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# Diagnosis Of Ovarian Cancer Using Artificial Neural Network

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***Abstract* - Ovarian cancer arises from the ovary indicates growth of cancer. More than 91%) ovarian cancers are known as "epithelial" which start from the surface epithelium, the thin tissue forming the outer layer of a body's surface and lining the alimentary canal and other hollow structures of the ovary. The intention of this study is to observe the performance of the ANN algorithm over Genetic Algorithm on the diagnosis of ovarian cancer using proven ovarian dataset fig 2. Ovarian cancer [2] accounts for the most caused cancer diagnoses among women. We propose a comparison between Genetic Algorithm and ANN[1] for preoperative guess of enmity in ovarian tumors. Most of the present methods do not meet the requirements which deal with the drawbacks like accuracy and noise. Gene ranking methods like T-Score, ANOVA, went for wrong prediction the rank when large database is applied. The typical ANN is proposed to form part of a trustworthy tool to distinguish between kind and unkind ovarian tambours. This may help doctors to fix on the applicable treatment for the patients.**

***Keywords*--- Gene Ranking, Trustworthy tool, ovarian tambours**

## I .INTRODUCTION

The diagnosis of complex genetic diseases like cancer has conventionally been done based on the non-molecular characteristics like kind of tumor tissue, pathological characteristics and clinical phase. Cancer precedents to almost 27% of all mortalities, making it the leading cause of death in America and also around the world. Timely and exact detection of cancer is life-threatening to the comfort of patients. Examinations of gene expression data precedents to cancer recognition and categorization, which will make ease appropriate treatment selection and drug development.

A major application of microarrays has been to the study of cancer. Recognition of the signals that are symptoms for the disease phenotype and its progression requires the use of hardy techniques.Cancer can be identified through the analysis of genetic data. The human genome contains almost 10 million single nucleotide polymorphisms which will be in charge for the difference that lies between human beings. The microarray technology is used to achieve gene expression levels and SNPs of an individual. In this paper two methods are used namely Artificial Neural Network and Genetic algorithm and use techniques such as dimensionality reduction to improve the accuracy rate of the classifier .A genetic algorithm is a search experiment that reduces the process of natural selection. This experiment is regularly used to provide useful solutions to enhance and search issues. Genetic algorithms [4] are appropriate to the huge class of evolutionary algorithms, which obtain solutions to enhancement problems using techniques that attract by natural progress, like heritage, alteration, collection, and boundary. Artificial neural networks are extensively used with appliances in science and technology An Artificial neural networks is a mathematical illustration of the human neural design, representing its "learning" and "generalization" capability. For this cause, Artificial neural networks have its place in the area of artificial intelligence. Artificial neural networks are extensively applied in research for the reason that they can model highly non-direct systems in which the relationship among the variables is undetermined or very complex.

## II. RELATED WORK

There are different techniques proposed by different authors for the prediction of cancer regions. Every technique has its own advantages and disadvantages. Some of the existing techniques are presented in this section.

Rui *et al.*, [12] proposed a multiclass cancer classification using semisupervised ellipsoid ARTMAP and particle swarm optimization with gene expression data [11]. It is critical for cancer prediction and treatment to perfectly categorize the site Of origin of a cancer. With huge progress of DNA microarray Techniques, creating gene expression profiles [8] for various cancer kinds has previously turn out to be a capable way for cancer classification [10]. In addition to research on binary classification like normal versus tumor samples that focuses on various issues from a mixture of disciplines, the discrimination of multiple tumor kinds is also essential. In the meantime, the choosing of genes that are appropriate to definite cancer kinds not only enhances the performance of the classifiers, but also offers molecular insights for treatment. Here, the author utilizes the semisupervised ellipsoid ARTMAP (ssEAM) for multiclass cancer discrimination and particle swarm optimization for informative gene selection. SsEAM is a neural network technique [14] embedded in adaptive resonance theory and applicable for classification purpose.

## III. BACKGROUND STUDY

Classification of cancer by gene expression data is known to hold the keys for indicating the basic troubles relevant to cancer analysis and drug identification. The latest advent of DNA microarray method has made simultaneous care over of thousands of gene expressions probable. With the lavishness of gene expression data researchers have started to discover the chances of cancer recognition using gene expression data. Recently, many methods have been proposed with promising results.

In order to achieve in-depth knowledge into the cancer classification problem, it is must to have a close observance which look at the problem the proposed method and the relevant problem all together. In this paper present a widespread indication of numerous proposed cancer classification methods and estimate them based on their calculated time, recognition accuracy and ability to reveal biologically useful gene information.

