

A Fuzzy-Neural-Genetic Algorithm Approach for Gene Expression and Micro Array Analysis for Breast Cancer Identification

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Abstract

The machine assisted medicinal finding of intricate enclosed works, for example, Breast Cancer (BC) is measured as the most adamant hazard and the main source of death among ladies all in all. The superior part of the precedent work concerning this matter was on the study of disease transmission, learning of (BC) and routine with regards to breast self-examination (BSE), etiological variables, and rate of survival. Earlier detection of Breast Cancer saves enormous lives, crashing and burning which may provoke to other extraordinary issues expediting sudden deadly end. Its cure rate and desire depend predominantly on the early recognizable proof and finding of the contamination. A champion among the most surely understood sorts of remedial demonstrations of disregard universally is a screw up in determination. Today, there is immense use of information mining methods and process like Knowledge disclosure improvement for expectation. Critical taking in can be found from use of data mining techniques in social protection system. Untimely prediction and identification of Breast Cancer (BC) is a vital, certifiable therapeutic issue. In this paper, we suggest a genetic algorithm approach for the order of small scale cluster information utilizing quality expression to assemble a Breast Cancer (BC) analysis framework with high capacities and to predict the tumor accurately. A few investigations were directed utilizing these calculations. The accomplished forecast exhibitions are practically identical to existing systems. In any case, we discovered that proposed algorithm has a vastly improved execution than the different systems. The predictive investigation strategies of information mining assemble an information forecast display by examining the present history of

patients in order to break down what's to come information. This paper audits the consequences of different arrangement systems that have been shown in the look into articles from quite a long while and makes a correlation between the displayed yields of the before works. In addition, experimentation is additionally directed to check the realness of the best clustering algorithm as a verification of idea. We concentrate on joining fuzzy-neural thoughts and Genetic algorithms to obviously create indicative structures to help and to comprehend and assess its outcomes with high characterization execution with accuracy. Our outcomes demonstrate that the proposed fuzzy-neural genetic qualities approach produces frameworks that accomplish high grouping execution, with basic and well interpretive standards and a decent level of certainty giving best results when compared with the available genetic algorithms.

Key words

Breast cancer, Analysis troubles, Fuzzy-neural systems, Genetic algorithms, Machine assisted diagnosis.

1. Introduction

In therapeutic science, conclusion of a tumor syndrome is a convoluted issue and affirming a determination is troublesome notwithstanding for restorative specialists. This has offered ascend to automated supported symptomatic apparatuses, proposed to help the doctor in settling on essential medicinal choices. A noteworthy region for such modernized apparatuses is in the space of breast growth, to know at an opportune time if the patient undergoing diagnosis displays the side effects of a considerate, or a threatening case decides an appropriate treatment for the cancer. The programmed determination ought to achieve the most noteworthy conceivable execution, which implies they should accurately arrange cases with a decent level of certainty with efficient result sets.

Three fundamental components are turned out to be basic for the achievement of Medical Diagnosis.

1. A Fast and precise info parceling technique that endeavors to locate the delicate class limits via naturally handling a progression of agent illustrations.
2. A Verbally interpretable information portrayal outline work that permits the check and incorporation of produced rules.
3. Producing the reliable and accurate prediction of breast cancer compared to other algorithms.

New fuzzy-neural justification is found to have an assortment of uses in different fields, for example, invigorating determination. Fuzzy-neural Logic framework depends on the choices on inputs considered from the enrollment capacities which are formulae to decide the fuzzy-neural set.

Survivability of a specific malady is conceivable by separating the information from the information identified with that illness. One of these information sources is SEER [2] (Surveillance Epidemiology and End Results), which is a novel, solid and fundamental asset for researching the distinctive parts of cancer. The Soothsayer database joins tolerant level data on cancer site, tumor pathology, stage, and reason for demise [3, 4].

