Fusion Based Mining Incorporation In Brain Mapping

S.Saranya, S.Ambika

Abstract--- A human brain is a complex organ with unimaginable convolutions consisting of 86 billion neurons. In which identifying a brain related physiological problem is a challenging task. It can be done through functional MRI (fMRI). It is very difficult to extract the exact information needed for a neurological disorder from fMRI because it involves combined work of multiple organs in a human body that resides under the control of different parts of the brain. The brain mapping plays important role in mapping the neurons that are responsible for such problem. The neuron concentration helps to locate the functional activities in the human body that is responsible for inexpressive pain the patient is experiencing in his medical situation and also assist the physiotherapist to take significant level of diagnosis. This paper focuses on Fusion technique that combines graph mining and data mining in mapping process and also helps in understanding the brain mapping strategy. The sample data is used in this paper for clear understanding of the proposed approach.

Index Terms--- Functional MRI (fMRI), Brain Mapping, Fusion based mining, graph mining, Data mining, Association Rule Mining (ARM), Graph matching.

1 INTRODUCTION

1.1 Brain Mapping

All human activities like motor, speech, memory, sensory process are associated with brain. In order to determine precisely which part of the brain is handling critical functions such as thought, speech, movement and sensation is explained through the concept called *brain mapping* [1]. The initial process of brain mapping involves the following stages [9]. First in the experimental laboratory a deceased person's brain is got for study. Then the brain is sliced, frozen and the small portion of grey matter is again sliced. On microscope this grey matter contains plenty of neurons. Further these neurons are processed for micro dissections and we term them as *micro array*. Each neuron has protein content and further the protein content has the DNA that controls the functional characteristics of the human.

So determining the normal structural image can help in identifying the tumor and other physical disorders of the brain which is shown in fig 1(a). But to understand the psychological disorder like pain, depression and psychosis can be determined only through functional images and they are significant with activated regions. Such a functional image is shown in fig 1(b) which shows the neurons connection in brain.

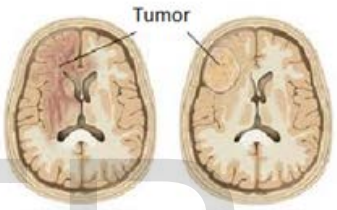
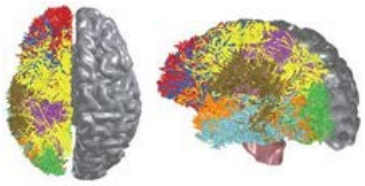


Fig.1. (a) Structural images signifying tumors and other physical disorder of the brain



(b) Functional images signifying activated regions of the brain

1.2 Functional MRI (fMRI)

A Functional MRI is best methodology to implement brain mapping [1], [2]. Normal anatomical image represents the satellite view of the brain and it helps in analyzing the physical brain damages, occurrence of brain clots, tumors etc. In order to analyze a brain activity related to pain, malfunctioning, alzheimer disease, psychological disorder and other such impairments can only be determined with the help of functional images.

There are many brain mapping methods like Functional MRI (fMRI), Positron Emission Tomography (PET), Single Photon Emission Tomography (SPECT), Electroencephalography (EEG), Magneto encephalography (MEG), Optical Intrinsic Imaging Techniques etc. Among all those methods fMRI is the best because it has no ionizing

- *S.Saranya is currently pursuing masters degree program in Computer Science and Engineering in Kumaraguru College of Technology, Anna University ,Coimbatore, Tamilnadu,, India . E-mail: sadhasaran5@yahoo.com*
- *S.Ambika is Assistant Professor of Mathematics, Government Arts College, Coimbatore, Tamilnadu,India.E-mail: ambisadha@yahoo.com.*

radiation and uses the concept of *echo planar imaging*. The most common fMRI techniques used to capture functional images of the brain is employed on the basis of Blood Oxygenation level Dependent (BOLD) contrast. In the BOLD effect, a neural activity in the brain caused by some sensory or motor tasks produces localized changes in the blood flow thereby resulting in changes in oxygenation level. Functional activation in fMRI studies by mapping changes in cerebral venous oxygen concentration that correlate with neuronal activity.

