Brain's Doing in Its Resting-State: Default Mode Network as an Inside Story within the Brain

Jian-Qin Liu*and Katsunori Shimohara+

*Kobe Advanced ICT Research Center
National Institute of Information and Communications Technology,
588-2, Iwaoka, Nishi-ku, Kobe, Hyogo 651-2492, Japan
(Tel : 81-78-969-2227; Fax : 81-78-969-3928)
(Email address liu@nict.go.jp)

+Department of Information Systems Design,Faculty of Science and Engineering,
Doshisha University,
1-3 Tatara Miyakodani, Kyotanabe City, 610-0394 Japan
(Tel : 81-0774-65-6973; Fax : 81-0774-65-6801)
(Email address kshimoha@mail.doshisha.ac.jp)

Abstract: As a promising research field after the turn of the new century, Default Mode Network (abbreviated as DMN) of the brain shows the strong potential of a new breakthrough to neuroscience, which emphasizes the baseline of the brain's activities when the brain is awake but without any external input signal to it. This study is highlighted recently and expected to provide keys to understanding the mental disorders. This paper consists of following two sections: (1) A brief tutorial on the DMN is presented with necessary fundamental knowledge of neuroscience on the brain. (2) A framework of network informatics for DMN is proposed based on network dynamics; models of information networks are discussed by bridging the gap between the level of regions and the level of neurons of the brain; and major issues on analyzing the DMN by brain imaging technologies are discussed as well. In a word, one of the inspirations from DMN is how spontaneous collective behavior is emerged within an autonomous system, which is crucial to systematically understand the brain's function and exploring new design principles of autonomous robotics to demonstrate complex life-like behaviors in engineering.

Keywords: Default Mode Network, Neuroscience, Brain's Function**.**

I. INTRODUCTION

As one of most mysterious phenomena, the human's intelligence from the brain is always an important theme for sciences, in which the psychological aspect of the human's behaviors has a relative long history. With the advances in brain imaging technologies such as fMRI, MEG, PET, NIRS, EEG and others, nowadays the images constructed by the signals of the brain's activities with certain degree of the spatial and temporal resolution are obtained. Consequently, it becomes feasible to quantitatively analyze the informatics network mechanism for the brain's function.

It is well known that autonomy exists in the nervous systems such as autonomous sympathetic and parasympathetic nervous systems. In the artificial life community, the brain as a complex system is one of the kernel contents of the study on innovating new core design principles of autonomous robot systems inspired by artificial life, where the informatics network is expected to play an inevitable role.

II. BASIS OF NEUROSCIENCE

1. The Levels of Neuroscience

By means of neuroscience, the brain is studied at the cognitive, functional, (functionally-specified) sub-systems, cellular and molecular level in terms of reductionism. Here the sub-systems refer to those nervous systems such as sensory, motor and regulatory systems.

2. Quantitative Analysis of Neuron Interactions

The quantitative analysis of neuron activities can be carried out at the level of the regions of the brain and used as the reference for modeling the dynamics of the neurons and their interactions. Here one of the methods for modeling the dynamics of neuron activities is the nonlinear differential equations under the condition of the mean field theory. Column-centered model is an important method to bridge the gap between the regions and neurons and shows high efficiency in analyzing the dynamics mechanism of the signaling processes among interacted neurons. In order to understand how the interactions of neurons contribute to the dynamical behavior of the neural signaling leading to systematical modeling of nervous system, systematically modeling for computational neuroscience is necessary and imperative.

3. Integrating Dynamics and Signal Processing

By integrating the methodology of systems biology and principle of computational neuroscience, the neuron interaction mechanism can be inferred by using the correlation degree of the time series signals observed by brain imaging technologies. As an example of quantitative analysis on the above mentioned dynamical signaling process, blind identification is expected to be used to identify the structure the network that consists of the neurons where correlated signaling processes are based on the self-oscillation phenomenon. In order to systematically understanding the underlying dynamics of the interacted neuron activities, the methodology of complex science is helpful when the signaling network of the brain is modeled in terms of complex systems.

