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Rheumatoid Arthritis (Ra) Using Hybrid Artificial Bee Colony (Hyarbc) of Fuzzy Cognitive Map (Fcm) (Hyarbc-Fcm) With Gene Datasets

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Abstract--- *Rheumatoid Arthritis (RA) is a severe autoimmune syndrome that damages both the joints and muscles of the body and can lead to disruption of joints and its function. Initial prediction of RA is very significant for avoiding the progression of the disease. Single Nucleotide Polymorphism (SNP) techniques utilize RA biomarkers to show the importance of the outputs. The major target of this study is to build prediction of Hybrid Artificial Bee Colony (HYARBC) of Fuzzy Cognitive Map (FCM) (HYARBC-FCM) technique that identifies the crucial part of RA taking the medical experts knowledge into consideration and further experience with the help of HYARBC and FCM methods to easily predict the RA for the purpose of gene profiles. This work uses the type named decision support which is built for the diagnostic process of RA with gene expression using HYARBC and the soft computational method of FCM. The FCM type is constructed by the HYARBC technique. There is a possibility of stabilizing the predetermined FCM topology and determined weights as per the stated topology. The changes carried out in the HYARBC algorithm have two significant aspects. Initially, the local search is guided efficiently by the data from the global optimal outputs and its gradient as a step by step process. The global optimal output provides maximum efficiency of ABC algorithm, by losing its diversity. Following that, with the inspiration of genetic algorithm, the resource nectar is converted into an innovative matrix with the process of selection the nectar resource is converted into an innovative adjacency matrix with 3 processes namely selection, crossover and mutation, that produces diversity of individuals and utilization of prior adjacency matrix for enhancing the broad search capability of the ABC technique. It is possible to elaborate the general correlation between the significant (concepts) that identify the system's behaviour dynamically. Meanwhile, RA issue can be avoided from passing through modern phases and the risk of building persistent and erosive arthritis for these victims would be minimized.*

Keywords--- *Mobile Computing, Pervasive Computing, Urban Development, Virtual Reality, Mobile Crowd Sourcing Technologies.*

I. INTRODUCTION

Almost one percent of entire population of the globe is affected by the defect called Rheumatoid arthritis (RA) which is an inflammatory arthritis disease [1]. It is shown by symmetric poly articular inflammation of the synovial, such that of hands, small joints, wrists and feet [2]. This symptom of inflammation leads to severe stiffness with

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pain, and can result in progressive joint damage, leads in deformities and functional loss. The related organ damage also takes the victim to severe disability. Moreover, the chronic inflammation secondary to RA can take the patient to high risk of cardiovascular attack and modifies the metabolism of the bone. Certain victims with high RA may be at greater risk for the problems like infection, problems in gastrointestinal organs, heart disease, and cancer [3]. But these problems may be co-related to other effects of the medical treatments than to the effect produced by RA.

For the past few years, the RA treatment has been reformed by modern understanding of the pathological methods and the manufacture of drugs that targets them. These innovative treatments have proved remarkable changes in the disease, with the side effects that can cause prolonged treatment and the delimits in the preoperative scenario. Initial and crucial medications of RA can result in better outputs [4]. This causes earlier prediction and the medication of RA is essential. The initial prediction of RA is a tedious job for GPs because of the symptom of wider spectrum and drastic changes in the direction of disease from time to time. This facilitates easy diagnosis and importance of RA medication. Few prediction and classification methods for RA have been improved after years [5–6] to help GPs. Also still debate continues regarding the implementation phase in the prediction process [7-8].

The RA prediction depends on the fusion of (1) The portrait of the joints that are involved, (2) The feature of joint stiffness during the early morning, (3) the factor which is positive of the rheumatoid (RF) and antibody namely citrulline, and (4) the rheumatoid module recognition and modifications in the radiography. RA has no specific treatment. Till date, the treatment of RA is (a) minimize the inflammation of the joint and its pain, (b) increase the function of the joint, and (c)avoid the destruction of the joint and its deformity. Treatment is advanced due to several factors like activities of the disease various joint types involved, physical health, age of the patient and work nature of patients. Due to the development of the disease, the disease's re-characterization in pathological and physiological terms using biomarkers is an alternate to future's medicine.