An fMRI experiment can be performed on the MR scanner. A fast MR imaging technique such as Echo-planar imaging (EPI) is employed in order to detect the neural activity and the resulting oxygenation levels. It is important that a single image obviously does not give any functional information.

In fact, a variation in the image intensity levels is recorded with respect to time, for the desired functional information. Therefore, a number of images of the brain are recorded consecutively with respect to time in a single fMRI experiment which is shown in fig 2.

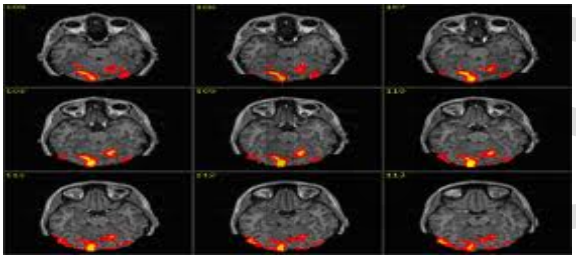


Fig.2. An fMRI scanned image that represents the consecutive recorded images and the red spots signifies the activated regions in the brain

fMRI is a relative technique that it compares the images taken during two different states of the task. During the ON state the subject performs some task (the activation state) where as no task is performed during OFF state (the base line state). Images recorded during the activation periods and those recorded during the baseline states are then compared. Typically a mean difference image is formed and then tests for statistical significance are carried out to obtain the activation maps. Activation maps show the brain regions that are responsible for a given sensory or motor task as shown in the fig 2.This provides a meaningful picture of the neural activity from the perspective of the brain function. Color pixels indicate the activated regions in the brain.

1.3 Graph Mining

A graph is a structured data representation with vertices or nodes which are connected by links or edges. A process of extracting useful information from graph is called *graph mining* [3]. Since brain is a collection of neurons focused on different zones on the brain; we can represent each of those focused areas by nodes in brain graph [2].

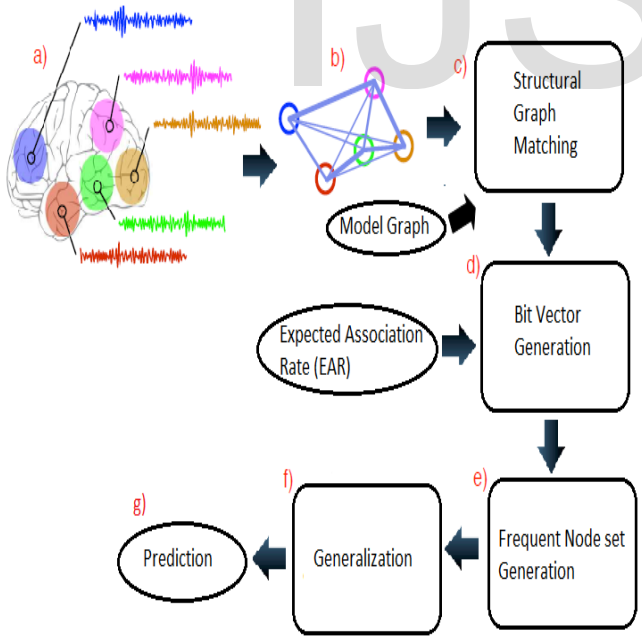
The most natural form of knowledge that can be extracted from graphs is also a graph; we referred it as *patterns* [5].Frequent pattern mining (FPM) is an important part of graph mining that helps to discover patterns based on relations. Developing algorithms that discover all frequently occurring sub graph in a large graph dataset is particularly challenging and computationally intensive. We classify the finding of frequent pattern from the given graph into two types as Apriori-Based Approach and Pattern-Growth Approach. *Apriori-Based Approach* uses a generate-and-test approach, which generates candidate item sets and tests if they are frequent. Whereas Pattern-Growth Approach uses frequent item set discovery without candidate generation by tree construction. In this paper, we apply Apriori based approach than pattern growth approach because time and space complexity generated in pattern growth approach is high due to tree construction. There are several graph generating models which comes under the two classes: Degree based and Procedure based [6]. Degree based is less powerful for pattern discovery whereas procedure based focuses on new patterns. In general, majority of generators fail to meet one or more of the following goals: (a) The generator should be procedural. (b) There should be a way to estimate its parameters. (c) It should be able to generate all types of graphs (directed/undirected, bipartite, and weighted). (d) It should satisfy more criteria (like diameter, eigenvalue plots) in addition to the degree distribution.

