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Establishing Effective Connectivity in Brain using Dynamic Bayesian Network

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ABSTRACT: Dynamic connectivity is shown essential for normal brain function. It is difficult to develop model for inferring brain effective connectivity from non invasive (fMRI) data. Author prefers DBN because its suitability and flexibility and it has solid base on statics. the proposed method detect the statistically significant, biological plausible connectivity between task related region of interest(ROIs) that difference between schizophrenic and normal subject, finding more knowledge which consist of prior neuroscience knowledge. Determine highly reproducible DBN node/edges across subjects seem promising for inferring altered functional connectivity within a group.

Keywords: Dynamic Bayesian Network, fMRI, Causal Modeling, BIC, Effective Connectivity, MDL, AIC

I. INTRODUCTION

For effective brain connectivity, the neural influence that one brain region exerts over another, is important for brain function, and its impairment may be related with neurodegenerative diseases such as alzeeimers, schizophrenic and PD. Some mathematical methods such as structural equation modeling (SEM), multivariate auto regressive modeling and dynamic causal modeling (DCM) have been proposed for effective connectivity using functional magnetic resonance imaging (fMRI) data [1]. DCM is the only approach to attempt model the "neuronal" and "hemodynamic" levels, due to the stability of the parameters specifying the relation between the neuronal and hemodynamic levels, especially in older diseases subject remain to be established. Recently (dynamic) Bayesian networks have been proposed to discover brain connectivity in fMRI. The BN approach is attractive due to its solid bases in statistics. DCM uses in older disease where Author have to specify "neuronal" and "hemodynamic" level but in DBN where region of interest is "neuronal activity" is represented by hidden node [1-3]. In DBN framework is the DCM can be regarded as particular case. Where each ROI's "neuronal activity" is represented by a hidden node, the observe nodes represent the "hemodynamic level" of the model [4].

Previous works on DBNs have show connectivity in schizophrenic may be altered given data from a single subject. However, ultimately extrapolating BN results from one subject to entire population e.g. patients with schizophrenic disease first requires methods to meaningfully integrate results from several subjects and rigorously compare BNs across different populations [5-6]. This inter-subject variability, a common and critical problem in many biomedical studies, remains a challenging problem. One study assumed that averaging the fMRI time-series over all subjects in an effective representation of the study population, another suggested applying the same model to all subjects and hence treating group of subjects data as being from the same subject and another applied analysis to only a single subject. These approaches may fail to distinguish connectivity patterns which are truly robust across individual as they may be sensitive to outliers. Goncalves have demonstrated the difficulty of interpreting fMRI data when inter-subject variability has been successfully dealt with in positron emission tomography studies, suggesting it is possible and important to address in fMRI studies Employing large, multi-subject SEM networks was proposed to address inter- subject variability, where all subjects were modeled with fully connected SEMs. The basic idea was to infer differences between normal subject and schizophrenic subject by comparing model [3-8].

II. LITERATURE SURVEY

Friston and Rajapakse describe the brain areas involved in various active tasks can now be identified quite accurately and reliably through functional Magnetic Resonance Imaging (fMRI) experiments. However, functional specialization of the brain does not provide a realistic view of brain function and does not describe how different brain regions communicate and interact with one another [4-5].

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Suppose multiple processes taking place in various region of brain which interacting with each other for doing specific task and discover the various brain connectivity with the help of fMRI data through which brain function easily understandable, recently there has been stress on functional integration studies to infer brain connectivity, especially for high order brain functions. In fMRI, the activity of brain is measured by time-series of signals depending on blood-oxygenation-level dependent (BOLD) contrast. Given multivariate voxel based time-series, to characterize the effective brain connectivity of the brain several techniques have been proposed to use fMRI. Structural equation modelling (SEM) decomposes interregional covariance of fMRI time-series to find functional interactions among brain regions. The covariance structure models the interactions of underlying neural systems only in second-order statistical sense and therefore does not render effective connectivity or the "cause and effect" relationships among brain regions. Dynamic causal modelling (DCM) characterizes the dynamics of interactions among states (of brain regions) with bilinear approximations of intrinsic coupling (among neuronal states) and the influence of external inputs. An extended balloon model is used in DCM to model hemodynamic response, which enables inference of interactions at the neuronal level. Both SEM and DCM are confirmatory in the sense that the analysis of brain connectivity requires a priori model to begin with and is inapplicable for higher-order functions unique to human such as language or cognition. Granger causality mapping (GCM) extends the vector autoregressive (VAR) technique to capture interactions among brain regions, assuming a causal and dynamic system of linear interactions, driven by stochastic innovations. A graphical approach linking the notions of graphical models and Granger causality has been applied to describe dynamic dependencies in neural systems [2-6].