Accuracy is the major factor in cancer classification, where it alone only the objective that wants to achieve. Biological significance is another issue, since any biological information obtained during the process can support in further gene function exploration and other research studies. Some useful information can be gained from the classification process is the purpose of the genes that work as a group in resolving the cancerous tissues or cells or the genes that are under-expressed or over-expressed in certain tissues or cells. Dealing with a huge amount of unrelated attributes is a challenging factor. Though unrelated attributes are exists in almost all kind of data sets, researchers have with earlier dealings, but the ratio of unrelated attributes to the related attributes is not as bulk as that in the gene expression data.

## IV. METHODOLOGY

In the medical research, Cancer research is one of the foremost research areas. Exact predictions of various tumor types has great value in granting better treatment and reduce harmfulness on the patients. In earlier days, cancer identification has always been morphological and clinical based. These typical cancer classification methods are boomed to have several demerits in their diagnostic capability. The cancer training gene data set is divided into several subsets with almost 1000 genes in each subset as shown in Fig.1. The division of the data sets can be taken place unintentionally.

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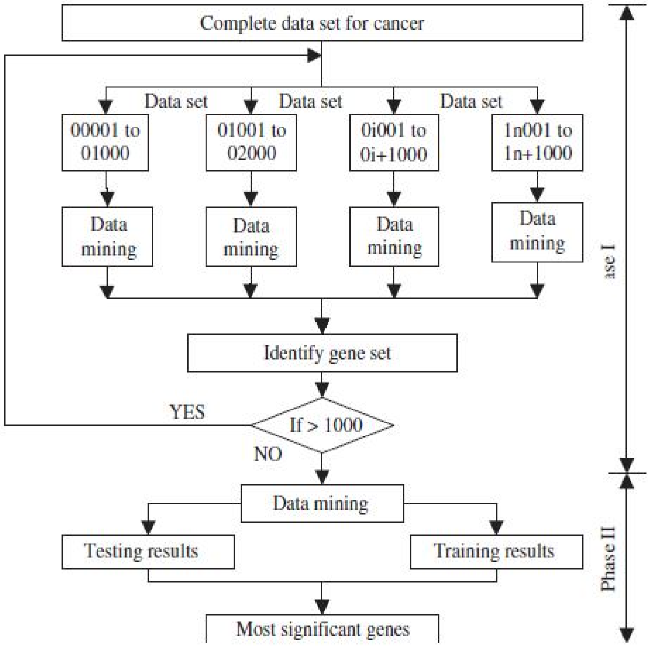
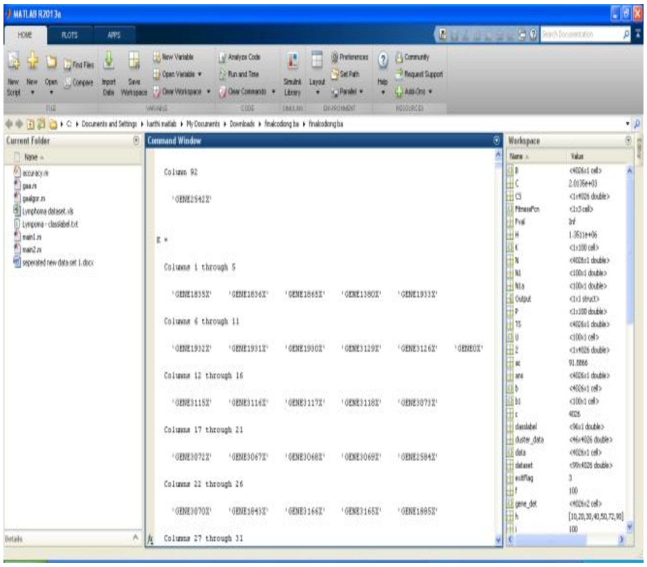


