Classifying Squint Risk Level of Squint Eye Patients from Pattern Visual Evoked Potential Signals

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Abstract: Classification of squint risk level of squint eye patient is a classical problem. In this study, genetic algorithm(GA) and adaptive neuro fuzzy inference system (ANFIS) are used in the classification of squint risk level from pattern visual evoked potential (P-VEP) signal parameters. The squint risk level is classified based on the extracted parameters like energy, variance, peaks, sharp and spike waves, duration, events, covariance and P100 latency from the P-VEP of the patient. This paper focuses on comparison of genetic algorithm (GA) and adaptive neuro fuzzy inference system(ANFIS) in classification. Genetic algorithm (GA) and ANFIS are applied on the code converter's classified risk levels to optimize risk levels that characterize the patient. The Performance Index(PI) and Quality Value (QV) are calculated for these methods. A group of ten patients with known squint findings are used in this study. High PI such as 93.33% and 97.83% for GA and ANFIS are obtained at QV of 20.14 and 24.59.

Keyword: P-VEP Signals, P100 latency, Squint eye, Genetic Algorithm, Adaptive Neuro Fuzzy Inference System, Risk Level.

1. Introduction:

The recognition of specific waveforms and features in the Pattern Visual Evoked Potential (P-VEP) for classification of squint risk levels has been the subject of much research. Techniques used are ranged from statistical methods to syntactic and knowledge based approaches. All of these methods require the definition of a set of features (or symbols and tokens) to be detected, and a pattern matcher to compare the observed values with the ideal, prototypical ones. An alternative approach, inspired by the configuration of the human brain, involves the use of artificial neural networks and fuzzy inference system (ANFIS). One specific ANFIS architecture is Sugeno FIS and RBFN(Radial Base Function Neural Network) with five layers between the input and output nodes. Training ANFIS is achieved by generalized least mean square algorithm. This research focused on classification of squint risk levels from PVEP signals through ANFIS and Genetic Algorithm (GA). The GA is a type of natural evolutionary algorithm that models biological process to optimize highly complex cost functions by allowing a population composed of many individuals to evolve under specific rules to a state that maximizes the fitness. John Holland developed this method in 1975 [1]. Many researchers share the intuitions that if the space to be searched is large, is known not to be perfectly smooth and unimodal (i.e., consists of a single smooth 'hill'), or is not well understood, or if the fitness function is noisy, and if the task does not require a global optimum to be found, i.e., if quickly finding a sufficiently good solution is enough – a GA will have a good chance off being competitive with or surpassing other optimization methods [2]. A comparison of GA and ANFIS as a classification and optimization tools for bio medical engineers with a useful application of squint risk level classification is analyzed.

1.1 Back Ground:

Visual evoked potential (VEP) is an evoked electrophysiological potential that can be extracted, using signal averaging, from the electroencephalographic activity recorded at the scalp. The VEP can provide important diagnostic information regarding the functional integrity of the visual system. Pattern reversal is the preferred technique for most clinical purposes. The results of pattern reversal stimuli are less variable in wave form and timing than the results elicited by other stimuli. Diagnosis of presence of squint is rarely difficult, but objectively determining what the symptomatic patient sees can be challenging. The pattern reversal stimulus consists of black and white checks that change phase (i.e., black to white and white to black) abruptly and repeatedly at a specified number of reversals per second. There must be no overall change in the luminance of the screen. This requires equal numbers of light and dark elements in the display. Background luminance of screen and room should approximate the mean for onset/offset of each check.

When a patient is diagnosed with squint, the latent potential of vision improvement is very important when deciding on therapy. Recently, various attempts have been made to assess which factors present at the time of diagnosis reflect the final visual outcome after squint treatment.[28-33] It has been reported that pattern visual-evoked response acuity correlates with the best-corrected Snellen acuity in normal subjects.[33] [34] Increases in the amplitude on

pattern visual evoked potential (P-VEP) appear to reflect vision improvement during squint treatment. [30] Among patients with squint, strabismus amblyopia, those with an eccentric fixation had a relatively delayed P100 latency and less vision improvement after 6 months of squint treatment when compared with patients who had a central fixation [28].

