An Intelligent Agent for Detection of Erythemato-Squamous Diseases using Co-Active Neuro-Fuzzy Inference System and Genetic Algorithm

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***Abstract*— In this paper, a new approach based on Coactive Neuro-Fuzzy Inference System (CANFIS) is presented for detection of erythemato-squamous diseases. The domain contained records of patients with 34 features and known diagnosis of six disease indications. Given a training set of such records, the CANFIS classifiers learned how to differentiate a new case in the domain that may be difficult even for experienced doctors to make correct diagnosis because many symptoms look very similar to each other, even though they are caused by different diseases. The proposed CANFIS model combined the neural network adaptive capabilities and the fuzzy logic qualitative approach which is then integrated with genetic algorithm. The performances of the CANFIS model were evaluated in terms of training performances and classification accuracies and the results showed that the proposed CANFIS model has great potential in detecting the erythemato-squamous diseases.**

Keywords- Artificial Neural Networks, Coactive Adaptive Neuro-Fuzzy Inference System (CANFIS), Fuzzy Logic, Erythemato-Squamous diseases, Genetic Algorithm (GA)

I. INTRODUCTION

In recent years the need for tools to process automatically and manage information drove researchers to make use of intelligent systems capable of dealing with the uncertainty typical of real data [1]. The integration of neural networks and fuzzy logic provides an effective way to exploit the powerful processing capabilities of a neuro-computing system and to organize the knowledge embedded into the system in an easily accessible form [2], [3]. These significant features, which characterize neuro-fuzzy systems, enable to tackle a wide range of problems related to many fields, including economy, control theory, engineering, industrial application, neuro-science and medicine [4], [5], [6], [7], [8]. Neuro-fuzzy systems lend themselves well to prognosis and diagnosis and find application in an increasing number of biomedical domains, since the human experts can check and verify the learned classification knowledge before using it in real world problems.

The differential diagnosis of erythemato-squamous diseases is a difficult problem in dermatology. The diseases in this group are psoriasis, seboreic dermatitis, lichen planus, pityriasis rosea, chronic dermatitis and pityriasis rubra pilaris. They all share the clinical features of erythema and scaling with very few differences [9]. This is where fuzzy set theory plays an important role in dealing with uncertainty when making decisions in medical applications. Fuzzy sets have attracted growing attention and interest in modern information technology, production technique, decision making, pattern recognition, diagnostics, data analysis, etc. [10–13]. Neuro-fuzzy systems are fuzzy systems which use artificial neural networks (ANNs) theory in order to determine their properties (fuzzy sets and fuzzy rules) by processing data samples. Neuro-fuzzy systems harness the power of the two paradigms: fuzzy logic and ANNs, by utilizing the mathematical properties of ANNs in tuning rule-based fuzzy systems that approximate the way man processes information.

A specific approach in neuro-fuzzy development is the coactive adaptive neuro-fuzzy inference system (CANFIS), which has shown significant results in modelling nonlinear functions. In CANFIS, the membership function parameters are extracted from a data set that describes the system behavior. The CANFIS learns features in the data set and adjusts the system parameters according to a given error criterion [2], [14]. Successful implementations of CANFIS in biomedical engineering have been reported for classification [15],[16] and data analysis [17]. In this study, a new approach based on CANFIS is presented for the detection of erythemato-squamous diseases. The dermatology database investigated in this study consisted of 358 cases of erythemato-squamous diseases compiled by Guvenir et al. [9]. The proposed CANFIS model was then evaluated and performance was reported. We were able to achieve significant improvement in sensitivity, specificity and total classification accuracy by applying CANFIS model compared to other neural networks reported in literature. [21].The paper is organized as follows. In Section II we present the

description of the domain and Section III about the diagnostic system using CANFIS and Genetic Optimization. In Section IV we describe the results and discussion and Section V conclusions were drawn.

II. DOMAIN DESCRIPTION

Erythemato-squamous diseases are frequently seen in the outpatient departments of dermatology. At the first sight, all the diseases look very much alike with the erythema and scaling. When inspected more carefully some patients have the typical clinical features of the disease at the predilection sites (localization of the skin where a disease preters) while another group has typical localization. The adopted dataset has been obtained from the UCI Machine Learning repository (http://www.ics.uci.edu/□mlearn/MLRepository.html) and has been employed in [21].