The attributes of a populace can be seen to build up the variables related with a particular result. Observational examinations, for example, factual learning and information mining, can build up the relationship of the factors to the result, however they don't generally set up the circumstances and end results relationship of the affiliation. Information driven factual investigate is turning into a typical supplement to numerous logical zones like drug and biotechnology. This drift is ending up increasingly noticeable as in the studies [6].

Kinds of breast cancer arranged basically malignant tumor and benign tumor. The decision of the arrangement method is particularly vital as the precision of the grouping as threatening or considerate shifts from calculation to calculation. The task includes the utilization of various order systems to arrange a specific tumor as threatening or amiable. The outcome is later thought about and the most precise of them is chosen. This will figure out which calculation is best fit for a specific arrangement of pictures.

2. Literature Survey

Ying Xie [1] proposed an improved KNN approach, which is signified as KNN++, for arranging multifarious information with heterogeneous perspectives. Any kind of view can be used while applying the KNN++ strategy, the length of a separation capacity can be characterized on that view. The KNN++ incorporates a basic learning part that takes in the heaviness of each view. Moreover, the KNN++ strategy considers the preparation information, as well as the obscure case itself while evaluating the significance of various perspectives in arranging the obscure case.

Given an obscure occasion, the KNN++ technique figures out how to weight each view by analyzing its K closest neighbors found by the separation work characterized on that view. Each case of the K closest neighbors of the obscure occasion by that separation capacity will seek its own K closest neighbors by utilizing a similar separation work, so as to check what number of its

K closest neighbors really has a similar class mark as this occurrence. The last weight of the separation work is the total of such numbers over all K closest neighbors of the obscure example by that separation work. The last K closest neighbors of the obscure occasion will be chosen from all unique K closest neighbors of the obscure occurrence found by various separation capacities with considering in the weights that are found out for those separation capacities.

However, they neglected to enhance the stock expectation execution by consolidating diverse sorts of stock data, for example, the conclusion data acquired from stock-situated informal communities, for example, stocktwits.com. The proposed method is not reasonable for different applications with complex information, for example, Alzheimer's initial location.

Be that as it may, both calculations experience the ill effects of a few insufficiencies exhibited in picking the estimation of count of Genes which are selected (K) and the suitable piece of work. To beat these disadvantages, the requirement for new strategy that naturally picks the restrictions of the capacity and it likewise has a suitable calculational intricacy is basic. They additionally neglected to build up a strategy that naturally picks the parameters of the capacity and it likewise has a fitting computational intricacy is basic.

BadrulSarwaret.al [3] proposed a Singular Value Decomposition(SVD)- based suggestion calculations which can rapidly deliver brilliant proposals, yet needs to experience exceptionally costly network factorization steps. They tentatively approve a method that can possibly incrementally construct SVD-based models and guarantees to make the recommender frameworks exceedingly versatile. They had done analysis with an incremental model-building system for creating SVD-based proposals that has the guarantee of being profoundly versatile while delivering great prescient exactness.

They neglected to see precisely why SVD functions admirably for some recommender applications, and less well for others. Additionally, there are numerous different routes in which SVD could be connected to recommender frameworks issues, including utilizing SVD to make lowdimensional perceptions of the evaluations space or utilizing SVD to recognize noteworthy items that would help bootstrapping the recommender frameworks.

Huihui Li et al. [4] proposed a novel mixture attribution technique, called Recursive Mutual Imputation (RMI). In particular, RMI misuses worldwide connection data and nearby organization in the information, caught by two famous techniques, Bayesian Principal Component Analysis (BPCA) and Local Least Squares (LLS), separately. Common methodology is executed by allocating the assessed information groupings at each iterative procedure. In the interim, we consider the ascription grouping in view of the quantity of missing sections in the

objective quality. Besides, a weight based incorporated strategy is used in the last collecting venture.