To investigate whether P100 latency could predict visual outcomes in patients with functional squint including, patients were grouped by P100 latency on P-VEP at the time of initial diagnosis, and visual improvement was compared after occlusion therapy between the two groups. Also, differences in P100 latency by type of amblyopia were sought.

2. Methodology

10 patients whose visual abnormalities could not be explained by the findings of ophthalmological, neurological and psychiatric examinations were included. Control group comprised of 24 age and gender matched normal volunteers. Examinations of patients and subjects included visual acuities with Landolt rings, tests of pupillary reaction to light, visual fields tests looking for signs of tubular constriction, ophthalmoscopic examination and presence of squint eye tests.

P-VEP was always performed with appropriate refractive correction. This investigation was performed according to the standard guidelines after informed consent was obtained from all subjects. For P-VEP recording, each subject viewed a white and black checkerboard pattern on a television monitor. One experimenter monitored the patients' ocular fixation, which was directed toward the TV screen in a shielded room as a monocular P-VEP was recorded. The check sizes were 1^o, 30`and 15`. Visual acuity of 0.2 corresponded to 1^o pattern, 0.4 corresponded to the 30` pattern and 0.7 to the 15` pattern.

The checks were reversed at 0.7 Hz. The computer analysis time of the P-VEP was 512milliseconds. One hundred P-VEP responses were averaged per session. The latency and amplitude of P100 for 3 consecutive check size were measured in both groups. The P100 component was used to estimate objective visual acuity.

A paper record of 16 channel P-VEP data is acquired from a clinical P-VEP monitoring system through 10-20 international electrode placing method. The PVEP signal was band pass filtered between 0.5 Hz and 50Hz using five pole analog Butter worth filters to remove the artifacts. With an P-VEP signal free of artifacts, a reasonably accurate detection of squint is possible; however, difficulties arise with artifacts. This problem increases the number of false detection that commonly plagues all classification systems. With the help of neurologist, we had selected artifact free PVEP records with distinct features. These records were scanned by Umax 6696 scanner with a resolution of 600dpi. Since the EEG records are over a continuous duration of about thirty seconds, they are divided into epochs of two second duration each by scanning into a bitmap image of size 400x100 pixels.

A two second epoch is long enough to detect any significant changes in activity and presence of artifacts and also short enough to avoid any repetition or redundancy in the signal [1] [2] [3]. The P-VEP signal has a maximum frequency of 50Hz and so, each epoch is sampled at a frequency of 200Hz using graphics programming in C. Each sample corresponds to the instantaneous amplitude values of the signal, totaling 400 values for an epoch. The different parameters used for quantification of the P-VEP are computed using these amplitude values by suitable programming codes.

The parameters are obtained for three different continuous epochs at discrete times in order to locate variations and differences in the presence of squint activity. We used ten P-VEP records for both training and testing. These P-VEP records had an average length of six seconds and total length of 60 seconds. The patients had an average age of 31 years. A total of 480 epochs of 2 seconds duration are used. General features of the test records are as follows.

Record 1and 4: High risk level with peaks and spikes.
Record 3 and6: Patient under clinical observation after two weeks of intensive drug therapy. Record 2and 8: Very High risk level with energy, Peaks and spikes.
Record 5and 7: Medium risk level with variance, energy, peaks and spikes.
Record 9and 10: Low risk level with variance, energy, peaks and spikes with occasional medium risk levels

2.1 Feature Extraction and Code Converter System

The various parameters obtained by sampling are given as inputs to the code converter system as shown in fig. 1. These parameters are defined as follows [9], [10], [11].

1. The energy in each two-second epoch is given by

$$E = \sum_{i=1}^{n} x_i^2 \quad \ldots\ldots(1)$$

Where x_i is signal sample value and n is number of samples. The normalized energy is taken by dividing the energy term by 1000.

2. The total number of positive and negative peaks exceeding a threshold is found.

3. Spikes are detected when the zero crossing duration of predominantly high amplitude peaks in the P-VEP waveform lies between 20 ms and 70 ms and sharp waves are detected when the duration lies between 70ms and 120ms.