1.4 Data Mining

Data Mining is a technique of extracting the useful information that is based on the area of interest and the type of data from which information is extracted. Data mining is often known as Knowledge Discovery in Databases (KDD), which is a nontrivial extraction of implicit, potentially useful information from data in databases.

Data mining task involves two types which are descriptive data mining and predictive data mining. First

type describes the general properties of the existing data whereas the other attempts to predict based on the inference on available data. One of the popular descriptive mining technique is Association Rule Mining (ARM) [8],[11].There are several algorithms exists such as Apriori algorithm, association graph construction, primitive association rule mining, generalized association rule mining, Link analysis ranking, association rule mining without pre-assigned weights etc [8]. Since the bitwise operations are very fast to operate and also number of transactions is limited to a table, we make use of ARM [7]. A typical and widely-used example of association rule mining is Market Basket Analysis. Association rules find interesting association and/or relationships among large set of data items. It shows attributes value conditions that occur frequently together in a given dataset. They allow capturing all possible rules that explain the presence of some attributes according to the presence of other attributes. Generally, Rules are a type of the most human-understandable knowledge, and therefore it is most suitable for deciphering new rules corresponding to data associated with medical applications. Association rule mining is a general purpose rule observation scheme that has been widely used for observing rules in medical applications. One such application is detection of breast cancer using association rules and neural network is used



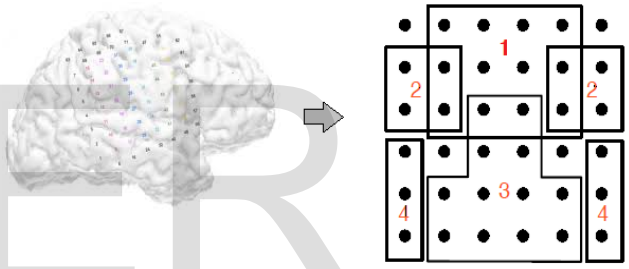
[13] and detect the occurrence of brain tumor [11]. Hence it can be applied in identifying the co-occurrence of different brain locations.

2 FUSION BASED MINING

This paper is formed based on the idea that "A complex organ needs a multidimensional/ multifarious methodology". In order to exactly identify which neurons in a particular region of a brain coordinates together to cause physical pain in a patient can be determined and visualized with the help of Fusion based mining technique as shown in fig 3.

Fig.3. Fusion based technique that couples the brain graph and generalized association rule.

Initially the image data is preprocessed and brain is divided to regions with time series, which is shown in fig. 3(a).Based on the series a graph is constructed and labeled corresponding to the region dependency which is shown in fig. 3(b). The obtained graph is compared with model graph for structural matching and correctness of graph as in fig.3(c).Then the adjacency matrix is computed from graph



for bit vector table generation which represents the number of occurrences of vertices in binary form is shown in fig.3(d) . With the Expected Association Rate (EAR) on bit vector table, a frequent node set table is generated as in fig. 3(e) which is based on rule mining and association with other nodes is determined. Generalization is done to construct the association graph is shown in fig. 3(f). Fig. 3(g) shows the final prediction of useful relationships from generalized graph.