Fig 1.Integrated gene-search algorithm

### A. Ovarian cancer

Ovarian cancer is a cancerous growth rise from the ovary where the indications are often very faint at initial stage on and may have bloating, pelvic pain, difficulty eating and frequent urination, and other disease. More than 90% of ovarian cancers are categorized as "epithelial" and are supposed to arise from the base (epithelium) of the ovary. In some case, suggests that the fallopian tube might be the cause for ovarian cancers. Meanwhile, the ovaries and tubes are tightly connected to each other; it is assumed that these fallopian cancer cells can simulate ovarian cancer. The Genetic algorithm was autonomously implied to the data set to extent the involvement of each individual gene. When the number of expressive genes was more than 1000, the Genetic algorithm was applied one more time for experiment, which reduces the number of significant genes by **85.12%.**



```
Column 92

  'GENE2542X'


x =

  Columns 1 through 5

  'GENE1835X'    'GENE1836X'    'GENE1865X'    'GENE1380X'    'GENE1933X'

  Columns 6 through 11

  'GENE1932X'    'GENE1931X'    'GENE1930X'    'GENE3129X'    'GENE3126X'    'GENE0X'

  Columns 12 through 16

  'GENE3115X'    'GENE3116X'    'GENE3117X'    'GENE3118X'    'GENE3073X'

  Columns 17 through 21

  'GENE3072X'    'GENE3067X'    'GENE3068X'    'GENE3069X'    'GENE2584X'

  Columns 22 through 26

  'GENE3070X'    'GENE1843X'    'GENE3166X'    'GENE3165X'    'GENE1885X'

  Columns 27 through 31
```

Fig 2. Dataset

### B. Artificial Neural Network

Neural network is the proposed algorithm, in which there will neural network for each stage. The code takes the preferred picture and implements it through the neural networks one by one, each time outcomes in a score. For each network we can review the most important methods. Artificial Neural Networks represent a powerful method to support clinical researchers to perform diagnosis and other enforcements. Here, Artificial Neural Networks have many advantages which are listed below

- The capability of processing huge amount of data
- Minimized possibility of un-related information
- Consumption of analysis time

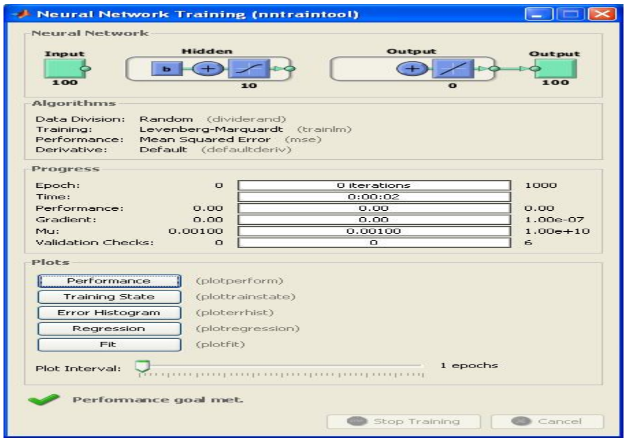
Artificial Neural Networks have confirmed suitable for adequate analysisof various diseases, addition to that, their use makes the analysis more trustworthy and therefore increases patient satisfaction. In despite their spread over application in modern analysis, they must be considered only as a device to make ease the final decision of a clinician, who responsible for essential evaluation of the Artificial Neural Network results as shown in Fig 3. Methods of summarizing and detailed information and intelligent data are continuously improving and can provide greatly to successful, complete and swift medical analysis

*c. Training and Testing stages*: The method and its parameters below are used to experimented our neural network: **net = train (net, inputs, targets);** The function parameters are:

1. **net:** the neural network which created previously.

2.**Inputs:** inputs of the created neural network as defined before.

3. **Targets:** stated target the neural network.



Algorithms

Data Division: Random (dividerand)
Training: Levenberg-Marquardt (trainlm)
Performance: Mean Squared Error (mse)
Derivative: Default (defaultderiv)

Progress

| | | | |
|---|---|---|---|
| Epoch: | 0 | 0 iterations | 1000 |
| Time: | | 0:00:02 | |
| Performance: | 0.00 | 0.00 | 0.00 |
| Gradient: | 0.00 | 0.00 | 1.00e-07 |
| Mu: | 0.00100 | 0.00100 | 1.00e+10 |
| Validation Checks: | 0 | 0 | 6 |

(plotperform)
(plottrainstate)
(ploterrhist)
(plotregression)
(plotfit)

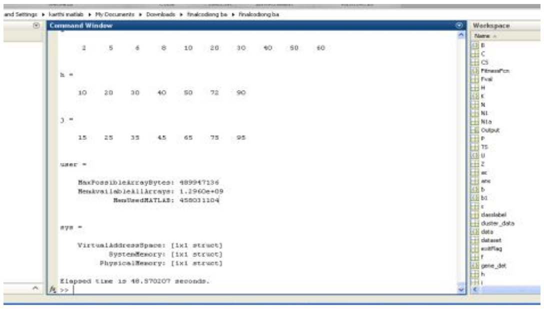
Plot Interval: 1 epochs

Performance goal met.