RA biomarkers utilize single nucleotide polymorphism (SNP) methods to show the importance of the outputs. SNPs are sequence type of variation in genomes. Mostly, SNPs can act as valuable genetic biomarkers; guiding biologists in the identification of genes that are correlated to general diseases [9]. In this study, the SNPs with help of biomarkers for recognizing the RA. The change in these nucleotides has greater level of frequency in affected victims when compared to normal individuals. Almost every nucleotide is fixed within genes or close to the genes. Many genes take part in the regulation of the immune system. As RA is considered as an autoimmune disease, genes are suggested as a significant group of processes involved in RA pathogenesis [10].

This work is proposed to overcome the limitations that are stated above by improving a model called DSS type [11] for initial prediction of RA utilizing Hybrid artificial Bee Colony (HYARBC) and the model of computational technique of Fuzzy Cognitive Map (FCM). It is possible to establish the casual relationships among the significant concepts that identify the dynamic characteristics of a system. Meanwhile, the RA diseases can be avoided from moving via modern phases and the complication of acquiring constant and erosive arthritis for these victims are minimized.

II. BACKGROUND

Saad et al [12] formulated an innovative genetic technique of autoimmune diseases shows a domain that

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develops with surpassing biomarker produces the outputs rapidly. The work carried on large numbers may produce remarkable outputs. Many researchers in the sector involving determination of RA biomarkers utilize Single Nucleotide Polymorphism (SNP) methods to bring the importance of their outputs. In future haplo type block techniques play significant task corresponding to that area. Shim et al [13] formulated groups of genomic density of the single-nucleotide polymorphism (SNP) which are analyzed using the application of haplo type-based techniques in the genome wide association studies (GWAS) lets. To calculate the relative potential of the two criteria to identify the associations within them uses huge sets of data from the consortium namely North American Rheumatoid Arthritis.

Singwe-Ngandeu et al [14] proposed the study on citrullinated peptides/proteins (ACPA) and to identify the sustainability of HLA-DRB1 shared epitope alleles (SE) in the patients of African country with rheumatoid arthritis (RA) so to analyse the diagnostic effectiveness of auto antibodies on. Polymerase chain reaction and hybridization with series oligonucleotide probes on micro beads arrays was carried out by Genotyping of HLA-DRB1 alleles for 51 patients with other chronic diseases and50healthy individuals were added as a control. Diogo et al [15] analysed a severe variation in coding with an average signal of relation with RA ($p < 0.05$) after fine tuning for the optimal signal of relation at the loci (penrichment = $6.4 \times 10{-}4$). The final outputs prove that variants (distributed across the allele-frequency spectrum) within the protein-coding part of a subset of biological candidate genes determined by GWASs take part on the risk factor of RA. It has also proved that huge sizes of samples are essential for the purpose of efficiently recognizing the single alleles subjecting to the leaving out RA heritability.

Dolcino et al [16] proposed a method of prediction of Psoriatic arthritis (PsA) in which the significant medical and detective biomarkers are unavailable. The major task of this work to describe certain criteria of the disease pathogenesis and also in the determination of the particular gene signatures, which is paired peripheral blood cells (PBC) and synovial biopsies of patients with PsA. As a final step, these predictions have let the determination of a probable disease biomarker, osteoactivin, easily predictable in PsA serum. Dolcino et al [17] performed the study on 6 responders and 4 non responder victims Peripheral Blood Cells (PBC) before and after the therapy. The significantly emphasised by ADA treatment and included genes involved in mitogen activated protein (MAP) kinase, wingless related integration site (Wnt), fibroblast growth factor (FGF) receptor, and Toll-like receptor (TCR) signalling determined 3 modules. Salmeron et al [18] proposed a modern tool-based decision support, and the experienced medical experts consultations with set of (i.e. orthopedic surgeons and rheumatologists) and utilizing Fuzzy Cognitive Maps (FCMs),a popular soft computing method. At last, a small-scale test has been carried out at a Shahoda hospital in Iran, for the purpose of accuracy evaluation of the formulated tool.