Naturally looking into the structure of the brain a complex graph connection can be visualized, so focusing on that idea a brain graph is first constructed. Human brain sends signals within fraction of seconds, so the primary step of diagnosis is by using BOLD time series. The brain image is first converted to bold time series by using parcellation technique [4].

Fig.4. Grouping of voxels in brain

We perform voxel to voxel correspondence (node to node correspondence) across time i.e., time series of all voxel within region is compared for brain graph

construction. For this purpose either clustering methodology or Spatial Independent Component Analysis (ICA) approach is used to determine the strengthness of the region. For clustering a combination of Self Organized Map (SOM) and K-means clustering is used for grouping time series of voxels within a region. But Spatial ICA approach is used in this paper because of significant correlation of time series data can be achieved. The voxels are grouped based on the temporal dependency which avoid curse of dimensionality. This ensures the generation of vertex of the graph. A sample grouping of voxel in brain is shown in fig. 4.

Each voxel in group has its own time series that correspond to the BOLD signal. For signal processing, the wavelet transform which is the improved version of fourier transform is used because it is computationally fast and produce fine details of signal[10]. The use of this transform function is to enhance each timeseries of voxels to a representive timeseries. Each wavelet deals with both temporal extent of the signal and the frequency spectrum of the signal which is an added advantage. The wavelet transform function is represented in (1).

$$X = \sum_{k\in\mathbb{Z}} C_{J,k}\,\phi_{J.k} + \sum_{j\le J}\sum_{k\in\mathbb{Z}} d_{j,k}\psi_{j,k} \qquad (1)$$

Where j=1, 2...J is a scale of time series, k is the time point, $C_{j,k}$ is the approximation coefficient at scale J located at time point k, $d_{j,k}$ is the detail coefficient at scale j and time point k, $\varphi_{j,k}(t) = 2^{-\frac{j}{2}}\varphi(2^{-j}t-k)$ and $\psi_{j,k}(t) = 2^{-\frac{j}{2}}\psi(2^{-j}t-k)$.

To construct two dimensional graph structures it is necessary to uniquely name the edges of (nodes) vertices. The similarities between nodes need to be measured to know the dependency or correlation of nodes in brain region. Based on level of correlation, edge width in graph may vary. The similar nodes have thicker edge width than dissimilar nodes. The Karl-Pearson's correlation coefficient in (2) is used to best represent the correlation between two nodes is given by,

$$r = \frac{\frac{1}{N}\sum(x-\bar{x})(y-\bar{y})}{\sqrt{\left\{\frac{1}{N}\sum(x-\bar{x})^2\right\}\left\{\frac{1}{N}\sum(y-\bar{y})^2\right\}}} \qquad (2)$$

Here x and y are representative timeseries using wavelet transform. The rank r is the resultant output whose value range between [-1, 1] i.e., -1<r<1 .Taking into account of positive correlation, perfect correlation is when r=1 and dissimilarity is when r=0. When positive correlation A methodology for direct conversion of timeseries to correlation matrix uses relative similarity of time points is found unsuitable since it lacks in significant correlation [4].A sample Pearson's correlation representation for graph construction using assumed edge weight (width) is shown in table I.

The table I mentioned above is sufficient for graph construction. Let G (V, E) be a graph where V is set of vertices or nodes and E is set of edges. The graph computed is a labeled undirected simple graph which is suitable for computation. A simple graph has properties such as no loop, no parallel edges. Each edge width marks the level of dependencies between nodes of the graph. The perfect correlation has assumed edge weight is five and it decreases as degree of correlation decreases till zero correlation is reached. The zero correlation represents dissimilarity has assumed edge weight be zero i.e., no real edge between two nodes with r=0. A sample graph with different edge weights is shown in fig 5.