They obviously showed that RMI altogether beats similar strategies as far as Normalized Root Mean Square Error (NRMSE), particularly for data clusters with huge misplaced rates and low entire qualities. The proposed technique can't plainly show how RMI fundamentally outflanks similar strategies as far as Normalized Root Mean Square Error (NRMSE), particularly for datasets with vast missing rates and less total genes. They had not focused on applying more refined ascription strategies in the iterative common procedure and to enhance our current itearative shared attribution structure.

Gilles Meyer et.al [5] proposed a settled rank estimation strategy and given an answer for taking in a straight relapse show whose parameter is a settled rank network. The Riemannian complex geometry of the arrangement of settled rank lattices and create productive line-look calculations. The proposed calculations have numerous applications, scale to high dimensional issues, appreciate nearby merging properties and present a geometric premise to late commitments on learning fixedrank networks. Numerical trials on benchmarks recommend that the proposed calculations rival the cutting edge, and that complex streamlining offers a flexible structure for the plan of rank-obliged machine learning calculations.

Nonetheless they bombed in creating a straight regression for the informational collections with irregular prority where the informational indexes are looked over an extensive information group. The proposed calculation does not deal with the informational indexes with gigantic information substances.

Aristidis Likaset.al [6] recommended an incremental technique for display determination and learning of Gaussian blends in view of the as of late proposed variational Bayes approach. The technique adds parts to the blend utilizing a Bayesian part test method: a segment is part into two segments and after that variational refresh conditions are connected just to the parameters of the two segments. Therefore, either both parts are held in the model or one of them is observed to be excess and is wiped out from the model. In this approach, the model choice issue is dealt with locally, in an area of the information space, so we can set more enlightening priors in view of the nearby information appropriation. A changed Bayesian blend show is exhibited to execute this approach, alongside a learning calculation that iteratively applies a part test on every blend segment.

They had not focused on refining the strategy by expounding on and testing two issues. The first is to investigate elective approaches to indicate the neighborhood accuracy earlier. Aside from this, it is conceivable to play out different part tests for a similar segment, with the scale

network slowly expanding keeping in mind the end goal to acquire a measure of power for the part test. The second issue is to consider elective approaches to introduce the methods for the two subcomponents amid split (e.g., in [13] split bearing is chosen haphazardly). Additionally, it is conceivable to play out various part tests for a particular segment with various subcomponent instatements each time. At long last, different issues to be considered are the versatility of the technique, the likelihood to simultaneously perform part tests for some segments, and its utilization in a few application areas (e.g., picture division).

3. Fuzzy-Neural Systems Mechanisms

Fuzzy-neural justification is a computational technique controlling data in a way that takes after human consistent thinking forms [23][24]. A fuzzy-neural identifier is portrayed by its fuzzy-neural variable A_n and the participation elements of these factors; with an enrollment esteem $(, to a given genuine esteem $u(R)$. A fuzzy-neural induction framework is a decision related framework that utilizations fuzzy-neural justification, instead of Boolean justification [26][27].$

The structure incorporates four primary parts: a fuzzifier, which deciphers fresh (genuine esteemed) contributions to fuzzy-neural esteems, a deduction motor that applies a fuzzy-neural thinking instrument to acquire a fuzzy-neural yield, a prediction of tumor, that makes an interpretation of the yield over into a fresh esteem, and an information base, having both an outfit of fuzzy-neural guidelines (the lead base), and a gathering of association enrollment works (the database); see Figure 1. which describes the organization of proposed Genetic algorithm.

Utilizing the undeviating fuzzy-neural method with learning with help of a human master, the fuzzy-neural reenactment distinguishes the restrictions of a fuzzy-neural surmising framework, with which coveted choice is made of. This errand is troublesome where the issue break is unpredictable and extensive; in this manner, persuading us to utilize Genetic algorithms to deliver fuzzy-neural methods. In the writing, there are a few ways to deal with fuzzy-neural displaying in light of neural systems [10][12], Genetic algorithms [1][6][8], and other half breed strategies [25]. Determination of important factors and sufficient tenets is basic for acquiring a decent precise characterization framework. The most significant issues in fuzzy-neural reproduction is the measure of calculation develops accordingly with the quantity of factors.