III. PROPOSED METHODOLOGY

To assist GPs, this work proposed a modern DSS tool focussed on FCM. As stated earlier, FCMs are constructed to be supervised learning neural systems, and capable in involving knowledge of the experts and their experience. In this work, the construction of five-step framework of methodologies is depicted in Fig. 3. The procedures are (1) choosing the genes of RA profiles, (2) formulating the FCM type, (3) learning FCM with HYARBC, (4) validating the learned FCM, and (5) examining the outputs. The steps 1, and 5 interruption of human, but steps 2–4 do not.

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Moreover, the steps 2–4 are FCM and HYARBC related one. The explanations of every step are discussed in the forthcoming sections.

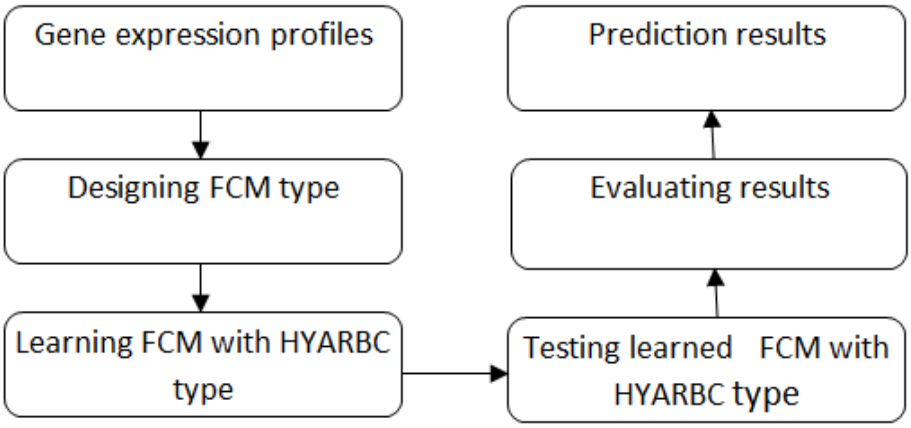

Figure 1: HYARBC-FCM Methodological Framework

FCMs have developed as a significant method to type the system which is complicated. With the of digraph a Fuzzy Cognitive Map type is designed consisting of group of composed by a group of concepts (nodes) associated by means of edges. The impact among the variables or nodes is formulated through by edges, where the edge direction depicts the direction of the impacts. The feature of an edge is its sign, that may be positive (typing a promoting effect) or negative (an inhibitory effect) [19]. A FCM designs the behaviour of a complicated system by means of concepts (nodes); every concept shows an entity, a variable, a state, or the system's features [20]. The FCM nodes (ci) would show concepts like speed, temperature, medical disease's symptoms, radiation, potential of failure, or marketing strategy, between one another. The directed edges show the relationships among the nodes. An edge joining 2 nodes designs the causal impact of the causal variable on the variable which is on the effect. (e.g. the temperature's impact failure). But the FCMs alternate these symptoms by a fuzzy value within −1 and +1, where the zero value shoes the absence of causality. Also, it has the feedback, where the effect of modification in a concept node may disturb other concept nodes. In another way an FCM is shown by a 4-tuple.

$$\boldsymbol{\Omega} = \langle \boldsymbol{N}, \boldsymbol{A}, \boldsymbol{f}(.), \boldsymbol{r} \rangle \qquad (1)$$

where N is the d of nodes $N = \{n_i\}^{i}_{m=1}$ with m the number of nodes, $A = [w_{ij}]_{m\times m}$ is the adjacency matrix showing the edges between nodes as $\{w_{ij}\}_{ij,\,=1}{}^{m}$, f (·) the activation function, and r the nodes' range. An adjacency matrix A is also considered as a square matrix showing the connectivity of the FCM nodes.