Nevertheless, a multi-step procedure fitting autoregressive models at each step is required to identify networks and therefore limits its applicability for large networks. Recently, two techniques based on Bayesian networks (BN) were proposed to derive effective connectivity of the brain from functional MRI data in an exploratory manner. Bayesian networks do not provide an explicit mechanism to represent temporal dependencies among multiple processes at brain regions and instead give one snapshot of brain connectivity, taking into consideration the whole experiment. Therefore, neural systems derived with BN do not fully describe causal relationships among brain regions. Moreover, because of equivalent properties of BN, directions of some edges are indeterminate and could be bi- directional propose by Chickering in 1995 [6-8]. In this paper, author proposes dynamic Bayesian networks (DBN) to derive the effective connectivity of the brain by modeling fMRI time-series in a Markov chain. DBN, an extension of BN, admits a class of nonlinear continuous time interactions and provides a direct mechanism to model temporal relationships among brain regions. Functional MRI time-series of activated voxels are modeled with first-order stationary Markov chains. The inter-scan interval of fMRI is used as the interval between two consecutive instances of the Markov chain. The connectivity between two time instances is modeled in a transition network of two layers of brain regions (or nodes). In a stationary setting, the connectivity of the transition network renders the effective connectivity of the brain [5]. Dynamic Bayesian networks may assume a known or unknown structure, and full or partial observe of states at the nodes. The states of activated brain regions are fully observed as intensity variations of fMRI time-series. Beginning with an unknown connectivity structure, author find the best structure fitting fMRI data in an exploratory manner. A greedy search or expectation maximization (EM) provides only a local search of the structure of DBN. Starting with a partly connected structure, Author uses a Markov chain Monte Carlo (MCMC) method to derive the structure of the connectivity among brain regions from fMRI data. The MCMC method attempts to find a globally optimal solution by sampling a collection of highly probable structures from the equilibrium distribution of the Markov chain [3-7].

III. PROPOSED SYSTEM DESIGN

Dynamic Bayesian Network based framework is proposed to infer the effective connectivity between various regions of brain. fMRI is technique to capture the range of measurements and extract quantitative information from various functional regions of brain. Proposed system works on fMRI images to generate feature vector which ultimately used to generate final model as shown in Fig. 1 [1].

A. Pre-processing

fMRI data is corrected for acquisition delays and for motion. Various regions are obtained by averaging all voxels within the region. Pre-processing step is applied to fMRI images to generate the feature vectors [3].

B. Dynamic Bayesian Network

It is graphical model for stochastic process. Dynamic Bayesian Network models dynamic system, not the model itself changes over time. The very good example of Dynamic Bayesian Network is first order Markov model. Markov model is fully specified by initial distribution $P(Z_1)$ and transition distribution $P(Z_{t+1}|Z_t).Z_t$ is state variable at time t. Temporal dependence relationship is represented using directed graph. Relationship is shown using arrow from Z_t to Z_{t+1} (t=1, 2, 3, …) [1].

fMRI signals from various regions are considered as feature vector. DBN models Proposed System as a vector-valued Markov process. DBN can model higher order Markov

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process but here only first order Markov processes are considered. DBN represents temporal dependence between brain regions as well as association at the same time. DBN generates the final model. The developed model is evaluated against various performance metrics and the results are captured [1-2].

