

A Hybrid System for Automatic Infant Cry Recognition II

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INTRODUCTION

Automatic Infant Cry Recognition (AICR) process is basically a problem of pattern processing, very similar to the Automatic Speech Recognition (ASR) process (Huang, Acero, Hon, 2001). In AICR first we perform acoustical analysis, where the crying signal is analyzed to extract the more important acoustical features, like; LPC, MFCC, etc. (Cano, Escobedo and Coello, 1999). The obtained characteristics are represented by feature vectors, and each vector represents a pattern. These patterns are then classified in their corresponding pathology (Ekkel, 2002). In the reported case we are automatically classifying cries from normal, deaf and asphyxiating infants.

We use a genetic algorithm to find several optimal parameters needed by the Fuzzy Relational Neural Network FRNN (Reyes, 1994), like; the number of linguistic properties, the type of membership function, the method to calculate the output and the learning rate. The whole model has been tested on several data sets for infant cry classification. The process, as well as some results, is described.

BACKGROUND

In the first part of this document a complete description of the AICR system as well as of the FRNN is given. So, with continuity purposes, in this part we will concentrate in the description of the genetic algorithm and the whole system implementation and testing.

A genetic algorithm refers to a model introduced and investigated by John Holland (John Holland, 1975) and by students of Holland (DeJong, 1975). Genetic algorithms are often viewed as function optimizers, although the range of problems to which genetic algorithms have been applied is quite broad. Recently, numerous papers and applications combining fuzzy concepts and genetic algorithms (GAs) have become known, and there is an increasing concern in the integration of these two topics. In particular, there are a great number of publications exploring the use of GAs for developing or improving fuzzy systems, called genetic fuzzy systems (GFSs) (Cordon, Oscar, *et al*, 2001) (Casillas, Cordon, del Jesus, Herrera, 2000).

EVOLUTIONARY DESIGN

Within the evolutionary techniques, perhaps one of the most popular is the genetic algorithm (AG) (Goldberg, 1989). Its structure presents analogies with the biological theory of evolution, and is based on the principle of the survival of the fittest individual (Holland, 1975). Generally, a genetic algorithm has five basic components (Michalewicz, 1992). A representation of potential solutions to the problem, a form to create potential initial solutions, a fitness function that is in charge to evaluate solutions, genetic operators that alter the offspring's composition, and values for parameters like the size of the population, crossover probability, mutation probability, number of generations and others. Here we present different features of the genetic

algorithm used to find a combination of parameters for the FRNN.

Chromosomal Representation

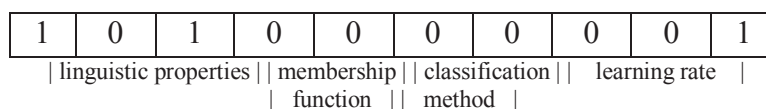
The binary codification is used in genetic algorithms, and Holland in (Holland, 1975) gave a theoretical justification to use it. Holland argued that the binary codification allows having more schemes than a decimal representation. Scheme is a template that describes a subgroup of strings that share certain similarities in some positions throughout their length (Goldberg, 1989). The problem variables consist of the number of linguistic properties, the type of membership function, the classification method and the learning rate. We are interested in having between 3 and 7 linguistic properties, so, the number of linguistic variables is encoded into a binary string of 3 bit length. The membership function is represented as a 2 bit string, where [00] decodes the Trapezoidal membership function, [01] decodes the Π function, [10] decodes the Triangular function, [11] decodes the Gaussian membership function. The classification methods are also coded as a 2 bit string, where [00] represents the max-min composition, [01] represents the geometrical mean and [10] represents the relational square product. Finally, the learning rate is represented as a binary string of 3 bit length, where [000] decodes to 0.1 learning rate, [001] decodes to 0.2 learning rate, [010] decodes to 0.31 learning rate, [011] decodes to 0.4 learning rate, and [100] decodes to 0.5 learning rate. A larger learning rate is not desirable, so all other bit values are ignored. The chromosome is obtained by concatenating all the above strings. Figure 1 shows an example of the chromosomal representation. Initial population is generated from a random selection of chromosomes, a population size of 50 was considered.

Genetic Operations

We use four genetic operations, namely elitism, roulette wheel selection, crossover and mutation. **Elitism:** In order to ensure that the members with highest fitness value of the population stay in the next generation we apply elitism. It has been demonstrated (Günter, Rudolph, 1994), that a genetic algorithm must use elitism to be able to show convergence. At each iteration of the genetic algorithm we select the members with the four highest fitness values and we put them in the next generation.

Selection: In the genetic algorithm the selection process is made in a probabilistic way, it is to say, the less apt individuals even have a certain opportunity to be selected. There are many different types of selection approaches; we use the roulette wheel selection, where members of the population have a probability of being selected that is directly proportionate to their fitness. **Crossover:** In this work we use a single point crossover. Observing the performance of different crossover operators, De Jong (De Jong, K., 1975) concluded that, although increasing the number of points of crosses affects its schemes from a theoretical perspective, in practice this does not seem to have a significant impact. The crossover is the principal operator in the genetic algorithm. Based on some experiments we decided to determine the crossover point randomly and the crossover probability was fixed at 0.8. **Mutation:** This operator allows the introduction of new chromosomal material in the population. We selected a gene randomly and we replaced it by its complement, a zero is changed by a one and a one is changed by a zero. Some authors suggest that the mutation probability equal to $1/L$, where L is the length of the chain of bits is an inferior limit acceptable for the optimal percentage of mutation (Bäck, Thomas, 1993). In this work the mutation probability is fixed at 0.05.

Figure 1. Chromosomal representation



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