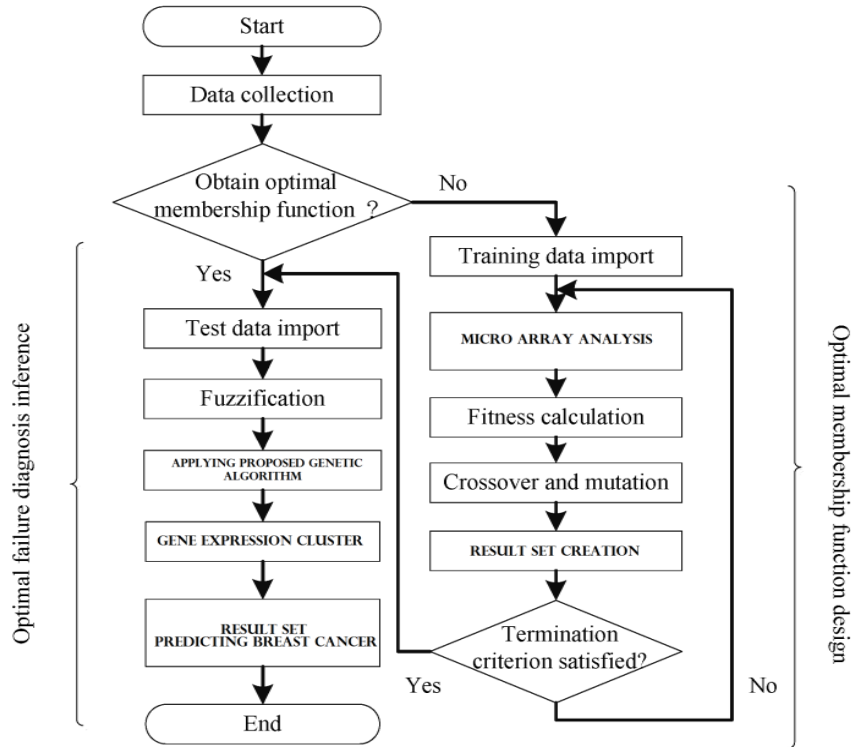


Fig.1. Organization of Proposed Genetic algorithm

4. Proposed Genetic Algorithm

A Genetic Algorithm (GA) is a hunt heuristic which impersonates the procedure of characteristic choice. Genetic algorithms are utilized to produce answers for streamlining and inquiry issues. The genetic calculation technique is a repeated system that includes a populace speaking to the look for answers for the issue, as people, every one spoken to by a limited series of images, called genome. The fundamental strategy continues as takes after: an underlying populace of people is created indiscriminately or heuristically. In each developmental stride (era), the people in the momentum populace are decoded and assessed by a wellness work that portrays the streamlining issue in the pursuit space.

Various decision philosophies are open, in that minimum complex being health balanced assurance, where individuals are picked with a probability comparing to their comparative wellbeing. Along these lines, high-health individuals stand a better open door than mimic and pass on new individuals to the masses, while low-wellbeing won't. Genetic algorithms are stochastic repetitive methods, and are not by any means guaranteed to center, and the stopping condition may be resolved with high number of periods or a picked level of the health.

A new Genetic Algorithm illustrated in Fig-2 which is developed by combining the features of fuzzy-neural logic and neural networks is designed which is applicable on data sets of Gene Expressions and predicting tumor accurately.