TABLE I

GRAPH CONSTRUCTION

		H
	(pts)	
1	5	
0.9	4.5	
0.8	3	
0.7	2.25	
0.6	1.5	
0.5	1	
0.4	0.75	
0.3	0.5	
0.2	0.25	
0.1	0.125	
0	0	NO

Fig.5.Edge weights representation in different graphs.

The brain graph obtained need to be analyzed for predicting the chance of co-occurrence of brain location. The direct conversion of brain graph to matrix form is possible but drawback of matrix methods is their inability to cope with graphs of different sizes. This means that they cannot be used when significant levels of structural corruption are present. So to handle such drawback statistical matching of graphs into a matrix representation and to exploit singular value methods to efficiently recover correspondences is handled in paper [12]. We commence by developing a likelihood function for the graph-matching problem. This treats the graph to be matched (the brain graph) as observed data and the set of correspondences with the available model (the model-graph) as hidden variables. Accordingly, we construct a mixture model over the set of correspondences between the nodes of the data-graph and those of the model-graph. The correspondence errors encountered in matching the data-graph to the model-graph is handled using Bernoulli model.

Consider a data graph $G_D = (V_D, E_D)$ where $V_D = \{x_1, x_2, \ldots, x_{|V_M|}\}$ is set of nodes in G_D used for matching against model graph $G_M = (V_M, E_M)$ where $V_M = \{y_1, y_2, \ldots, y_{|V_M|}\}$ is set of nodes in G_M. The matching function is represented as $f : V_D \rightarrow V_M$ that maps nodes of both graphs. The structure of two graphs is represented using adjacency matrix D for data graph and M for model graph whose order is $|V_D| \times |V_D|$ and $|V_M| \times |V_M|$ respectively. The elements of data graph D and model graph M are defined as

$$D_{ab} = \begin{cases} 1 \ if \ (a,b) \epsilon \ E_D \\ 0 \ otherwise \end{cases} \quad (3)$$

$$\text{and} \quad M_{\alpha\beta} = \begin{cases} 1 \ if \ (\alpha,\beta) \epsilon \ E_M \\ 0 \ otherwise \end{cases} \quad (4)$$

Since graphs are undirected the adjacency matrices are symmetric in nature i.e. $D=D^T$ and $M=M^T$. The Matching matrix S of order $|V_D| \times |V_M|$ whose elements are assignment variables which is,

$$s_{a\alpha} = \begin{cases} 1 \ if \ f(a) = \alpha \\ 0 \ otherwise \end{cases} \quad (5)$$

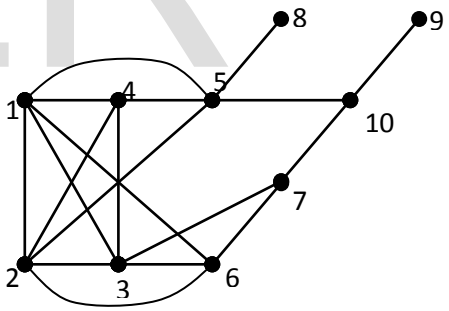
The corresponding log-likelihood function for matching matrix along with Bernoulli distribution is represented as

$$\mathcal{L}(S) = \sum_{a \epsilon V_D} \log \left\{ \sum_{\alpha \epsilon V_M} K \ exp \left[\mu \sum_{b \epsilon V_D} \sum_{\beta \epsilon V_M} D_{ab} \, M_{\alpha\beta} \, s_{b\beta} \right] \right\} \quad (6)$$

Where $= \ln \frac{1-P_e}{P_e}$, K= $P_e^{|V_D| \times |V_M|}$ and P_e is parameter for probability of correspondence error. Here 1-P_e represent correct correspondence and P_e represent error. In order to handle incomplete data likelihood the Expectation-Maximization algorithm can be used. This processing ensures the correctness of the graph determined. The adjacency matrix of brain graph S obtained from graph matching is for making association which in the form of binary matrix. The model graph M used previously for correspondence is processed to obtain brain locations which is a categorical attribute.