4. The total numbers of spike and sharp waves in an epoch are recorded as events.

5. The variance is computed as σ given by

$$\sigma^2 = \frac{\sum_{i=1}^{n} (x_i - \mu)^2}{n} \quad \ldots\ldots(2)$$

$$\mu = \frac{\sum_{i=1}^{n} x_i}{n}$$

Where is the average amplitude of the epoch.

6. The average duration is given by

$$D = \frac{\sum_{i=1}^{p} t_i}{p} \quad \ldots\ldots(3)$$

Where t_i is one peak to peak duration and p is the number of such durations.

7. Covariance of Duration which is defined as the variation of the average duration is

$$CD = \frac{\sum_{i=1}^{p} (D - t_i)^2}{pD^2} \quad \ldots\ldots.(4)$$

8. P100 latency are calculated using standard deviation.

$$s = \sqrt{\frac{\sum_{i=1}^{N} (x_i - \bar{x})^2}{N-1}} \quad \ldots\ldots..(5)$$

In this formula, x is the value of the mean, N is the sample size, and x_i represents each data value from i=1 to i=N.. The $\sum$ symbol indicates that you must add up the sum $(x_1 - x)^2 + (x_2 - x)^2 + (x_3 - x)^2 + (x_4 - x)^2 + (x_5 - x)^2$. . . + $(x_N - x)^2$.

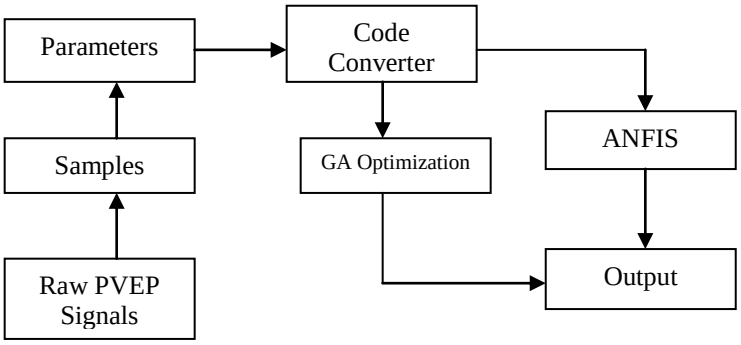

Figure.1. Block diagram of Genetic Algorithm and ANFIS based Classification system

The average values of extracted parameters in each 2 seconds epoch over sixteen channels of the patient record 5 is listed in the Table I

Table I Average values of Extracted Parameters from Patient Record 5

Parameters	Epoch1	Epoch2	Epoch3
Energy	5.2869	8.581	10.10
Variance	1.1397	2.121	2.322
Peaks	1	2	2
Total	9	38	35
Sharp & Spike	8	6	6
Total	122	91	87
Event	12	10	10
Total	185	154	145
Average duration	3.798	4.042	3.883
Covariance	0.5793	0.5123	0.5941
P100 latency(SD)	0.04	0.05	0.03

With the help of expert's knowledge and our experiences with the references [12],[13],[14], we have identified the following parametric ranges for five linguistic risk levels (very low, low, medium, high and very high) in the clinical description for the patients which is shown in table II

Table II Parameter Ranges for Various Risk Levels

Risk levels / Normalized Parameters	Normal	Low	Medium	High	Very High
Energy	0-1	0.7-3.6	2.9-8.2	7.6-11	9.2-30
Variance	0-0.3	0.15-0.45	0.4-2,2	1,6-4.3	3.8-10
Peaks	0-2	1-4	3-8	6-16	12-20
Events	0-2	1-5	4-10	7-16	15-28
Sharp Waves	0-2	1-5	4-8	7-11	10-12
Average Duration	0-0.3	0.15-0.45	0.4-2.4	1.8-4.6	3.6-10
Covariance	0-0.05	0.025-0.1	0.09-0.04	0.28-0.64	0.54-1
P100 latency (msec)	120	< 120	120 - 130	130 - 140	> 140

The output of code converter is encoded into the strings of seven codes corresponding to each P-VEP signal parameter based on the squint risk levels threshold values as set in the table II. The expert defined threshold values are containing noise in the form of overlapping ranges. Therefore we have encoded the patient risk level into the next level of risk instead of a lower level. Likewise, if the P100 latency is 130 – 140 msec then the code converter output is High risk level instead of Normal level [12].