$$A = \begin{matrix} \\ c_1 \\ \vdots \\ c_m \end{matrix} \overbrace{\begin{pmatrix} w_{11} & \cdots & w_{1m} \\ \vdots & \ddots & \vdots \\ w_{m1} & \cdots & w_{mm} \end{pmatrix}}^{c_1 \quad \cdots \quad c_m} \qquad (2)$$

FCMs are automatic systems having the feedback, where the changing effects may disturb other nodes resulting in the node initiating the change. The study starts with the typeling of the initial vector state (c (0)), which shows the starting value of every variable or concept (node) [21-22]. The starting vector state c (0) with m nodes is shown as: c (0) = (c_1(0) c_2 (0) … c_m (0)), where c_1(0)is the value of the concept i = 1 at instant t = 0. The new values of the nodes

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are estimated n an iterative modification process with a function called activation, which is utilized to set monotonically the node value into a normalized range [0, 1] or [−1, +1]. The sigmoid function is maximum used [23] when the concept (node) value sets in the range [0, 1]. The vector state *c* (*t* + 1) at the beginning t+ 1 would be

$$c(t+1) = f(c(t).A) = (c_1(t+1)c_2(t+1) \dots c_m(t+1)) \qquad (3)$$

where c(t) is the state of the vector at the t instant, $c_i(t)$ is the value of the i concept at the t instant, f (.) is the sigmoid operation and A the adjacency matrix. The state modifies at every stage of process. The component i of the vector state $c_i(t + 1)$ at the instant $t + 1$ can be estimated as depicted in Eqs. (4) and (5). Eq. (4) computes $c_i(t + 1)$ just with presynaptic computation:

$$c_i(t+1) = f\left(\sum_{j=1}^{m} w_{ij}.c_j(t)\right) \qquad (4)$$

Eq. (4) estimates the presynaptic impacts and joins the state of the postsynaptic node in the earlier iteration. In that case, the node has memory of its earlier state:

$$c_i(t+1) = f\left(c_i(t) + \sum_{j=1}^{m} w_{ij}.c_j(t)\right) \qquad (5)$$

If f (·) is unipolar sigmoid and the modification is estimated as Eq. (4), then the component i of the state of vector state c(t) at a point t would be

$$c_i(t+1) = \frac{1}{1+e^{-\lambda\left(c_i(t)+\sum_{j=1}^{m} w_{ij}.c_j(t)\right)}} \qquad (6)$$

where λ is function slope constant (degree of normalization). If f (⋅) is the hyperbolic tangent function and Eq. (4) is used to update the function, then the component i of the state of the vector c(t) at the instant t would be as follows:

$$c_i(t+1) = \frac{e^{2\lambda\left(c_i(t)+\sum_{j=1}^{m} w_{ij}.c_j(t)\right)} - 1}{e^{2\lambda\left(c_i(t)+\sum_{j=1}^{m} w_{ij}.c_j(t)\right)} + 1} \qquad (7)$$

Once the inference gets over, the FCM attains either one of two states with the repeated iterations. It solves to a constant node value pattern and the so-called hidden pattern or fixed-point attractor (c (t) = c (t − 1)). In other hand, it allows cycling among many fixed states, which is called a limit cycle. With the continuous transformation function, a next possibility called as a chaotic attractor currently exists.