The adjacency matrix of S is considered for generation of bit vector generation. The Sample graph obtained from output of graph matching and corresponding adjacency matrix is shown in fig 6.

The bit vector is generated from adjacency matrix which is symmetric because the graph is undirected. Similar to transaction table generated in Market Basket Analysis, the generation of Diagnosis table is made. A sample diagnosis table representation for fig 6 is shown in table II.



$$A(S) = \begin{pmatrix} 0 & 1 & 1 & 1 & 1 & 1 & 0 & 0 & 0 & 0 \\ 1 & 0 & 1 & 1 & 1 & 1 & 0 & 0 & 0 & 0 \\ 1 & 1 & 0 & 1 & 0 & 1 & 1 & 0 & 0 & 0 \\ 1 & 1 & 1 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 1 & 1 & 0 & 1 & 0 & 0 & 0 & 1 & 0 & 1 \\ 1 & 1 & 1 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 1 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 1 & 0 & 1 & 0 & 1 & 0 \end{pmatrix}$$

Fig.6.Sample Graph at left side and corresponding adjacency matrix generated is shown right side.

TABLE II

SAMPLE DIAGNOSIS TABLE GENERATED FOR FIG. 6

Brain Functions	Number Assignment (item)	Bit vector (BV)
Balance	1	0111110000
Arm	2	1011110000
Chest	3	1101011000
Eyes	4	1110100000
Leg	5	1101000101
Neck	6	1110001000
Jaw	7	0010010001
Knee	8	0000100000
Tongue	9	0000000001
Mouth	10	0000101010

In table 2, brain functions on structural matching (for this sample only some sensory and motor functions are included) are got from model graph and corresponding adjacency matrix is obtained from brain graph is represented in bit vector. Also numbers are assigned for each brain function based on the vertex of the graph as in fig 6 and is used as item in following description.

Expected Association Rate (EAR) determines the frequency level to which the association is expected. It is similar to the minimum threshold condition that the frequent sets must satisfy. For frequent node set generation, Association Rule mining (ARM) is used. The algorithm follows: The logical OR operation and bitwise AND is used for every item. The vertices that satisfy EAR are chosen as Large 1- set. From Large 1- set item two large items i, j such that i<j is chosen. If item j is not the ancestor of item i and number of 1's in BVi ∧ BVj (i>j) achieve EAR then item set (i, j) is chosen as Large 2-set. Similarly the operation is continued for n number of set till it satisfies the EAR. If no more item sets are frequent i.e. item sets do not satisfy EAR then the operation of frequent node set generation stops. It is assumed that if an item set say X is a large item set, then any item set generated by replacing an item in item set X with its ancestor is also a large item set. The ARM algorithm is as follows,

```
ARM ()
Input: Diagnosis table
Output: Frequent item sets that satisfy EAR
Begin
Select BV for each item and perform logical OR operation to produce sum
  Step 1: For each item i
   {
    If (sum ≥ EAR)
    {
      Add this item i to Large 1-set
    }
   }
  Step 2: For each item set (i, j) from Large 1-set
    {
      If (i<j and sum (BVi ∧ BVj) ≥ EAR)
      {
        Add this item (i, j) to Large 2-set
      }
    }
  Step n:  For each large n-set
  {
    Repeat the step 2 for nth set
  }
End
```

A sample frequent item set generation is shown below. Assume the EAR is taken to be 30%.By applying ARM algorithm for table II, the generation is considered. In this sample the algorithm stops after Large 3-set.

Large 1-set: {1, 2, 3, 4, 5, 6}

Large 2-set: {{1, 2},{1, 3},{1, 4},{2, 3},{2, 4},{3, 5},{3, 6},{4, 6}}

Large 3-set: {1, 2, 3}

A generalized graph construction is made based on the frequent item set is shown in fig 7. For each Large 2-set (i, j) an edge is drawn between vertices i to j is carried out. Similarly edges are drawn for Large n-set. With this graph association between items i.e. the brain functions can be identified. From the generalized graph, predicting of association of brain functions is possible.