TABLE 1: THE DATA SET USED IN THE PRESENT STUDY (EXTRACTED FROM UCI MACHINE LEARNING REPOSITORY)

Erythemato - squamous diseases	Features	
	Clinical	Histopathological
Psoriasis (111)	Feature 1: Erythema	Feature 12: Melanin incontinence
Seboreic dermatitis (60)	Feature 2: Scaling	Feature 13: Eosinophils in the infiltrate
Lichen planus (71)	Feature 3: Definite borders	Feature 14: PNL infiltrate
Pityriasis rosea (48)	Feature 4: Itching	Feature 15: Fibrosis of the papillary dermis
Chronic dermatitis (48)	Feature 5: Koebner phenomenon	Feature 16: Exocytosis
Pityriasis rubra pilaris (20)	Feature 6: Polygonal papules	Feature 17: Acanthosis
	Feature 7: Follicular papules	Feature 18: Hyperkeratosis
	Feature 8: Oral mucosal involvement	Feature 19: Parakeratosis
	Feature 9: Knee and elbow involvement	Feature 20: Clubbing of the rete ridges
	Feature 10: Scalp involvement	Feature 21: Elongation of the rete ridges
	Feature 11: Family history	Feature 22: Thinning of the suprapapillary epidermis
		Feature 23: Pongiform pustule
		Feature 24: Munro microabcess
		Feature 25: Focal hypergranulosis
		Feature 26: Disappearance of the granular layer
		Feature 27: Vacuolization and damage of basal layer
		Feature 28: Spongiosis
		Feature 29: Saw-tooth appearance of retes
		Feature 30: Follicular horn plug
		Feature 31: Perifollicular parakeratosis
		Feature 32: Inflammatory mononuclear infiltrate
		Feature 33: Band-like infiltrate
		Feature 34: Age

Patients are first evaluated clinically with 12 features. The degree of erythema and scaling, whether the borders of lesions are definite or not, the presence of itching and koebner phenomenon, the form of the papules, whether the oral mucosa, elbows, knees and the scalp are involved or not, whether there is a family history or not are important for the differential diagnosis. For example, the erythema and scaling of chronic dermatitis is lesser than that of psoriasis with the koebner phenomenon present only in psoriasis, lichen planus and pityriasis rosea. Itching and polygonal papules are for lichen planus and follicular papules are for pityriasis rubra pilaris. Oral mucosa is predilection site for lichen planus, while knee, elbow and scalp involvement are of psoriasis. Family history is usually present for psoriasis. The pityriasis rubra pilaris usually starts during childhood.

Some patients can be diagnosed with these clinical features only, but usually a biopsy is necessary for the correct and definite diagnosis. Skin samples were taken for the evaluation of 22 histopathological features. Another difficulty for the differential diagnosis is that a disease may show the histopathological features of another disease at the beginning stage and may have the characteristic features at the following stages. Some samples show the typical histopathological features of the disease while some do not. Melanin incontinence is a diagnostic feature for lichen planus, fibrosis of the papillary dermis is for chronic dermatitis, while exocytosis may be seen in lichen planus, pityriasis rosea and seboreic dermatitis. Acanthosis and parakeratosis can be seen in all diseases in different degrees. Clubbing of the rete ridges and thinning of the suprapapillary epidermis are diagnostic for psoriasis. Disappearance of the granular layer, vacuolization and damage of the basal layer, saw-tooth appearance of retes and a band like infiltrate are diagnostic for lichen planus. Follicular horn plug and perifollicular parakeratosis are hints for pityriasis rubra pilaris [9].

In the dataset, the family history feature has the value 1 if any of these diseases has been observed in the family and 0 otherwise. The age feature simply represents the age of the patient. Every other feature (clinical and histopathological) was given a degree in the range of 0 to 3. Here, 0 indicates that the feature was not present, 3 indicates the largest amount possible, and 1, 2 indicate the relative intermediate values. The dataset used in the experiment is summarized in Table 1. All of the test cases had one of the six erythemato-squamous diseases. The features of a patient are represented as a vector of features which has 34 entries for each feature value.

