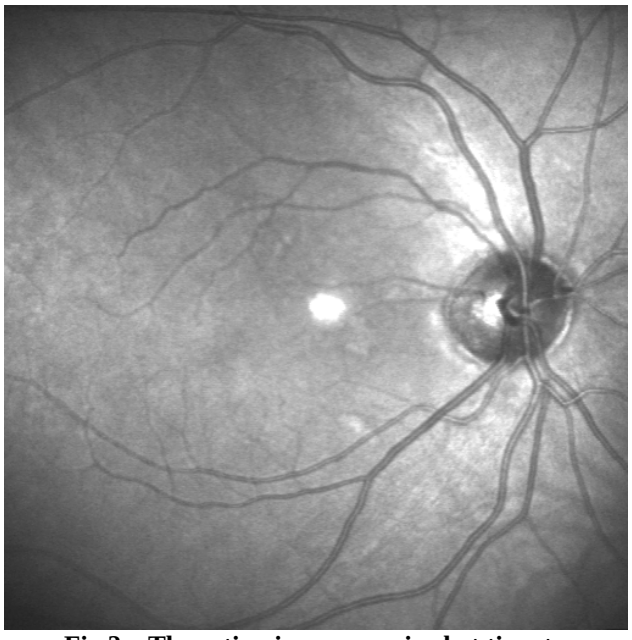

Fig.2 – The retina image acquired at time t_1.

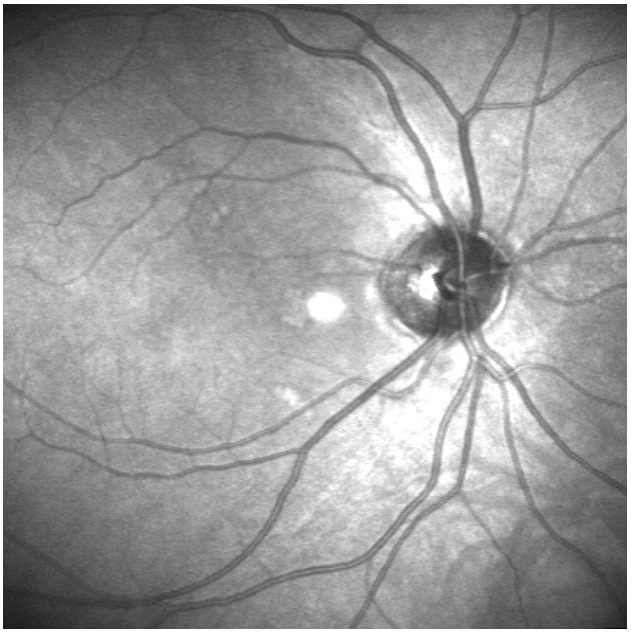

Fig.3 – The retina image acquired at time t_2.

4. Experimental setting and results

Pre-processing consists in tone extraction and spatial mean.

We explore input image by rectangular partition of variable dimensions and constant width – height ratio that we say window. Every window is partitioned in a fixed number of blocks (8 x 14). Then we assign windows pixels to each block, so we calculate mean of them and compare it with prearranged threshold.

Individual

Each individual has a chromosome with three genes (x0,y0,h) that corresponds to window position and height that determines a solution as a candidate of the best overlapping region, taking one of the two images as geometric reference.

Constraints

Domain and linear constraints allow considering only windows entirely into image. Non-linear constraints restrict search space and allow starting from population closer. In the new iterations domain constraints are restricted to allow searching next character into contiguous windows.

Evaluation function

Evaluation function is a multi-objective function to be minimised and it has two additive parts, that work in a competitive way to allow the exploitation of different kind of useful information. First term is involved to find windows fit and to avoid that the best solution was a very small overlapping region, the second term implements the maximum likelihood method.

Then, for each region individuated thanks to the first term, the optimisation algorithm modify the localisation of the overlapping region minimising the percentage of change in the difference image. Actually, to improve the performances of the unsupervised technique that analyzes the difference image between the original ones in order to determine change percentage, the image at time t2 has been spectrally corrected by using the following linear transformation:

$$\left(\frac{X_{t_2}-\mu_{t_2}}{\sigma_{t_2}}\right)\cdot\sigma_{t_1}+\mu_{t_1}=\frac{\sigma_{t_1}}{\sigma_{t_2}}\cdot X_{t_2}-\left(\frac{\sigma_{t_1}}{\sigma_{t_2}}\mu_{t_2}-\mu_{t_1}\right)$$

where $\mu_{t_i}, \forall i=1,2$ is the mean value and $\sigma_{t_i}, \forall i=1,2$ is the standard deviation of X_i.

Successively the optimisation algorithm is applied and the so obtained experimental results are reported in Table 1

%		Row Shift					
		44	45	46	47	48	49
Col Shift	14	16.00	15.99	16.04	16.15	16.29	17.01
	15	16.02	15.98	15.98	16.07	16.20	16.96
	16	16.18	16.07	16.05	16.39	16.69	17.10

Tab.1 – Change percentage in the neighbourhood of correct registration point.

5. Conclusions

In this paper we have presented an application of a multi-objective handling constraints genetic algorithm in which the adoption of a maximum likelihood method allows to take into account both the spectral and geometrical information to provide the best overlapping of two different images. Future work will provide the implementation of a Pareto multi-objective optimisation to reach better results in term of convergence of the proposed algorithm.

References:

[1] V. Bevilacqua, G. Mastronardi, A. Colaninno, A Character Recognition Handling Constraints Genetic Algorithm: the license plate case study. *Proceedings of the Iasted International Conference on Artificial Intelligence and Applications*, 2004, 109-113.

[2] J.B.A. Maintz, M.A. Viergever, A survey on Medical Image Registration, *Medical Image Analysis*, *2*(1), 1998, 1-37.

[3] G.E.Christensen, A.A. Kane, J.L. Marsh, M.W. Vannier, Synthesis *of an individual cranial atlas with dysmorphic shape*, Mathematical methods in biomedical image analysis, Los Alamitos, CA,1996, 309-318.

[4] F. Kruggel, P. Bartenstein, *Automatical registration of brain volume datasets* in Y. Bizais, C. Barillot, R. di Paola eds. *Information processing in medical imaging*, Kluwer, 389-390.

[5] Z. Michalewicz, *Evolutionary Computation Techniques for Non-Linear Programming Problems*, ftp://ftp.uncc.edu/coe/evol/p6.ps.

[6] Z. Michalewicz, C.Z. Janikow, *Handling Constraint in Genetic Algorithms*, Proceedings of the Fourth ICGA, Morgan Kaufmann, 1991.
ftp://ftp.uncc.edu/coe/evol/icga91.ps

[7] Z. Michalewicz, Survey of Constraint Handling Techniques in Evolutionary Computation Methods, *Proceedings of the 4th Annual Conference on EP*, MIT Press, Cambridge, MA, 1995,
ftp://ftp.uncc.edu/coe/evol/p17.ps

[8] L.Bruzzone, & D.F. Prieto, Automatic analysis of the difference image for unsupervised change detection, *IEEE Trans. Geosci. Remote Sensing, 38*(3), 2000, 1171-1182.

[9] L.Bruzzone, & D.F. Prieto, An adaptive semi-parametric and context-based approach to unsupervised change detection in multi-temporal remote-sensing images, *IEEE Trans. Image Processing*, *11*(4), 2002, 452-466.

[10] A.P.Dempster, N.M.Laird, & D.B.Rubin, Maximum likelihood for incomplete data via the EM algorithm, *J. Roy. Statist. Soc.*, *39*(1), 1977, 1-38.