2.2 Code Converter as a Pre Classifier

The encoding method processes the sampled output values as individual code. Since working on definite alphabets is easier than processing numbers with large decimal accuracy, we encode the outputs as a string of alphabets. The alphabetical representation of the five classifications of the outputs is shown in table III.

Table III Representation of Risk Level Classifications

Risk Level	Representation
Normal	N
Low	L
Medium	M
High	H
Very High	V

By encoding each risk level one of the five states, a string of seven characters is obtained for each of the sixteen channels of each epoch. A sample output with actual patient readings is shown in fig. 2 for eight channels over three epochs. It can be seen that the Channel 1 shows low risk levels while channel 7 shows high risk levels. Also, the risk level classification varies between adjacent epochs**.** There are sixteen different channels for input to the system at three epochs.

This gives a total of forty-eight input output pairs. Since we deal with known cases of patients, it is necessary to find the exact level of squint risk in the patient. This will also aid towards the development of automated systems that can precisely classify the risk level of the squint patient under observation. Hence an optimization is necessary. This will improve the classification of the patient and can provide the P-VEP with a clear picture [15].

The outputs from each epoch are not identical and are varying in condition such as [HHVMMMM] to [LHVHHHH] to [HHVVHHH]. In this case energy factor is predominant and this results in the high risk level for two epochs and low risk level for middle epoch. Channel five and six settles at high risk level. Due to this type of mixed state output we cannot come to proper conclusion, therefore we group four adjacent channels and optimize the risk level. The frequently repeated patterns show the average risk level of the group channels. Same individual patterns depict the constant risk level associated in a particular epoch. Whether a group of channel is at the high risk level or not is identified by the occurrences of at least one V pattern in an epoch.

Epoch 1	Epoch 2	Epoch 3
LHHLHHH	LHHLHHH	LVHHLLL
HVVHMMM	HHHHMMM	HHHMHHH
HHVMHHH	HHHHHHH	HHHHHHH
HVVHMHH	MVVMHHH	HHHHHHH
VVVHHHH	LHHHMMM	HHHMHHH
HHVMMMM	LHVHHHH	HVVHHHH
VVVHHHH	HHHHHHH	VVVHHHH
HHHHMMM	HHHHMMM	HHHMVHH

Figure. 2. Code Converters Output

The Code converter‘s classification efficiency is evaluated from the following parameters. The Performance of the Code converter is defined as follows [6],

$$PI = \frac{PC - MC - FA}{PC} \times 100 \quad (6)$$

Where PC – Perfect Classification, MC – Missed Classification, FA – False Alarm. The Performance of code converter is 40%. The perfect classification represents when the physician agrees with the epilepsy risk level. Missed classification represents a High level as Low level. False alarm represents a Low level as High level with respect to physician’s diagnosis. The sensitivity *Se* and specificity *Sp* are defined as [17],

Se= [PC/(PC+FA)]*100 ……(7)

(0.5/0.6)*100=83.33%

Sp= [PC/(PC+MC)] *100…..(8)

(0.5/0.7)*100=71.42%

Due to the low values of performance index, sensitivity and specificity it is essential to optimize the out put of the code converter. In the following section we discuss about the GA based optimization of squint risk levels.

3. Genetic Algorithm

Genetic algorithm is a population-based search method. The general scheme of a GA can be given as follows:

begin
INITIALIZE population with random candidate solutions;
EVALUATE each candidate;
repeat
SELECT parents;
RECOMBINE pairs of parents;
MUTATE the resulting children;
EVALUATE children;
SELECT individuals for the next generation

until TERMINATION-CONDITION is satisfied
end

It's clear that this scheme falls in the category of generate-and-test algorithms. The evaluation function represents a heuristic estimation of solution quality and the search process is driven by the variation and the selection operator. GA has a number of features:

- GA is population-based
- GA uses recombination to mix information of candidate solutions into a new one.
- GA is stochastic.