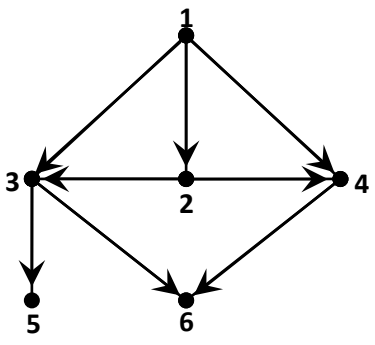


Fig.7. Generalized graph construction

TABLE III

SAMPLE OUTPUT OF FREQUENT ITEM SET GENERATION WITH SUPPORT AND CONFIDENCE CALCULATION.

Item set	Bit vector	Support	Confidence
1	0111110000	0.5	-
2	1011110000	0.5	-
3	1101011000	0.5	-
4	1110100000	0.4	-
5	1101000101	0.5	-
6	1110001000	0.4	-
1 2	0011110000	0.4	0.8
1 3	0101010000	0.3	0.6
1 4	0110100000	0.3	0.4
2 3	1001010000	0.3	0.6
2 4	1010100000	0.3	0.6
3 5	1101000000	0.3	0.6
3 6	1100001000	0.3	0.6
4 6	1110000000	0.3	0.75
1 2 3	0101010000	0.3	0.75

A Support is the fraction of frequency of occurrence of an item set (support count) to total number of items in diagnosis table. Based on the Support value of each frequent item set, it is possible to prioritize the level of diagnosis is shown in table 3. Support is simply a probability that a randomly chosen transaction t contains both item sets A and B. In brain mapping t is considered as time point. Mathematical notation is,

$$\text{Support } (A \Rightarrow B)\ t = P\ (A \subseteq t \ \wedge\ B \subseteq t) \quad (7)$$

Or Support $(A \Rightarrow B)\ t = P\ (A \wedge B)$

A confidence (or accuracy) is strength of implication in the rule. It is simply the probability that an item set B occurs in a randomly chosen transaction t given that item set A has occurred. Mathematically,

$$\text{Confidence } (A \Rightarrow B)\ t = P\ (B \subseteq t \mid A \subseteq t) \quad (8)$$

Or Confidence $(A \Rightarrow B)\ t = P\ (B \mid A)$

This calculation gives the strength of associate rate of brain functions thereby showing the co-occurrence of brain functions in a person is shown in table III. For example, a patient has strong association of brain functions in arm, chest, and balance then on diagnosis prediction, patient have chances of either heart attack or stroke. When previous brain functions have association with eyes, mouth, leg then the chance to stoke is higher than heart attack is the prediction result.

3 APPLICATION

In Clinical neuroscience, the root cause of a pain may be due to infection, injury, psychological stress and other such problems. The proposed technique helps the physiotherapist to limit their level of diagnosis and also help in diagnosis of patients with brain injury. The association of the neuron that involve together to cause such pain for a suffering person can be used.

This technique can be applied when we need to distinguish a person suffering from Mild cognitive impairment (MCI) to Alzheimer diseased person and with amnesia**.** Mild cognitive impairment (MCI) causes a slight but noticeable and measurable decline in cognitive abilities, including memory and thinking skills. A person with MCI is at an increased risk of developing Alzheimer's or another dementia. It is used in cancer patients to distinguish early stages of cancer. This methodology can be used to distinguish a patient from Cardiac arrest to heart attack and stroke.

4 CONCLUSION

This paper helps to identify the neurons that are responsible for a particular disorder in brain. Since neurons are grouped together in different regions of the brain and

each of the brain locations focus on different activities like vision, speech, emotion ,balance, skill, sensation ,behavior etc., we can also determine which activity is being associated with such disorder. The advantage of the proposed work is the use of fast association mining technique that is suitable for preliminary level of diagnosis of a patient and can be applied chemical structure in brain cells. Graph mining and data mining is coupled together for better understanding, easy implementation and quick processing.