Fig 3.Neural network model using Training Tool

## V. EXPERIMENTAL RESULTS

The Ovarian data sets were used in this research to identify affected that to differentiate the kind and malicious of ovarian cancer cases. The data sets consisted of 100 samples, 100 normal tissues samples, and 14 kind samples. Only the cancerous and noncancerous samples are included in this paper. Each sample consisted of 14.094 intensities with intensities of features. The proposed system results that Genetic algorithm and Neural Networks will be useful tool to distinguish affected or unkind, kind and normal cells. Furthermore, the Artificial Neural Network obtained the best performance, classifying those tissues, with a good success rate, accuracy and compassion. It may minimize the number of unwanted tissues and delayed cancer identification. Based on this performance, it is experimented that such features provide considerable assistance to a medical research, and the results were boosting when tissues were classified with Neural Networks.Genetic algorithm is used to hold those genes in the dataset that provide most to its conflict. The monetary and social values of Ovarian Cancer are very high and its outcome has the problem which impressed many researchers in the computational intelligence in recent times. Because of the significance of achieving exact classification, Artificial Neural Networks (ANNs) are the best then genetic algorithm.



```
      2     5     6     8    10    20    30    40    50    60


h =

     10    20    30    40    50    72    90


j =

     15    25    35    45    65    75    95


user =

    MaxPossibleArrayBytes: 489947136
    MemAvailableAllArrays: 1.2960e+09
            MemUsedMATLAB: 458031104


sys =

    VirtualAddressSpace: [1x1 struct]
           SystemMemory: [1x1 struct]
         PhysicalMemory: [1x1 struct]

Elapsed time is 48.570207 seconds.
>>
```

Fig 4. Memory and speed calculation

The experimental results show in Fig 5(a) & (b) that when Genetic algorithm is compared with Artificial Neural Networks, later is the best algorithm for classification of medical data. It is also observed that Artificial Neural Network performs well for classification on medical data sets of increased size.

Although the research described in this proposed paper has given an extensive comparison of models and techniques, and extended the work done previously it has not exhausted the possibilities of classification models

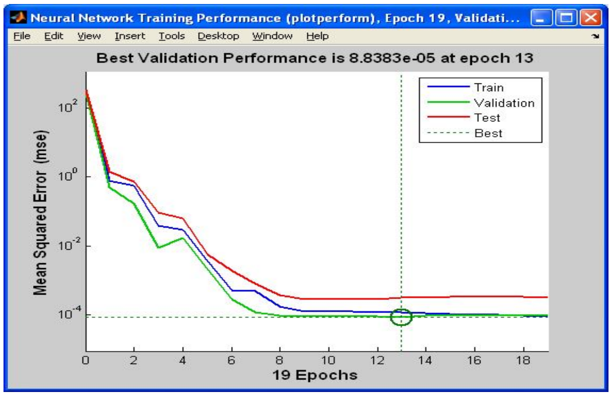


Fig 5(a). Performance of the data

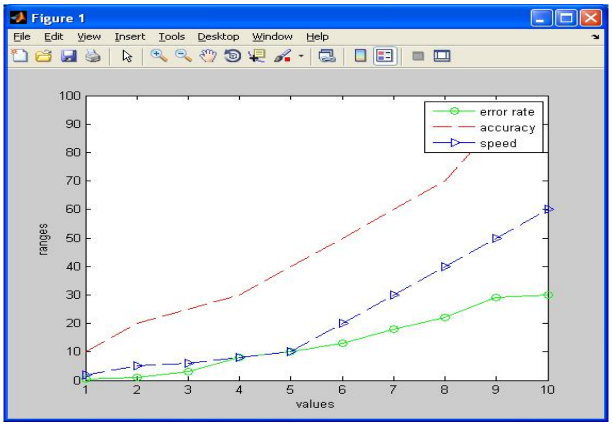


Fig 5(b). Performance of the Artificial Neural Network

## VI. CONCLUSION

In the past cancer categorization is generally depends on morphological and clinical analysis. To overcome those drawbacks in cancer classification, efficient technique in accordance with the global gene examination have been evolved. The microarray gene data must be preprocessed for classification with good accuracy using the classifier. This paper proposes a method for refinement and Categorizing the ovarian with kind, spreading and normal tissue using Genetic Algorithm and Artificial neural networks. This method was experimented for a ovarian dataset and radial basis operates neural networks. The best result was acquired with probabilistic neural networks resulting with high accuracy and good success results rate with 98% of performance for classification when compared to the conventional techniques.

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