The swarm intelligence optimization algorithm is ABC algorithm which simulates the behaviour of the bees of collecting the honey. The bees are partitioned in ABC algorithm into 3 types depending on their partition labour division: employees, onlookers and scouters. Nectars are looked out by the employees and distribute the nectars' adjacency matrix data with onlookers in dance area, onlookers choose their own nectar oriented towards the shared adjacency matrix data and scouters, duties are utilized to randomly look for nectars. At the process of recognizing in the ABC algorithm, employees and onlookers are entirely responsible for the purpose of exploration, while scouters have commitment towards the exploitation. The method of recognizing the potential adjacency matrix search space is the process of ABC algorithm for problem solving. To make sure of the diversity in population, employees are needed to perform a local search for good nectar resources around the relevant resources in every generation depending on the given formula,

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$$\bar{x}_{ij} = x_{ij} + rand(-1,1).\left(x_{ij} - x_{kj}\right) \quad (8)$$

Where $\bar{x}_{ij}$ is the value of extracted nectar resource in j[th] dimension of adjacency matrix, x_{ij} is the value of i[th] nectar resource in j[th] dimension, x_{kj} is the value of k[th] nectar resource in j[th] adjacency matrix dimension, in which k is a probability of the number and that is below adjacency matrix quantity of population which is not equal to i. Correlating the extracted nectar resource with the actual one, the one of greater fitness value is sustained by utilizing the greedy selection strategy. The fitness value of nectar resource generally relates with the objective function value, and the estimation is as follow,

$$Fit_i = \begin{cases} \frac{1}{1+f_i} if f_i > 0 \\ 1 + |f_i| \ , if f_i \leq 0 \end{cases} \quad (9)$$

wheref_i is the fitness value of i.As per the adjacency matrix information of nectar resources transferred by employees, each onlooker will select a nectar resource based on roulette criteria. The formula for probability of being chosen is shown as follow,

$$p_i = \frac{Fit_i}{\sum_{j=1}^{n} Fit_j} \quad (10)$$

Where Fit_i is the fitness value of i[th] nectar resource and n is the number of nectar resources. The onlookers look for an innovative nectar resource as per the Eq (10) after choosing the nectar resources by the roulette strategy. At the same time, the employees modify the nectar resources by fitness value on the foundation of the greedy selection technique. If any nectar resource is not modified within a given limit of generation, the related employee gives up the nectar resource, updates the role to be a scouter and finds for a new nectar resource randomly. The scouters find for new nectar resources as per the following formula,

$$x_{id} = x_{id}^{\min} + rand(0,1).\left(x_{id}^{\max} - x_{id}^{\min}\right) \quad (11)$$

Where x_{id} is the value of ith nectar resource in d[th] dimension, $rand(0,1)$ is the random vector.$x_{id}^{\min}$and$x_{id}^{\max}$are the lower and upper bounds of i[th] nectar resource in d[th] dimension.

The stabilized ABC algorithm's nearest search is carried out by the employees and onlookers in every generation and global searching is significantly reflected in the finding process of scouters. The nearest search depends on Eq (9) in standard artificial bee colony algorithm. It will be proved by surveying the Eq (9) that the standard ABC algorithm's local search is to choose one dimension of adjacency matrix from one nectar resource as its nearest optimization variable. In Eq (12), β coefficient is entirely a random number in [±1, 1], $x_{k,j}$ is a random individual in the adjacency matrix population and the possibility of choosing a better feasible solution is almost equal to that of choosing a bad solution. To find the solution for this, the literature [24] represents GABC to formulate the global optima into the search formula of artificial bee colony algorithm for enhancing the exploitation which points to particle swarm optimization and the specific is depicted in Eq (14). The longevity of this output has been confirmed in reference [24].

$$\bar{x}_{ij} = x_{ij} + \varphi_{ij}\left(x_{ij} - x_{kj}\right) + \beta\left(x_j^{global} - x_{ij}\right) \quad (12)$$