There are several directions for future research. A real time implementation of this technique should be deployed and verified on its working functionality. The future graph mining algorithm can be employed using query language for finding the desired pattern by querying graph data for high performance. A budding methodology of query processing through solr query can be used for real time implementation. A combination of K-means clustering and Kohonen Self-Organizing Maps (KSOM) can be deployed for improving the clustering of voxel. Visualization techniques can be used for quicker understanding of the brain activity of patient on the circumstances of unexpressive pain. Pearson correlation in this work accounts only positive correlation, but the work can be extended to handle negative correlation.

REFERENCES

[1] Nivedita Daimiwal, Dr.M.Sundhararajan, Revati Shriram, "Applications of fMRI for Brain Mapping", International Journal of Computer Science and Information Security (IJCSIS), pp.23-27, Vol. 10, No. 11, November 2012.

[2] Jonas Richiardi , Sophie Achard, Horst Bunke, and Dimitri Van De Ville, "Machine learning with brain graphs", IEEE Signal Processing Magazine (Author Copy Of Corrected Accepted Manuscript, V1.01).

[3] Harsh J. Patel1, Rakesh Prajapati, Prof. Mahesh Panchal, Dr. Monal J. Patel, "A Survey of Graph Pattern Mining Algorithm and Techniques", International Journal of Application or Innovation in Engineering & Management (IJAIEM),pp. 125-129,Volume 2, Issue 1, January 2013.

[4] Mason porter, Sang Hoon Lee,"Characterising patients and controls with brain graphs constructed from fMRI data", September 2012.

[5] Wei Wang, Chen Wang, Yongtai Zhu, Baile Shi, Jian Pei, Xifeng Yan, Jiawei Han, " Graph Miner: A Structural Pattern Mining System for Large Disk based Graph Databases and Its Applications", SIGMOD '05 Proceedings of the 2005 ACM SIGMOD international conference on Management of data , pp. 879-881.

[6] Deepayan Chakrabarti and Christos Faloutsos, "Graph Mining: Laws, Generators, and Algorithms", ACM Computing Survey (CSUR)., Volume 38, Issue 1, June 2006.

[7] Hemant kumar Sharma, Deepak Garg, "Graph based approaches used in association rule mining",thesis, Thapar university, June 2010.

[8] Srivatsan. M, Sunil Kumar. M, Vijayshankar. V, Leela Rani P, " Predicting Missing Items in Shopping Carts using Fast Algorithm", International Journal of Computer Applications(IJCA),pp.35-41, Volume 21–No.5, May 2011.

[9] Vasileios Megalooikonomou, James Ford, Li Shen, Fillia Makedon , Andrew aykin," Data mining in brain imaging", Statistical Methods in Medical Research 2000; 9: 359–394.

[10]*M. Sifuzzaman, M.R. Islam and M.Z.* Ali,"Application of Wavelet Transform and its Advantages Compared to Fourier Transform", *Journal of Physical Sciences, Vol. 13, 2009, 121-134*

[11] Dipankar Sengupta, Meemansa Sood, Poorvika Vijayvargia, Sunil Hota, and Pradeep K Naik, "Association rule mining based study for identification of clinical parameters akin to occurrence of brain tumor", Bioinformation 9(11): 555–559 June 2013.

[12] Bin Luo, Edwin Hancock ,"Structural Graph Matching using the EM Algorithm and Singular Value Decomposition", ACCV2002: The 5th Asian Conference on Computer Vision, 23–25 January 2002.

[13] Murat Karabatak, M. Cevdet Ince, "An expert system for detection of breast cancer based on association rules and neural network", Expert Systems with Applications 36 (2009) 3465–3469.