EXPERIENCES OF EVOLUTIONARY SOLUTIONS IN BIOMETRICS, BIOINFORMATICS AND KNOWLEDGE MINING APPLICATIONS

Vitoantonio Bevilacqua1,2, Lucia Cariello1,2, Marcello Castellano1,2, Giuseppe Mastronardi1,2

1 Department of Electrical and Electronics, Polytechnic of Bari, Via Orabona, 4 – 70125 Bari – Italy
2 e.B.I.S. s.r.l. (electronic Business In Security), Spin-Off of Polytechnic of Bari, Via Pavoncelli, 139 – 70125 Bari – Italy

The theory and applications of infinite dimensional dynamical systems have attracted the attention of scientists for quite some time. Dynamical issues arise in equations, said evolution equations, which attempt to model phenomena that change with time, and the infinite dimensional aspects occur when forces describing the motion are depended on spatial variables. There are several ways to write the evolution equations, and therefore there are also several ways to implement them numerically. So Beside their presence in various fields of mathematics, evolution equations have also made, the last 20 years, a big impact on science and technology. In particular, in this paper, the authors present some of their most important works of the last years concerning the application of this equations in the field of biometrics, bioinformatics and knowledge mining application.

Personal identification involves a very large type of life situations and this is the reason for the high interest given, in the last years, to the biometric methods that improves the accuracy which systems can identify individuals with. This technologies are based on measurements of physical or behavioural characteristics unique to an individual such as fingerprints, facial features, retinal fundus, iris, hand geometry, voice, handwritten signature. The authors have run many researches in particular in the retinal bifurcation and cross-over points and facial features extraction, and they show their most recently works on this field. In [1], an analysis of images of retinal fundus by means of a combination of soft-computing techniques, is carried out, in order to extract from blood vessels their bifurcation and crossover points. In particular, the implemented method is constituted of four steps: a pre-processing of the input image by using, in sequence, several filters to obtain a black and white image representing the template of retinal veins and arteries; applying to the so obtained image a genetic algorithm, it is extracted the edges’ template; a skeleton process of the contours making use of an empirical algorithm and finally the objective is caught up by characterising the searched points by means of a tracking algorithm. In [2], different Pseudo 2-dimension Hidden Markov Models (HMMs) are introduced for a face recognition, showing performances reasonably fast for binary images. The proposed P2-DHMMs are made up of five levels of states, one for each significant facial region in which the input frontal images are sequenced: forehead, eyes, nose, mouth and chin. Each of them has been trained by coefficients of an Artificial Neural Network (ANN) used to compress a bitmap image in order to represent it with a number of coefficients that is smaller than the total number of pixels. In [3], it is presented a software system for fully automatic alignment of the 3D model of a human face. Starting with the point cloud of a human head, previously segmented from the background, pose normalization is attended with a novel, purely geometric approach. In order to solve the degrees of freedom of this problem, the natural mirror symmetry of human faces is exploited, then front profile shape is analyze and finally model’s bounding box with nose tip position is aligned. The whole procedure is thought as a twofold, multivariable optimization problem, addressed by a multilevel genetic algorithm and a branch and bound like search stage, with the latter compared against standard PCA.

The bioinformatic is a multidisciplinary scientific research that involves the application of computational and statistical techniques to understand, organize, manage, extract and analyze biological information. Also in this field the authors lead a flourishing searches. In [4], a technique to infer gene regulatory networks from data is described. An enhanced evolutionary algorithms to stochastically evolve a set of candidate Bayesian Network (BN) structures, is used and the model that best fits data without prior knowledge is found. Various evolutionary strategies suitable for the task have been proposed and their choices has been tested using simulated data drawn from a gene simulator, which has been used in the literature for benchmarking. In particular the approach enhanced by Crossover-Two Point and Selection Roulette Wheel for the learning of gene regulatory networks with BN outperforms classical structure learning methods in elucidating the original model. These results are been obtained for the learning of a bio-realistic network and, more importantly, on various small datasets. In [5], a unified evolutionary approach to coplanar radiotherapy inverse planning is proposed. It consists of a genetic algorithm-based framework that solves with little modification treatment planning for three different kinds of radiation therapy: conformal, aperture-based and intensity modulated. Thanks to evolutionary optimization techniques, full beam configurations has been searched, that is beam intensity, beam shape and especially beam orientation. The proposed solution automatically determines exact beam angles not relaxing solely on a geometrical basis but involving beam intensity profiles, thus considering the effective delivered dose.

Data Mining is the process of extracting hidden patterns, relations, reporting and new useful trends from large amounts of data, using automatic or semiautomatic techniques of analysis such as pattern recognition, statistics methods and mathematics models. The authors describe the equations that formalize the evolutionary model of the neural networks through two their works. In [6], an intrusion detection system based on data mining techniques (association rules and neural networks) able to detect a possible intrusion and to report it to the security administrator, is illustrate. Detection was carried out through the analysis of internet traffic generated by users in a network computer system. In [7], is explained how to develop a decision support system based on mining techniques (Text Mining and Data Mining) and performed on a large biomedical textual documentation, in order to extract new knowledge about symptom and pathology bio-entities. Data mining algorithms based on association rules and ANN to find probabilistic relationships between symptoms and pathologies, are applied.

REFERENCES