III. DIAGNOSTIC SYSTEM USING CANFIS

A very promising paradigm in intelligent techniques is constituted by the neuro-fuzzy approach, in which fuzzy logic and neural networks are combined. Neuro-fuzzy hybrid systems combine the advantages of fuzzy systems, which deal with explicit knowledge that can be explained and understood, and neural networks which deal with implicit knowledge that can be acquired by learning. Neural network learning provides a good way to adjust the expert's knowledge and automatically generate additional fuzzy rules and membership functions, to meet certain specifications and reduce design time and costs.

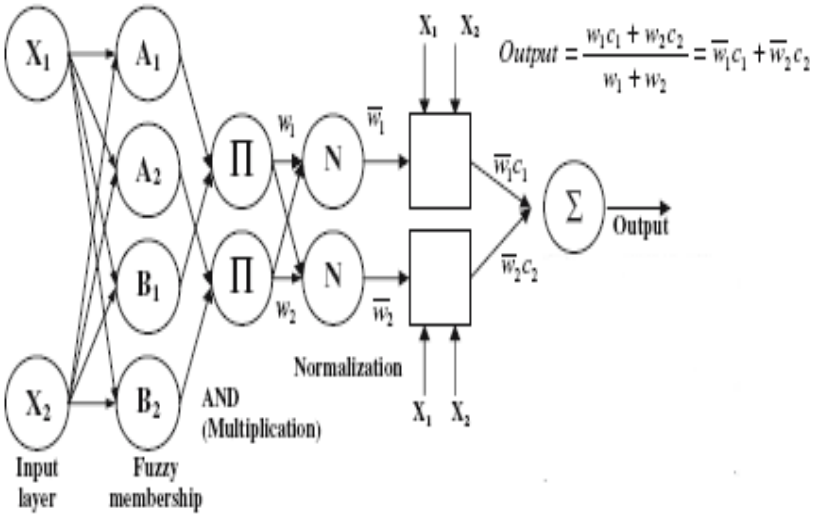

Figure 1. A prototype two-input one-output CANFIS network and output calculation

The CANFIS model integrates adaptable fuzzy inputs with a modular neural network to rapidly and accurately approximate complex functions. Fuzzy inference systems are also valuable, as they combine the explanatory nature of rules (Membership Functions) with the power of neural networks. These kinds of networks solve problems more efficiently than neural networks where the underlying function to model is highly variable or locally extreme [18].

The fundamental component of CANFIS is a fuzzy axon, which applies membership functions to the inputs. The output of a fuzzy axon is computed using the following formula:

$$f_j(x,w) = min\forall_i(MF(x_{i,} w_{ij})), \qquad (1)$$

Where i =input index, j =output index, x_i =input i, w_{ij} = weights (MF parameters) corresponding to the j th MF of input i and MF = membership function of the particular subclass of the fuzzy axon

This system can be viewed as a special three-layer feed forward neural network. The first layer represents input variables, the middle (hidden) layer represents fuzzy rules and the third layer represents output variables. The CANFIS architecture used in this study is shown in Fig 1.

A. CANFIS Architecture

Consider a CANFIS structure with n inputs and one output. For model initialization, suppose a common rule set with n inputs and m IF-THEN rules as follows [19]:

Rule 1: If z_1 is A_{11} and z_2 is A_{12} . . . and z_n is A_{1n}
then $u_1 = p_{11}z_1 + p_{12}z_2 + \cdots + p_{1n}z_n + q_1$

Rule 2: If z_1 is A_{21} and z_2 is A_{22} . . . and z_n is A_{2n}
then $u_2 = p_{21}z_1 + p_{22}z_2 + \cdots + p_{2n}z_n + q_2$

Rule m: If z_1 is A_{m1} and z_2 is A_{m2} . . and z_n is A_{mn}
then $u_m = p_{m1}z_1 + p_{m2}z_2 + \cdots + p_{mn}z_n + q_m$

The corresponding CANFIS structure is illustrated in Fig. 2. All layers in CANFIS structure are either adaptive or fixed. The function of each layer is described as follows:

Layer 1 (Premise Parameters): Every node in this layer is a complex-valued membership function (μ_{ij}) with a node function:

$$O_{1,ij} = |\mu A_{ij}(z_i)| \angle \mu A_{ij}(z_i) \text{ for } (1 \le i \le n,\ 1 \le j \le m). \qquad (2)$$

Each node in layer 1 is the membership grade of a fuzzy set (A_{ij}) and specifies the degree to which the given input belongs to one of the fuzzy sets.