4.1 Proposed Genetic Algorithm

```

Proposed Genetic Algorithm
{
    Randomly create a class label and initialize it
    Consider a dataset with numerous records of patients
    Assign a count value to every record
    Calculate Microarray result of dataset
    Form group of best result and calculate Gene Expressions of data sets
    WHILE NOT termination condition DO
    {
        Assign a priority value of the predicted record
        Apply the Gene Expressions set on the predicted result set
        Crossover predicted results sets
        Handle misplaced and lost data sets
        Apply the Gene Expressions set again on the result set
        Record the predicted data set
        Eliminate the worst records from the cluster
    }
    WHILE NOT termination condition DO
    {
        Compare the recorded set with available Genetic Algorithms
        Record the Compared result sets
        Display the Result sets
    }
    Display the best Result set
}

```

Fig.2. Proposed Genetic Algorithm

4.2 Proposed Algorithm Implementation

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STEP 1. for class label  $h_i \in H$ 
STEP 2. Initialize count  $h_{i,u}$  to be 0;
STEP 3. for all  $s_j \in S$ 
STEP 4. consider the weight of  $s_j$  as  $Qs_j$  and initialize to 0;
STEP 5. calculate the nearest neighbour cluster using  $d_i$  and them store in a set  $Ns_i(u)$ ;
STEP 6. for all  $u_i \in Ns_i(u)$ 
    calculate the nearest neighbor of  $u$  in the set of  $(u-r_{eM+1})$  by using  $d_i$  and store
    them in a new set  $Ns_i(u_i)$ ;
STEP 7. for each  $u_i \in Ns_i(u_i)$ 
    if  $u_i$  and  $u_i$  are having equal class label
         $Qs_j++$ ;
STEP 8. Initialize fl to be unknown;
STEP 9. Initialize flc to be 0;
STEP 10. for each class lable  $h_i \in H$ 
    if(count( $h_i, u$ ) > flc)
        flc=count( $h_i, u$ );
        fl= $h_i$ ;
    Output fl;

```

Fig.3. Implementation of Genetic algorithm

The proposed algorithm can be applied on a dataset of numerous patients for the prediction of breast cancer so that the diagnosis process will be much easier in early stages.

5. Results

Minimization investigates the test set, portrayed in Subsection 6.1, have been done keeping in mind the end goal to think about the conduct of the proposed ANIFSGA in the past area, the

calculations worked with a specific end goal to do this are depicted, lastly. Test Set For the analyses, we have considered three much of the time utilized test elements of Benchmark issues: Sphere display (f_{Sph}) ([7]):

$$f_{Sph}(x) = \sum_{i=1}^n x_i^2, \text{ and } -5.12 \leq x_i \leq 5.12.$$

A data cluster of numerous patients are considered and various parameters are considered which are shown in Table-1 which are strongly used for identification of breast cancer based on the gene expressions calculated from micro array data. The results are generated by applying the newly proposed Genetic algorithm to the data sets of patients and accurate results are generated.

Attribute	Values
Multiple family members who have had breast, ovarian and/ or prostate cancer	Yes = 2 No = 1
Menstrual cycles starts before 12	Yes = 2 No = 1
Birth control pills	Yes = 2 No = 1
Gone through menopause	Yes before 55 = 3 Yes after 55 = 2 No = 2
Gone through menopause	Yes = 2 No = 1
Breast diseases	Yes = 3 No = 1
breast feed	Yes = 1 No = 2
Undergone estrogen and prostogen hormone therapy	Yes = 3 No = 1

Table 1. General attributes for predicting tumor

The Process of calculating micro array data from the dataset represented in Table-3 and calculation of gene expressions where statistics of the prediction are shown in Table-2.

Table 2. Statistics of the tumor

	Yes	No
Menopause	45.5%	54.5%
1 st degree relative with breast cancer	17.6%	82.4%