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where φ_{ij} is the random value between zero to one, β adjustment value .The rate of convergence is minimized by fine tuning the modern steps in various situations as per the gradient direction of the G-best solution. The fine tuning is associated to the G-best solution's gradient and the distance between the feasible solution and G-best solution. Thus the formula for search can be expressed as follows,

$$x'_{ij} = x_{ij} + \varphi_{ij}(x_{ij} - x_{kj}) + \beta\left(x_j^{global} - x_{ij}\right) + (-1)^k \left|x_j^{global} - x_{ij}\right| . \left|grad_{e,j}^{global}\right| \quad (13)$$

$$k = \begin{cases} even if\, x_{ij} > \left(x_j^{global}\right) \\ odd if\, x_{ij} < \left(x_j^{global}\right) \end{cases} \quad (14)$$

Here, a normal distribution is chosen to denote the adaptive coefficients,

$$\gamma(t) = \frac{N}{\sqrt{2\pi}} e^{\left[-\frac{t^2}{2.\left(\frac{N}{4}\right)^2}\right]} \quad (15)$$

Where k is direction control parameter,$x_j^{global}$is the value of jth dimension of global optimal solution. $\gamma(t)$ is adaptive coefficients, $grad_{e,j}^{global}$is the value of jth dimension of unit gradient of global optimal solution. With the concepts of the genetic algorithm, the nectar resource that is extracted by the way of identification, crossover and mutation alternates the actual one while the employee is converted to be a scouter who looks for a new nectar resource, which will lead the scouter's global search. There is a huge possibility of crossover and a small fraction probability of the variance. The crossover function is to choose two parent chromosomes depending on the selection probability and then extract a new chromosome in coding method of real number (28-36). The search formula is formulated as follow.

$$x_{id} = \begin{cases} \lambda . x_{kd} + (1-\lambda) . x_{ld} \quad , if\ 0 \le p \le p_c \\ x_{id}^{min} + rand(0,1) . \left(x_{id}^{\max} - x_{id}^{\min}\right), if\, p_c \le p \le 1 \end{cases} \quad (16)$$

Where λ is random number and $p_c$is crossover probability. K and l are chosen based on roulette strategy viaEq (12).

IV. RESULT SUMMARY

Factors that is responsible for the development for radiographic severity of poor prediction of Rheumatoid Arthritis (RA) in African-Americans. To examine the genes whose expression in Peripheral Blood Cells (PBCs) is related with radiographic harshness of RA The gene expression signature, which looks to associate with the level of erosions at baseline and 36 months are degree of transcriptional action related with RA severity, nevertheless not significantly disease advancement.

Similarly, the related gene expression intensity with the updation of the erosion score amid baseline and three years disease period. The signal strongly apparent while checking the relationship of gene expression and erosions at baseline and 36 months, were specifically reduced while gauging the updation in erosions (37-43). The weak signal amid gene expression and disease advancement is due to the demerit of intrinsic to this unit of patients with premature RA.

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Table 1: Accuracy vs. Decision Learning Classifiers

Iteration	***Accuracy (%)***		
	FCM	***PSO–FCM***	***HYARBC-FCM***
10	85.63	87.28	89.79
20	86.21	88.79	90.85
30	86.51	89.53	91.79
40	87.41	91.201	93.25
50	88.12	92.56	94.79
60	89.41	92.89	95.62
70	90.51	93.25	95.98
80	91.15	93.52	96.14
90	91.89	93.85	96.58
100	92.63	94.24	96.79
Average (%)	**88.947**	**91.7111**	**94.158**

Table 2: MAE vs. Decision Learning Classifiers

Iteration	***MAE (%)***		
	FCM	***PSO–FCM***	***HYARBC-FCM***
10	14.37	12.72	10.21
20	13.79	11.21	9.15
30	13.49	10.47	8.21
40	12.59	8.799	6.75
50	11.88	7.44	5.21
60	10.59	7.11	4.38
70	9.49	6.75	4.02
80	8.85	6.48	3.86
90	8.11	6.15	3.42
100	7.37	5.76	3.21
Average (%)	**11.053**	**8.2889**	**5.842**