Layer 2 (Firing Strength): Every node in this layer is product of all the incoming signals. This layer receives input in the form of the product of all the output pairs from the first layer:

$$O_{2,j} = w_j = \mu A_{i1}(z_1)\mu A_{i2}(z_2), \ldots, \mu A_{i1n}(z_n), \quad \text{for } (1 \le i \le m \qquad (3)$$

Layer 3 (Normalized Firing Strength): Every node in this layer calculates rational firing strength:

$$O_{3,j} = \overline{w_j} = \frac{w_j}{\sum_{j=1}^{m} w_j} \quad \text{for } (1 \le j \le m). \qquad (4)$$

Layer 4 (Consequence Parameters): Every node in this layer is multiplication of Normalized Firing Strength from the third layer and output of neural network:

$$O_{4,j} = \overline{w_j}\, u_j = \overline{w_j}\,(P_{J1}Z_1 + P_{J2}Z_2 + \cdots P_{Jn}Z_{2n} + q_j) \quad \text{for } (1 \le j \le m) \qquad (5)$$

Layer 5 (Overall Output): The node here computes the output of CANFIS network:

$$O_{5,1} = \Sigma \overline{w_j}\ u_j \qquad (6)$$

Basically, two membership function types can be used (Gaussian or generalized bell). The bell fuzzy axon used in this study is a type of fuzzy axon that uses a bell-shaped curve as its membership function. Each membership function takes three parameters stored in the weight vector of the bell fuzzy axon (Eq. 7):

$$\mathrm{MF}(x,w) = \frac{1}{1+\left|\frac{x-w_2}{w_0}\right|^{2w_1}} \qquad (7)$$

where x =input and w=weight of the bell fuzzy axon.

Fuzzy axons are valuable because their MF can be modified through back propagation during network training to expedite the convergence. A second advantage is that fuzzy synapses help in characterizing inputs that are not easily discretized. The powerful capability of CANFIS stems from the pattern-dependent weights between the consequent layer and the fuzzy association layer.

The second major component of CANFIS is a modular network that applies functional rules to the inputs. The number of modular networks matches the number of network outputs and processing elements in each network are corresponding to the number of MFs. Two fuzzy structures are mainly used: the Tsukamoto model and the Sugeno (TSK)model. Finally, a combiner is used to apply the MF outputs to the modular network outputs. The combined outputs are then channeled through a final output layer, and the error is back propagated to both the MF and the modular network [20]

B. Genetic Optimization

In order to improve the learning of the *CANFIS*, viz., quicker training and enhance its performance, we use genetic algorithms to search for the best number of MF for each input, and optimization of control parameters such as learning rate, and momentum coefficient. This approach also is useful to select the most relevant features of the training data which can produce a smaller and less complicated network, with the ability to generalize on freshly presented data, due to the removal of redundant variables.

The GA combines selection, crossover, and mutation operators with the goal of finding the best solution to a problem by searching until the specified criterion is met. The solution to a problem is called a chromosome, which is composed of a collection of genes. In hybrid neuro-fuzzy-genetic applications, genes are the *CANFIS* parameters to be optimized. The GA creates an initial population and then evaluates this population by training a network for each chromosome. It then evolves the population through multiple generations in the search for the best network parameters.

GAs cause the initial population to evolve towards a population that is expected to contain the best solution [21]. We use the following reproduction evaluation cycle for each iteration-referred to as a generation. Chromosomes (individuals) from the current population are selected with a given probability; and copies of these chromosomes (individuals) are created. The selection of chromosomes is based on their fitness relative to the current population; that is, the stronger chromosomes will have a higher probability of being copied. The fitness is a function of the *CANFIS* model's response. Selected chromosomes are subjected to mutation and to crossover. Fig 2 shows the CANFIS/genetic algorithm cycle in search of optimum parameters of the model