Family member with other cancer	4.5%	95.5%
Breast trauma	4.0%	96.0%

Table 3. Samples of data sets

Observed	Predicted			Percentage Correct
	Negative	Uncertain	Positive	
Negative	0	13	0	0.0%
Uncertain	0	31	1	96.7%
Positive	0	1	0	0.0%
Overall Percentage	0%	97.8%	2.2%	67.4%

The wellness of the ideal is $f_{\text{Ros}}(x^*) = 0$. This test work is persistent, entirely raised, and unimodal. Summed up Rosenbrock's capacity (f_{Ros}) ([7]):

$$f_{\text{Ros}}(x) = \sum_{i=1}^{n-1} [100(x_{i+1} - x_i^2)^2 + (x_i - 1)^2] \quad \text{and} \quad -5.12 \leq x_i \leq 5.12$$

The wellness of the ideal is $f_{\text{Ros}}(x^*) = 0$. f_{Ros} is a consistent and unimodal capacity, with the ideal situated in a precarious allegorical valley with a level base. This element will presumably cause moderate advance in numerous calculations since they should persistently alter their hunt course to achieve the ideal. Summed up Rastling's capacity (f_{Ras}) ([4]):

$$f_{\text{Ras}}(x) = 10n + \sum_{i=1}^n (x_i^2 - 10 \cos(2\pi x_i)) \quad \text{and} \quad -5.$$

This capacity is a versatile, nonstop, distinguishable, and multimodal, which is created from by f_{SPH} adjusting it with $k \cdot \cos(wx_i)$.

5.1 Algorithm Comparisons

We contrast proposed genetic algorithm and a few strategies in different GA's that Herrera et al. utilized as a part of [9]. They had been viewed as a generational GA display that connected a basic hybrid administrator and a transformation timepiece administrator and determination likelihood count took after direct positioning (MIN = 0.5). The testing calculation was the stochastic widespread examining, and elitist methodology was considered. Additionally, the general characteristics of the fuzzy-neural justification control that they had been considered was the accompanying: the base administrator was utilized for conjunction of provisions in the IF part of a govern, the base administrator was utilized to flame each administer and the focal point of

gravity weighted by coordinating system as the defuzzification administrator was considered. Table 2 demonstrates these calculations.

The newly proposed algorithm is applied on the calculated Gene Expressions for identification of breast cancer and the same results are applied with the available genetic algorithms and the comparison table is shown in Table-4 which illustrates the accuracy rate of the algorithms. The proposed Genetic algorithm gives the highest accuracy rate on results set.

Table 4. comparison of accuracy rate of different algorithms on data sets

Algorithms	Features
GA1	$p_m = 0.001$ and $p_c = 0.6$ fixed during the run.
GA2	$p_m = 0.005$ and $p_c = 0.6$ fixed during the run.
GA3	$p_m = 0.01$ and $p_c = 0.6$ fixed during the run.
GA-RAN	$p_m \in [0.001, 0.01]$ for each generation. $p_c = 0.6$.
GA-DET	Deterministic Control of the Mut. Prob. $p_c = 0.6$.
GA-AIL	Adaptive Control at Individual-level of the Mut. Prob $p_c = 0.6$.
GA-SELF	Self-Adaptive Control of the Mut. Prob ($\delta = 0.001$) $p_c = 0.6$.
GA-FLC	Adaptive Control of the Mut. Prob. by FLC (G = 50) $p_c = 0.6$.
PROPOSED GA	$p_m \in [0.001, 0.2]$ for each generation and $p_c = 0.8$

Table 5. Result analysis of multiple genetic algorithms

Algorithm	f_{Sph}	f_{Ros}	f_{Ras}
GA1	2.4e -10	1.1e -01	5.9e +00
GA2	7.7e -08	8.5e -03	5.1e -05
GA3	8.0e -06	1.2e -05	6.0e -02
GA-RAN	2.2e -07	6.9e -04	8.4e -05
GA-DET	2.8e -10	5.6e -05	3.3e -02
GA-AIL	2.4e -10	4.3e -02	1.2e +00
GA-SELF	2.4e -10	4.5e -02	1.7e +00
GA-FLC	2.4e -10	6.4e -04	6.1e -08
PROPOSED GA	2.4e -10	1.3e -07	9.5e -09

With respect to the GA forms that we looked at in Table 5, we can state that: For the simple test function, f_{Sph} aftereffect of recently proposed system is the best consequence of different techniques.