The operation of fitness is the primary operation utilized to characterize, how nearer a particle provided or adjacency matrix is in the sequence that can gain the set that targets (44-52). The reduction is done in the fitness is the Mean Absolute Error (MAE) between the original and the given output values of the tools of prediction. The MAE is estimated as follows:

$$MAE = \frac{1}{M}\left(\sum_{i=1}^{N}\sum_{j=1}^{M}|c_{ij} - \hat{c}_{ij}|\right) \qquad (17)$$

where N is nodes count, M is the profiles count, c_{ij} is the actual value for the i^{th} node of the j^{th}profile, and $\hat{c}_{ij}$is the value of prediction for the i^{th} node of the j^{th} profile. The accuracy level of the outputs of the learning type is summarized as follows,

$$\text{Accuracy= 100-MAE} \qquad (18)$$

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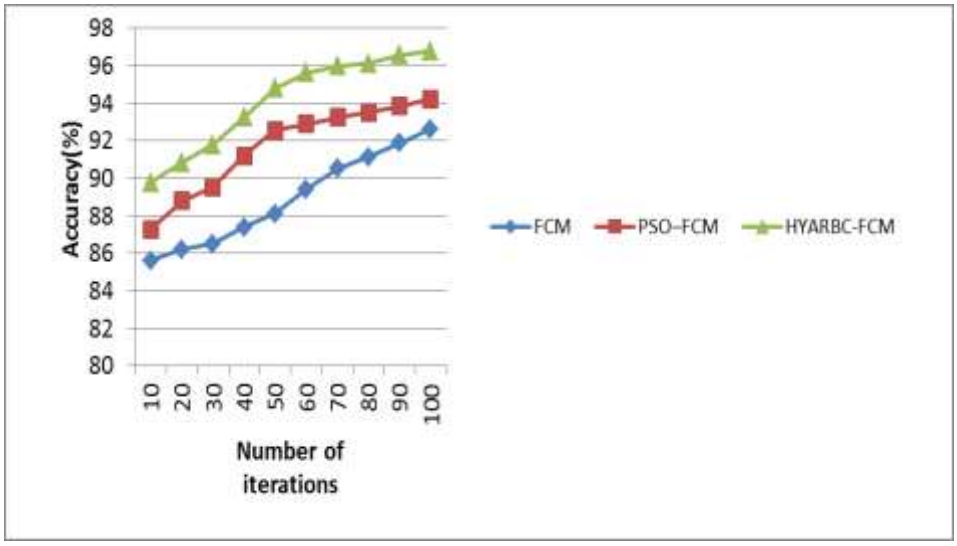