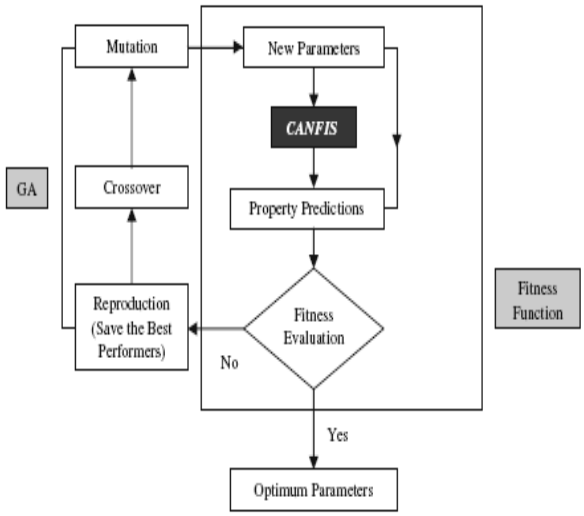

Figure. 2 The CANFIS /GA cycle for Optimization

These mathematical chromosomes could be operated upon by quasi-genetic processes of crossing over and mutation. To implement crossovers, chromosomes were randomly paired, and segments of paired chromosomes between two randomly determined breakpoints were swapped. Crossovers could be implemented either across genes, so that gene boundaries might potentially be breached by the exchange of genetic material; or within genes, so that gene boundaries would be preserved. Inversions could also be modeled, so that exchanged genetic material could be inverted before becoming incorporated into the recipient chromosome

Mutations were implemented by flipping a bit at a binary locus, so that a "0" bit was converted to a "1," or a "1" bit was converted to a "0." In this paper, for the optimization of the CANFIS model, GA used the serial method of binary type, roulette-wheel in the selection operator, tow-point crossover in the crossover operator, and boundary in the mutation operator. Automatic determination of the chromosomes length used for optimal search is one of the most important capabilities of the NeuroSolution software. Thus, all the chromosomes were automatically set in this software so that they contained the number of input neurons and membership functions, learning rate, and momentum. Neuro-Solution also automatically produced their initial values.

IV. RESULTS AND DISCUSSIONS

The simulations were realized by using MATLAB 6.0 Neural Network Toolbox and Neurosolution software. 50% of data (179 training data) were used to train the CANFIS network

model and the remaining 50% of data (179 testing data) were used to validate the accuracy of the CANFIS model for the detection of erythemato-squamous diseases. In classification, the aim is to assign the input patterns to one of several classes, usually represented by outputs restricted to lie in the range from 0 to 1, so that they represent the probability of class membership. While the classification is carried out, a specific pattern is assigned to a specific class according to the characteristic features selected for it. In this application, there were six classes: psoriasis, seboreic dermatitis, lichen planus, pityriasis rosea, chronic dermatitis, and pityriasis rubra pilaris. Classification results of the CANFIS model were displayed by a confusion matrix. The confusion matrix is defined by labeling the desired classification on the rows and the actual network outputs on the columns. The confusion matrix showing the classification results of the CANFIS model is given in Table2.

TABLE 2: CONFUSION MATRIX USING CANFIS FOR OUR DATA SET

Desired Result	Psoriasis	Seboreic dermatitis	Lichen Planus	Pityriasis rosea	Chronic dermatitis	Pityriasis rubra pilaris
Psoriasis	55	1	0	0	1	0
Seboreic dermatitis	0	29	0	0	0	0
Lichen Planus	0	0	34	0	0	0
Pityriasis rosea	1	0	1	23	0	1
Chronic dermatitis	0	0	0	1	23	0
Pityriasis rubra pilaris	0	0	0	0	0	9