The most important components in a GA consist of:

- representation (definition of individuals)
- evaluation function (or fitness function)
- population
- parent selection mechanism
- variation operators (crossover and mutation)
- survivor selection mechanism (replacement)

The complex and conflicting problems that required simultaneous solutions, which in past were considered deadlocked problems, can now be obtained with GA. However, the GA is not considered a mathematically guided algorithm. The optima obtained are evolved from generation to generation without stringent mathematical formulation such as the traditional gradient–type of optimizing procedure. In fact GA is much different in that context. It is merely a stochastic, discrete event and a non linear process. The obtained optima are an end product containing the best elements of previous generations where the attributes of a stronger individual tend to be carried forward into the following generation. The rule of the game is "survival of the fittest will win" [3].

A simple genetic algorithm can be summed up in seven steps as follows [16]:

1. Start with a randomly generated population of n chromosomes
2. Calculate fitness of each chromosome
3. Select a pair of parent chromosomes from the initial population
4. With a probability *Pcross* (the 'crossover probability' of the 'crossover rate'), perform crossover to produce two offspring
5. Mutate the two offspring with a probability *Pmut* (the mutation probability)
6. Replace the offspring in the population
7. Check for termination or go to step 2

Each iteration of the above steps is called a generation. The termination condition is usually a fixed number of generations typically anywhere from 50 to 500 or more. Under certain other circumstances, a check for global minimum is done after each generation and the algorithm is terminated as and when it is reached [4].The encoded genetic algorithm is a type of genetic algorithm that works with a finite parameter space. This characteristic makes it ideal in optimizing a cost due to parameters that assume only finite number of values. In case of optimizing parameters that are continuous, quantization is applied. The chief aspect of this method is the representation of the parameter as strings of binary digits of 0 and 1. This composition allows simple crossover and mutation functions that can operate on the chromosomes.

3.1 Encoding

The five risk levels are encoded as V>H>M>L>N in binary strings of length five bits using weighted positional representation as shown in table IV. Encoding each output risk level gives us a string of seven chromosomes, the fitness of which is calculated as the sum of probabilities of the individual genes. For example, if the output of an epoch is encoded as VVHMLVV, its fitness would be 0.419352.

Table IV. Encoded Risk Levels

Risk Level	Code	Encoded String	Weight	Probability
Very High	V	10000	16/31 =0.51612	0.086021
High	H	01000	8/31=0.25806	0.043011
Medium	M	00100	4/31=0.12903	0.021505
Low	L	00010	2/31=0.06451	0.010752
Normal	N	00001	1/31=0.03225	0.005376
		11111 =31	$\sum$ =1	

3.2 Operation on Data:

Using the above representation, we have developed a genetic algorithm that optimizes the output of the code converter and gives four risk level patterns in the five categories for each patient. This is obtained by the following procedure [16]

- Open three files having 16 strings each and process stage 1
- Divide into sets of 4 strings and iterate

1) Maximum of 128 generations
2) Two strings selected randomly
3) Single point crossover after 3rd position with probability Pcross = 0.75
4) Random mutation of any position to any state in the offspring with lower fitness and probability Pmut = 0.150535 which is the probability of XXXXXXX
5) Best two strings with higher fitness get selected for next stage

- Stage 2 operates on 24 chromosomes with 8 from each epoch
- Divide into sets of 4 strings and iterate in same way as stage 1
- Output of stage 2 is 4 best strings in each epoch
- Final stage is row-wise optimization in which each row of the epochs are iterated and one best output is taken
- Last iteration involving string of each row gives the final 4 output strings

By the application of the above procedure, the 48 risk level patterns obtained by the code converter are reduced to 4 risk level patterns, which define that of the patient. This process for a single patient is shown in table V.