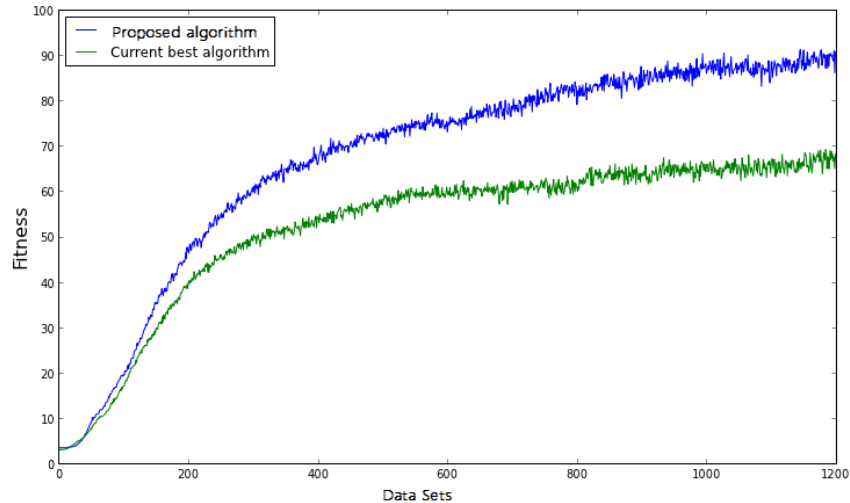


Fig.4. Comparison of proposed and existing genetic algorithms

For the capacity with many-sided quality, f_{Ras} and for the most complex capacity, f_{Ros} outcome of recently proposed genetic calculation framework is better of different techniques. Fig-4 shows the graph in which proposed a genetic algorithm has the highest accuracy rate. At that point recently proposed GA system, has the strongest practices, since for each capacity, it returns comes about that are fundamentally the same as the ones of the best GAs with middle of the road unpredictability, or superior to anything all them comes about for the capacity with moderate many-sided quality and for the most complex capacity.

6. Conclusion

In this article distinctive misplaced esteems ascription calculations are clarified. Distinctive metric procedures were utilized to quantify the execution of the calculations. Every calculation was tried under various informational indexes. In any case, to approve the execution of every calculation, more tests should have been directed. Besides, to make certain that the calculations are solid, similar informational collections ought to be utilized to run the tests. At long last, from the writing displayed, we presume that the results generated based on newly proposed genetic algorithm are accurate than LLS and SVR calculations. SVR can be considered as a supplement calculation for LLS particularly when connected to loud information. Be that as it may, both calculations experience the ill effects of a few lacks. LLS has the issue of allotting the parameter esteem K . Choosing distinctive K -values brings about various exhibitions which thus influences the last metric assessment for this calculation. Picking the ideal K -esteem ought to be completed each time the calculation is utilized. SVR, then again, has two hindrances, to begin with, the picking of the proper part capacity and secondly, its calculational intricacy. In future, the proposed work can be extended to beat these disadvantages, we require another technique that

consequently picks the parameters of the capacity and it likewise has a suitable computational unpredictability is basic.

With the developing examination of DNA microarray, which produces a substantial number of microarray expression information. Misplaced esteems, as a vital issue, affected the examination advance on this region. Various successful distinct strategies are proposed to gauge the misplaced esteems. In any case, they just use the worldwide data or neighborhood structure in the information lattice, which can't completely utilize the watched data. In this examination, enlivened from community preparing technique, by proposed genetic algorithm. To our best information, this work is the principal endeavor to concentrate on utilizing a recursive common methodology to gauge missing esteems and micro array data sets analysis using new genetic approach. Here, we consider the ascription arrangement in light of the quantity of missing passages in the objective quality.

Some further research bearings are worth for us to make a more profound examination. It incorporates applying more refined ascription strategies in the recursive shared procedure and to enhance our current recursive common attribution system. Another fascinating issue is the manner by which to pick the correct single techniques in RMI. In the meantime, the half breed technique is effortlessly stretched out to build up a various cross breed form by utilizing more than two single strategies, which is a particular suggestion undertaking.

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