4. DMN as an Instance for Brain Science

Default Model Network (abbreviated as DMN) [1~5] is an instance of complex systems. Both in nature and in engineering, various types of complex systems have been observed. In order to explore new information processing paradigm to understand unknown mechanism in brains, it is necessary to know what the brain is doing when it has no input signals when the brain is modeled as a system. This status is the baseline of the brain, which plays an important role on observation and analysis of the brain in nonlinear dynamics. In the eyes of complex systems, DMN provides us important information on the baseline state of the brain, which is a promising field of neuroscience.

II. BASIS OF DEFAULT MODE NETWORK

1. Concept of DMN

Default Mode Network is a network of signals within the brain when the system of the brain has no input. In informatics DMN is formulated as graph in topology $G = <V, E>$ where V is the set of the vertexes and E is the set of the edges. The vertex refers to the location of the regions of the brain, which is known in anatomy. The value of the vertex refers to the signals obtained from brain imaging, e.g., fMRI. The edge refers to the relationship among the vertexes, i.e., the functionally connection and structural interaction among regions. Here, functional connection means that the regions cooperate for certain functions of the brain; structural interaction means that the signals of the nodes located at specific regions of the brain are included in a function in nonlinear dynamics so that some of these signals influence other signals or all of these influence each other. The weight of the edges can be assigned by the value of the functional connectivity measure between the two nodes linked by the edge.

DMN is active under the condition of the resting state of the brain. In order to describe the corresponding dynamics of DMN, a dynamical graph is given as follows: $G = <V, E, Q>$ where Q is a function to describe the dynamics of the signaling process for the variables corresponding to the vertexes. The general form of Q is given as follows:

$$d/dt\, X_1 = f_1\,(X_1, X_2, \ldots, X_n)$$
$$d/dt\, X_2 = f_2\,(X_1, X_2, \ldots, X_n)$$
$$\ldots$$
$$d/dt\, X_n = f_n\,(X_1, X_2, \ldots, X_n)$$

where $X_1, X_2, \ldots, X_n$ are the variables that correspond to the vertexes, $f_1(.), f_2(.), \ldots, f_n(.)$ are the functions to describe the underlying dynamics. In computational neuroscience, one of the tasks is to identify these function based on the data of the variables. The information processing mechanism of DMN looks like the operating system of a computer or a network in metaphor. It is clear that the *dynamics* mechanism of DMN is one of the kernel topics in computational neuroscience.

2. Significance of DMN Study in Medicine

One of the direct applications of DMN research may be the medicine although there is still a long way to go, owing to the fact that DMN is related to the states of brains when diseases such as autism, schizophrenia and Alzheimer's disease occur [1].

3. DMN as a Topological Graph

In anatomy, the areas where DMN is located include: vMPFC – Ventral medial prefrontal cortex; PCC/Rsp – posterior cingulated/retosplenial cortex; IPL – Inferior parietal lobule; LTC – Lateral temporal cortex; dMPFC – dorsal medial prefrontal cortex; HF+ Hippocampal formation.

With the reference of the anatomical locations, a topological representation is summarized in [1], which is an undirected graph consisting of *the set of nodes* {IPL(R and L types of IPL), PCC/Rsp, vMPFC, dMPFC(negative), PHC(R,L types of PHC), HF (R and L types of HF), LTC (L and R types of LTC)} *and links* whose length is given according to the correlation measurement. Here dMPFC(negative) refers to that the signal of dMPFC is anti-correlated with the one of the medial temporal lobe subsystem [2]. This topological network shows an interesting feature – the structure of hubs in network structure and sub-systems in system structure.

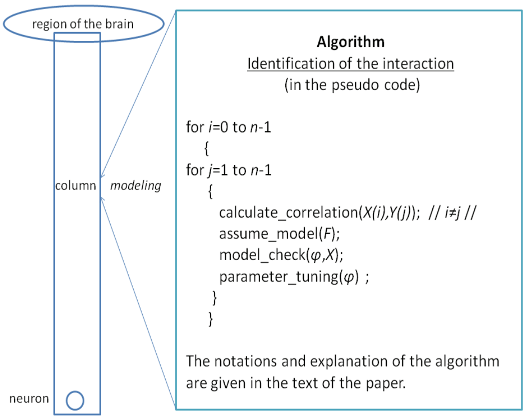

Fig. 1 The Identification Algorithm

III. NETWORK IFNORMATICS FOR DMN

1. Building Blocks of the DMN Dynamics

Multiple nodes and links for interaction among these nodes are the basis for networking. On the nonlinear dynamics, feedforward and feedback are two key factors. The node should be assigned with the signals constrained by nonlinear dynamics. The nonlinear dynamics here should be temporal and/or spatial. Considering an autonomous distributed (decentralized) system that consists of elements of information processing (e.g., agent in autonomous multi-agent systems), the local rules are defined and assigned to the elements, and no central control exists. The interaction among these autonomous components (elements) gives rise to the collective behavior, which reflects the emergence from the network with nonlinear dynamics.