Table V. Optimization by Encoding GA

EPOCH 3		
HHHMHVV		
HHHMHVV		
VHHHVVH		
HHHMMVH	HHHHVVH	
HHHHHVH	HHHMHVV	
HHHMHHH	HHHVVVH	VVHVHVH
HHHHHHH	VVHLHHH	HHHVVVH
VVHVVVV	VHHVHHH	HHHVVVH
HHHHHHH	HHHVHHH	VVHHHHV
HHHMHHH	VVHVVVV	
HHHHHHH	HHHVVVH	
VHHHHHH		
HHHHHHH		
HHHHMMM		
VVHVVVV		
VVHVVVH		

Final String for all epochs

Epoch 1	Epoch 2	Epoch 3	Epoch 4
VHHVHVV	VHHVVVV	VVHVHVH	VVVHVVV
HHHVVHH	HHHVVVV	HHHVVVH	HHHHVVV
HHHMVVV	VVHMVVV	HHHVVVH	HVHHLLV
HHHHHVV	VVHHMVV	VVHHHHV	VVVHHLL

From the table V, each epoch is first reduced to 4 strings, which give the optimized risk levels of the epoch. An operation on the 12 strings in the final stage by a row-wise optimization gives the final 4 strings, representing the risk levels of the patient.

The drawback in this optimization as evident from the table V is that even though there are lower risk level states in the intermediate stage, they get omitted while proceeding to the final stage. This is because the algorithm takes only the higher fitness strings, which are the strings that represent the higher risk levels. Since we deal with only known cases of epilepsy, it can be stated that this is not a disadvantage, as those states will result in false alarms, which are defined later. It can also be inferred from the table IV that the mutation taking place in the initial stages affects the final result in only a small extent. Also, the final four strings which are obtained as the risk levels of the patient matches with the initial strings to a large extent. These advantages of the algorithm outline its use for the optimization of the risk levels of squint. The optimization of squint risk levels using ANFIS network is analyzed in the following section of the paper.

4. Adaptive Neuro Fuzzy Inference System for Risk Level Optimization

In this paper, for the classification method the ANFIS algorithm used in order to classify the trial signals into signals coming out. ANFIS's network organizes two parts like fuzzy systems. The first part is the antecedent part and the second part is the conclusion part, which are connected to each other by rules in network form. If ANFIS in network structure is shown, that is demonstrated in five layers. It can be described as a multi-layered neural network as shown in Figure (4). Where, the first layer executes a fuzzification process, the second layer executes the fuzzy AND of the antecedent part of the fuzzy rules, the third layer normalizes the membership functions (MFs), the fourth layer executes the consequent part of the fuzzy rules, and finally the last layer computes the output of fuzzy system by summing up the outputs of layer fourth. Here for ANFIS structure (fig. (4)) two inputs and two labels for each input are considered. The feed forward equations of ANFIS are as follows [27]:

$$w_i = \mu_{A_i}(x) \times \mu_{B_i}(y), \quad i = 1,2$$

$$\overline{w_i} = \frac{w_i}{w_1 + w_2}, \quad i = 1,2$$

$$f = \frac{w_1 f_1 + w_2 f_2}{w_1 + w_2} = \overline{w_1} f_1 + \overline{w_2} f_2$$

Where $f_1 = p_1 \quad f_2 = p_2$

(10).

In order to model complex nonlinear systems, the ANFIS model carries out input space partitioning that splits the input space into many local regions from which simple local models (linear functions or even adjustable coefficients) are employed. The ANFIS uses fuzzy MFs for splitting each input dimension; the input space is covered by MFs with overlapping that means several local regions can be activated simultaneously by a single input. As simple local models are adopted in ANFIS model, the ANFIS approximation ability will depend on the resolution of the input space partitioning, which is determined by the number of MFs in ANFIS and the number of layers. Usually MFs are used as bells shaped with maximum equal to 1 and minimum equal to 0 such as [27]:

$$\mu_{A_i}(x) = \frac{1}{1+\left[\left(\frac{x-c_i}{a_i}\right)^2\right]^{b_i}}$$

$$\mu_{A_i}(x) = exp\left\{-\left[\left(\frac{x-c_i}{a_i}\right)^2\right]^{b_i}\right\} \quad \ldots.(11)$$