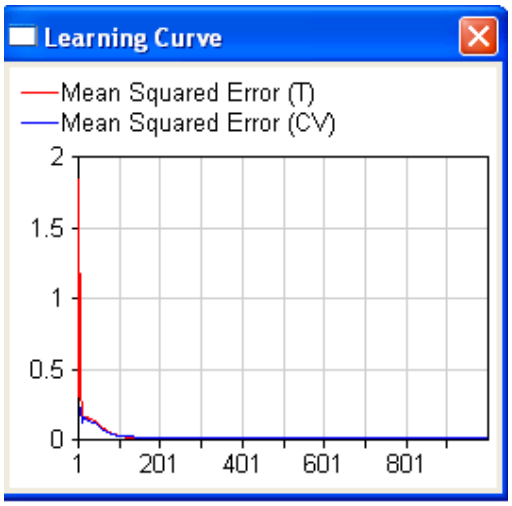

Figure 3 Learning Curve for our dataset

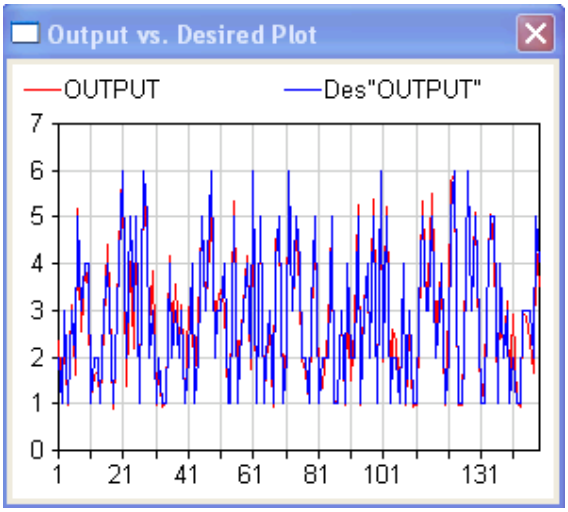

Figure 4: Output Vs desired plot for our dataset

According to the confusion matrix, one subject suffering from psoriasis was classified incorrectly by the CANFIS model as a subject suffering from pityriasis rosea, one subject suffering from seboreic dermatitis was classified as a subject suffering from psoriasis, one subject suffering from lichen planus was classified as a subject suffering from pityriasis rosea, one subject suffering from pityriasis rosea was classified as a subject suffering from chronic dermatitis, one subject suffering from chronic dermatitis was classified as a subject suffering from psoriasis and one subject suffering from pityriasis rubra pilaris was classified as a subject suffering from pityriasis rosea. The learning curve using CANFIS for our dataset is shown in Fig 3

TABLE 3: THE VALUES OF SENSITIVITY

Erythemato-squamous diseases	Sensitivity (%)
Psoriasis	98.2
Seboreic dermatitis	96.66
Lichen Planus	97.14
Pityriasis rosea	95.8
Chronic dermatitis	95.8
Pityriasis rubra pilaris	90.0

TABLE 4: THE VALUES OF SPECIFICITY

Erythemato-squamous diseases	Specificity (%)
Psoriasis	98.4
Seboreic dermatitis	100
Lichen Planus	100
Pityriasis rosea	98.1
Chronic dermatitis	99.4
Pityriasis rubra pilaris	100

Fig. 4 gives the output vs desired plot for our dataset and Mean Square Error (MSE) is found to be 0.0097247839. The test performance of the CANFIS model was determined by the computation of the statistical parameters such as sensitivity, specificity and total classification accuracy.

The sensitivity, specificity and total classification accuracy are defined as follows:

Sensitivity: Number of true positive decisions/number of actually positive cases.(Table 3)

Specificity: Number of true negative decisions/number of actually negative cases.(Table 4)

Total classification accuracy: Number of correct decisions/total number of cases which is 96.65% for our dataset. The values for sensitivity and specificity were shown in Table 3 and 4.

A true positive decision occurs when the positive detection of the network coincided with a positive detection of the physician. A true negative decision occurs when both the network and the physician suggested the absence of a positive detection. The total classification accuracy of the CANFIS model is found to be 96.65%.

V. CONCLUSIONS

This paper presented a new application of CANFIS model with genetic optimization for the detection of erythemato-squamous diseases. The obtained total classification accuracy of 96.65% is better than that of all reported in literature. The total classification accuracy of the stand-alone neural network was 85.50%.and that of the ANFIS model was 95.5%. [21] [22]. These results indicate that the proposed CANFIS model has great potential in detecting the erythemato-squamous diseases. Also another advantage of the CANFIS tool will be a guide to the doctors in making their own diagnosis mechanisms by examining the working methodologies of our algorithm. While encouraged by the performance of our methods, we believe further work is likely to yield much more comprehensive and accurate tool for diagnosis of erythemato-squamous disease.

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