Figure 2: Accuracy vs. Decision Tree Classifier

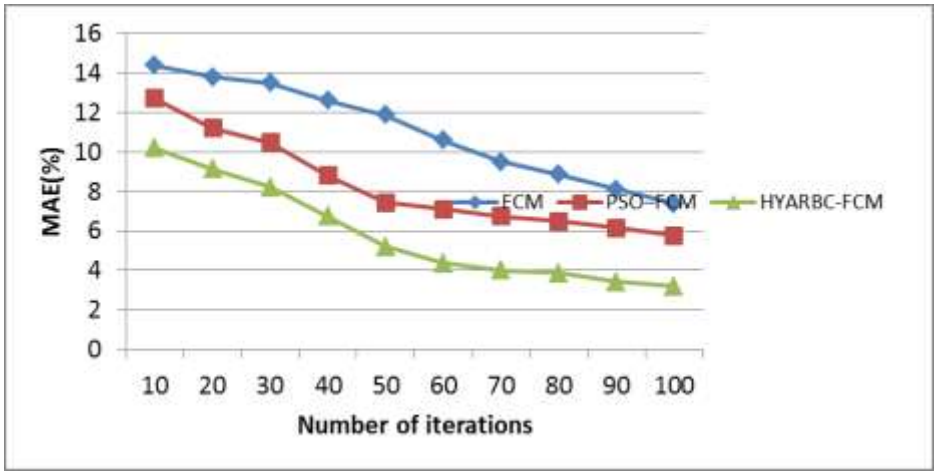

Figure 3: MAE vs. Decision Tree Classifiers

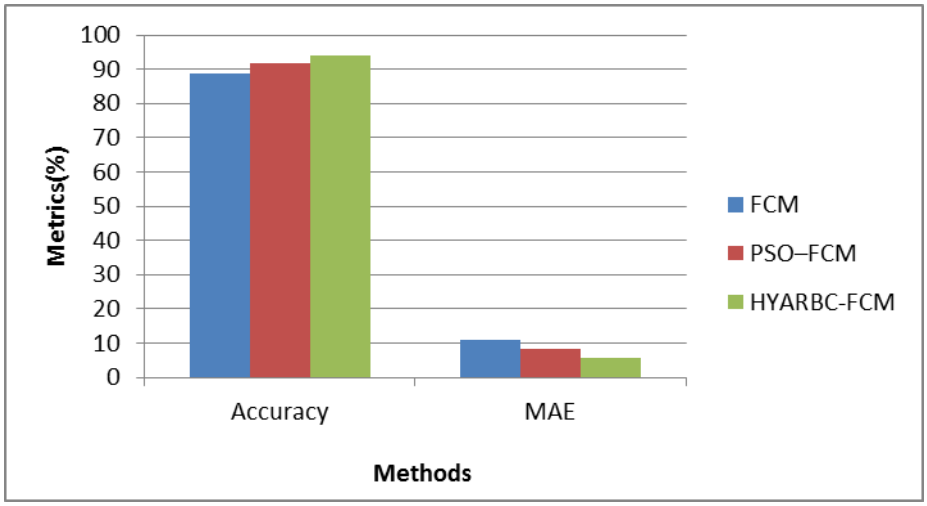

Figure 4: Classification Metrics vs. Decision Tree Classifiers

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Figure 2 depicts the efficiency comparison results of the FCM, PSO–FCM, and HYARBC-FCM in terms of the accuracy with respect to 100 numbers of iterations. Each one of the method is measured in terms of the ten different number of iteration. The iterations are varied from 10 to 100 with 10 intervals. The proposed HYARBC-FCM classifier produces higher accuracy results of 96.79%, whereas other classifiers FCM, and PSO–FCM classifier produces accuracy results of 92.63% and 94.24% methods respectively. Figure 3 shows the performance proposed HYARBC-FCM classifier produces lesser MAE results of 3.21%, whereas other classifiers FCM, and PSO–FCM classifier produces MAE results of 7.37% and 5.76% methods respectively. Figure 4 depicts the average efficiency comparison results of the FCM, PSO–FCM, and HYARBC-FCM in terms of the MAE and accuracy. The proposed HYARBC-FCM classifier produces lesser MAE results of 5.842%, whereas other classifiers FCM, and PSO–FCM classifier produces MAE results of 11.053% and 8.2889% methods respectively. The proposed HYARBC-FCM classifier produces higher accuracy results of 94.158%, whereas other classifiers FCM, and PSO–FCM classifier produces accuracy results of 88.947% and 91.7111% methods respectively.

V. Conclusion and Future Directions

Rheumatoid Arthritis is generally a health issue that shortens the life span, leading to significant disability and minimizes the life's quality. There may be broad parameters of spectrum, medical indications and outputs from the lab to study and predict RA but, prediction of the correct disease within the various patients simultaneously is certainly not an easy job for GPs. In the proposed study, the five-step methodological framework is developed. The steps are (1) choosing the genes of RA profiles, (2) formulating the FCM type, (3) studying FCM with HYARBC, (4) validating the learned FCM, and (5) examining the outputs. Then, the evaluated outputs are validated with connection with clinical experts in order to attain accuracy level and flexibility of the tool formulated. The further research process could include (i) indulging subjects (along with caregivers/families) in the various phases of study and correlating the outputs, (ii) carrying out the additional observations on different contexts to attain the efficiency of the tool is built on the decision support.

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