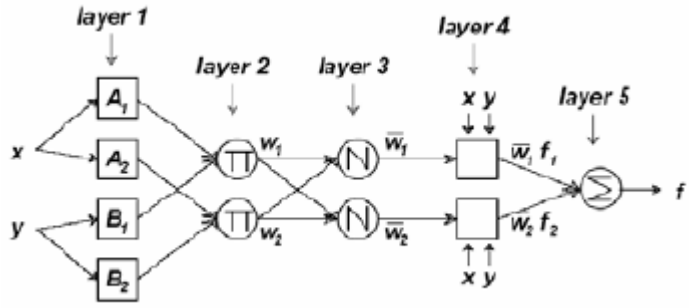

Figure (3): The equivalent ANFIS (type-3 ANFIS)

After applying the methodology and running the classification algorithm for 3 iterations, it reached the minimum RMSE value after the second epoch. The classification algorithm task is to classify and distinguish between the signals that are coming out. The primary aim of developing an ANN is to generalize the features (squint risk level) of the processed code converters outputs. We have applied different architectures of ANFIS networks for optimization. The simulations were realized by employing Neural Simulator 4.0 of Matlab v.7.0 [24]. Since our neural network model is patient specific in nature, we are applying 48 (3x16) patterns for each ANFIS model. There are ten models for ten patients. As the number of patterns in each database for training is limited, each model is trained with one set of patterns (16) for zero mean square error condition and tested with other two sets of patterns (2x16).

After network is trained using these, the classification performance of test set is recorded. The testing process is monitored by the Mean Square Error (MSE) which is defined as [19]

$$MSE = \frac{1}{N}\sum_{i=1}^{N}(O_i - T_j)^2 \quad \ldots..(12)$$

Where Oi is the observed value at time i, Tj is the target value at model j; j=1-10, and N is the total number of observations per epoch and in our case, it is 16. As the number of hidden units is gradually increased from its initial value, the minimum MSE on the testing set begins to decrease.

The optimal number of hidden units is that number for which the lowest MSE is achieved. If the number of hidden units is increased beyond this performance does not improve and soon begins to deteriorate as the complexity of the neural network model is increased beyond that which is required for the problem. Multilayer perceptrons (MLPs) are feed forward neural networks trained with the standard back propagation algorithm [20].

To reduce the training time, an advanced NN training algorithm, called Levenberg-Marquardt (LM) is used. This training algorithm is based on the Gauss-Newton method, and it reduces the training time dramatically. It provides a fast convergence, it is robust and simple to implement, and it is not necessary for the user to initialize any strange design parameters. It out performs simple gradient descent and other conjugate gradient methods in a wide variety of problems [21].

5. Results and Discussions:

The outputs are obtained for three epochs for every patient in classifying the squint risk level by the code converter, Genetic algorithm, and ANFIS approaches. To study the relative performance of these systems, we measure two parameters, the Performance Index and the Quality Value. These parameters are calculated for each set of the patient and compared.

5.1 Performance Index

The PI calculated for the classification methods are illustrated in table VII using (5)

Table VII. Performance Index

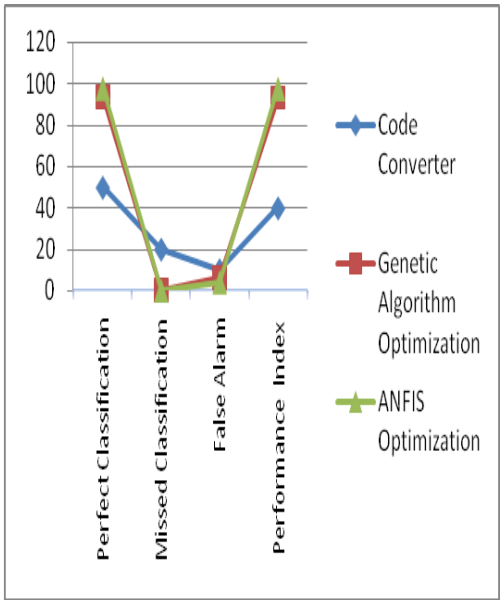

Figure 4: Performance Index

It is evident that the optimizations give a better performance than the code converter techniques due to its lower false alarms and missed classifications. For code converter classifier we have max detection of 50% with false alarm of 10% .Similarly for GA and ANFIS optimizations we obtained perfect detections of 93.75%and 97.83% with false alarms of 6.25% and 4.16%. This shows that the GA and ANFIS classifiers are performing better than the single code converter classifier.