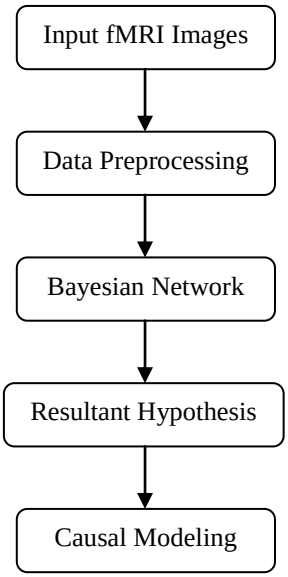

Fig. 1 Proposed System Design

IV. BAYESIAN NETWORKS

Bayesian Network is a graph which contains random variables and probabilities associated. BN is directed acyclic graph. The goal is to construct BN using the bellow tables containing experimental data about healthy and schizophrenic control. Two graphs will be generated one for healthy control and another for schizophrenic control. The common structure in graph of healthy control will shows the connections between different regions of brain in healthy person. In the same common structure in graph of schizophrenic control will show the connections between different regions of brain in schizophrenic person.

V. CAUSAL MODELING

Causality refers to "cause-and-effect" relations. It is a relationship that holds between events, variables, or state of affairs. Causality always implies dependency between the cause and the effect. Causal model focuses on causal factors. Causal modeling is used in Intelligence Analysis. For example, Military commander has intelligence assessment which contains most likely scenario as well as most dangerous scenario. Causal modeling useful to calculate probability of enemy courses of action based on specific conditions [9].

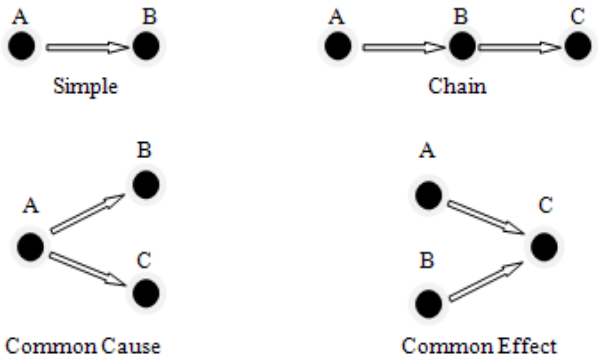

Fig. 2 Simple Causal Models [9]

Simple causal models are shown Fig. 2. These are graphical causal models. Graphical causal model has benefits of visual representation of models. Causal model can be build using following steps.

1. Data gathering
2. Building causal maps
3. Construct Bayesian causal maps using causal maps
4. Derive parameters of Bayesian causal maps

Data gathering is interview with a subject-matter expert. All the responses to such an interview are gathered and recorded in specific format. In second step, causal steps are identified from the knowledge acquired in step 1. Based on the steps identified, raw maps are built. In third step, modifying the causal maps has to consider four issues:

- Identification of conditional independencies
- Discern the underlying links between concepts
- Distinguish between direct and indirect relationships
- Eliminate circular relations.

Adjacency matrices are used to accomplish such issues [9].

Models are the representation of real life. Models even the best case models are limited, inaccurate and evolving. So, models need to be modified and the probabilities should be adjusted. There is possibility of previously hidden, unknown and ever-nonexistent factor will emerge. Existent factors may become irrelevant and need to be updated or even eliminated. Bayesian Theory provides the facility to do this automatically in mathematical context [9].

VI. EXPERIMENTAL SIMULATIONS

In this section, various brain regions for healthy control are shown in Table 1 and schizophrenic controls are shown in Table 2. The coordinates X, Y and Z were mapped to corresponding anatomical regions by using SPM (Statistical Parametric Mapping) tool. Brodmann Area is a region of cerebral cortex defined based on structure and organization of cells. Hemisphere shows the Left half or Right half of the

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brain. The software Talairach Client shows Talairach Labels for user defined coordinates.