5.2 Quality Value

The goal of this paper is to classify the squint risk level with as many perfect classifications and as few false alarms as possible. In Order to compare different classifiers we need a measure that reflects the overall quality of the classifier [15].Their quality is determined by three factors, Classification rate, Classification delay, and False Alarm rate. The quality value QV is defined as [5],

$$Q_V = \frac{C}{(R_{fa} + 0.2) * (T_{dly} * P_{dct} + 6 * P_{msd})}$$

Where, C is the scaling constant,
R_{fa} is the number of false alarm per set
T_{dly} is the average delay of the on set classification in seconds
P_{dct} is the percentage of perfect classification and
P_{msd} is the percentage of perfect risk level missed.

A constant C is empirically set to 10 because this scale is the value of QV to an easy reading range. The higher value of QV, the better the classifier among the different classifier, the classifier with the highest QV should be the best. The two different approaches give different results. Hence a comparative study is needed whereby the advantages of one over the other can be easily validated and the best method found out. A study of code converter method without and with GA optimization was performed and their results were taken as the average of all ten known patients was tabulated in table VIII.

Methods	Perfect Classification	Missed Classification	False Alarm	Performance Index
Code Converter	50	20	10	40
Genetic Algorithm Optimization	93.75	0	6.25	93.33
ANFIS Optimization	97.83	0	4.16	97.65

Table VIII. Results of Classifiers Taken As Average of All Ten Patients

Parameters	Code Converter Method	Genetic Algorithm	ANFIS
Risk level Classification rate (%)	50	92.75	97.83
Weighted delay(s)	4	0.482	0.463
False-alarm rate/set	0.4	0.0635	0.0416
Performance Index(%)	30	94.33	97.65
Quality value	5.25	19.14	24.59

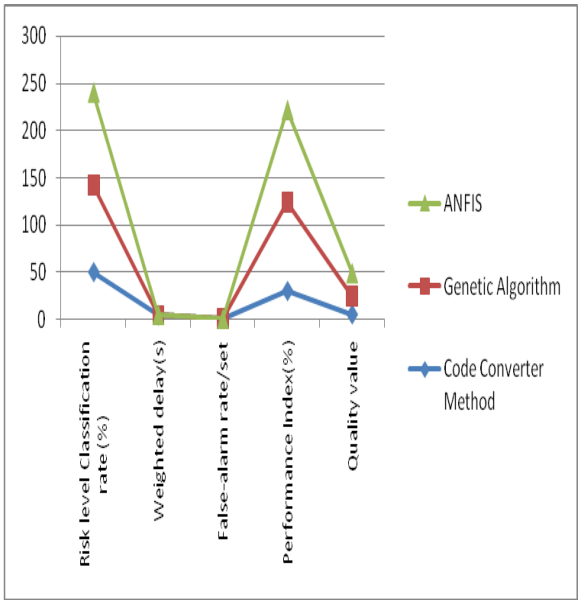

Figure 5: Classifiers Output

6. Conclusion:

This paper aims at classifying the squint risk level of squint patients from P-VEP signals. The parameters derived from the P-VEP signal are stored as data sets. Then the code converter technique is used to obtain the risk level from each epoch at every P-VEP channel. The goal was to classify perfect risk levels with high rate of classification, a short delay from onset, and a low false alarm rate. Though it is impossible to obtain a perfect performance in all these conditions, some compromises have been made. As a high false alarm rate ruins the effectiveness of the system, a low false-alarm rate is most important. Genetic algorithm and Adaptive neuro fuzzy inference system (ANFIS) optimization techniques are used to optimize the risk level by incorporating the above goals. The spatial region of normal P-VEP is easily identified in this classification method. The major limitation of GA method is that if one channel has a high-risk level, then the entire group will be maximized to that risk level. This will affect the non-squint spike region in the groups and for ANFIS its additional training cost involves in the learning procedures of the network. However, the classification rate of squint risk level of above 90% is possible in this method. The missed classification is almost 0% for a short delay of 2 seconds. From this method the inference is occurrence of High-risk level frequency and the possible medication to the patients. Also optimizing each region's data separately can solve the focal problem.

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