TABLE I

TALAIRACH ATLAS LABELS FOR HEALTHY CONTROL

Anatomical Region	Sub Region within Anatomical Region	X	Y	Z	BA	Hemisphere
Parietal Lobe	Supramarginal Gyrus	63	-43	26	40	R
Parietal Lobe	Supramarginal Gyrus	58	-15	30	40	R
Parietal Lobe	Precuneus	12	-71	34	7	R
Parietal Lobe	Inferior Parietal Lobule	-32	-52	44	40	L
Occipital Lobe	Middle Occipital Gyrus	47	-60	-7	19	R
Occipital Lobe	Cuneus	30	-78	32	19	R
Occipital Lobe	Precuneus	19	-63	22	31	R
Frontal Lobe	Precentral Gyrus	-59	-5	24	4	L
Frontal Lobe	Precentral Gyrus	42	-16	36	4	L
Frontal Lobe	Precentral Gyrus	62	-8	30	6	R
Frontal Lobe	Middle Frontal Gyrus	27	-6	56	6	R
Frontal Lobe	Inferior Frontal Gyrus	-46	39	13	46	L
Frontal Lobe	Superior Frontal Gyrus	-15	-3	70	6	L
Frontal Lobe	Middle Frontal Gyrus	-34	45	27	9	L

TABLE II

TALAIRACH ATLAS LABELS FOR SCHIZOPHRENIC CONTROL

Anatomical Region	Sub Region within Anatomical Region	X	Y	Z	BA	Hemisphere
Frontal Lobe	Middle Frontal Gyrus	-32	40	47	8	L
Frontal Lobe	Middle Frontal Gyrus	56	11	44	8	R
Temporal Lobe	Middle Temporal Gyrus	-36	-68	23	39	L
Frontal Lobe	Superior Frontal Gyrus	-27	44	47	8	L
Frontal Lobe	Superior Frontal Gyrus	-26	47	45	8	L
Parietal Lobe	Precuneus	-44	-78	41	19	L
Parietal Lobe	Precuneus	-46	-77	40	19	L
Frontal Lobe	Middle Frontal Gyrus	60	12	37	9	R
Frontal Lobe	Superior Frontal Gyrus	34	56	29	9	R

VII. METRICS

A. BIC (Bayesian Information Criterion)

Brain connectivity is learned from fMRI data as per the maximum a posteriori (MAP) criterion. It means to choose most probable structure after observing data. The structure is chosen with largest Bayesian information criterion (BIC) score is given by equation (1).

$$\mathrm{BIC}(S) = \sup_{\theta} \log P(X|S,\theta) - 0.5K \log N \qquad (1)$$

Where N is the sample size of data X. K is number of free parameters θ of the model S[1].

B. MDL (Minimum Description Length)

The basic idea is to minimally encode dataset D into two parts *i.e.* network structure and unexplained data. The model is encoded with tables storing conditional probability of all variables. It requires $\log N/2 * p$ bits, where $\log N/2$ is space

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required to store one probability value and p is total number of individual probability values. Unexplained data can be explained with $LL(D|B)$ bits. So, we can write penalty term for MDL as

$$\text{PenaltyMDL}(Xi, B, D) = \frac{\log N * p_i}{2} \quad (2)$$

Where p_i is the number of parameters for X_i[10]

C. AIC (Akaike's Information Criterion)

AIC is another scoring metric for Bayesian Networks based on the asymptotic behavior of models with sufficiently large datasets. The penalty of AIC differs from MDL by the log*N*term. So, the penalty for AIC is given as

$$\text{PenaltyAIC}(Xi, B, D) = p_i \quad (3)$$

As the penalty of AIC is less than MDL, AIC tends to be more complex network than MDL [10].

VIII. CONCLUSIONS

In the paper, Dynamic Bayesian Network is used for effective connectivity between different regions of brain. The connectivity gets disrupted in disease. So, the common structures generated for healthy control and schizophrenic control are different. By studying the pattern of connections in various regions of brain, it will help to identify the affected regions of brain. The research will help the practitioner to work on specific regions of brain which are affected.

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Biography

Shivaji Mutkule received his B.E. degree in Information Technology from Vidya Pratishthan's College of Engineering, Baramati, Pune University, India, in 2011 and pursuing M.E. degree in computer science and engineering from Government College of Engineering Aurangabad, India. His research interests include Data Mining, Network Security and Bioinformatics.

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M. B. Nagori has been working as an Assistant Professor in Computer Science and Engineering department since last 10 years. Currently author is carrying out research work in the area of developing models and methods for efficient detection and classification of Brain tumour.