2. The network informatics framework for DMN

The framework of network informatics for DMN is suggested as follows:

(1) The basic data structure for dynamical networks:

We can adopt the representation of dynamical networks as graph in topology and/or dynamical graph to describe the underlying network structure and corresponding dynamics mechanism for the signaling processes.

(2) Discrete Models:

Discrete mathematical models including automata are possible to describe the autonomy of the underlying network under the condition of the abstraction.

(3) Nonlinear Dynamics:

Considering the characteristics of the distributed system where each node is formalized by certain local rules and the interactions among these nodes give rise to the collective behaviors, a generalization of the entire network as a system is necessary. In principle, the ***Generalization*** takes the following form:

$$d/dt[\boldsymbol{X}_i(t+1)] = -\ \alpha \boldsymbol{X}_i(t) + \text{nonlinearity} + n\ (\text{noise}) \quad (1)$$

where i=0,1.,…, n-1 refers to the index of the node within the network. The study on the nonlinear dynamics aspect of DMN covers a broad scope from multiple disciplinary fields, e.g., stability and robustness are two issues to evaluate the performance of the system of DMN where the related parametric specificity is quantitatively analyzed. It will be also an interesting topic to investigate whether or not the chaos and/or bifurcation exist in DMN. In Fig.1, an identification algorithm is given in brief.

(4) Cognitive science aspect of the DMN

According to the relation between self-reference and DMN, the Bayesian model can be expected to model the function by using logical operation in computer science where the stochastic models and logic programming will be integrated.

(5) DMN-Inspired Routing for Computer Networks

Considering the dynamics mechanism of DMN and computer networks, a DMN-inspired routing algorithm for overlay networks in the field of computer networks is proposed as follows:

```
Algorithm (in the pseudo code)
  initialization ()
  WHILE NOT (V≠∅)
  // multiple path for multiple input and output //
   do
   {
   select (i,j)
   // select any two nodes i and j (i≠j) for a path from i
     to j //
   V ← V/{node(i), node(j)}
   l = i
```

```
    WHILE NOT (node (j) is reached)
    {
    single_path_generation
    // start from node i //
    calculate_correlation (node(l),  node(l+1))
    // return {correlation (node(l),  node(l+1))} //
    neighbor_find(l,(correlation
(node(l),node(l+1))<Tc))
    // select node (l) with correlation (flow (node(l),
      node(l+1))
      that satisfies certain threshold //
    // return (node (l+1)) //
    path (l, l+1)
    weight_of_path (l,l+1) ← capacity (path (l, l+1))
   for l' = 0 to M_l-1
      // l' is the node in the set of V except i, j, l (l≠i)
        and l+1  //
      {
      weight of link (l, l')
      // set by Monte Carlo method //
      // l' ∉ path (l,l+1) //
      path_set' (l') ← path_set ∪ {path (l')}
      V' = V' ∪ {l'}
      }
      return (matrix (l,l')) // the size of the matrix is M_l
     × M_l //
   path_set ← path_set ∪ path (l,l+1)
      l++
   }
   path_set' ← path_set ∪ path_set' (l')
   modeling_the_dynamics (V')
   // to estimate the signal of node (j) according to the
     path_set' //
  calcaulte_difference(correlation(path_set),correlation(
  path_set'))
// return diff(correlation(path_set), correlation(path_set'
  )) //
   diff_v ← diff (correlation(path_set),
     correlation(path_set'))
   if diff_v > Td
   {
   reconfigure()
     // the kernel operation is
          path_set ← path_set' //
   }
   routing_by_path (path_set)
}
```

Fig. 2 An algorithm of routing

Here the anti-correlated signal (time series) in DMN gives us the hint to select multiple routes that the related flows are with the complementary quantities. The total quantity of the traffic in the multiple routes is considered in this case. Normally in the transport layer, the knowledge of TCP dynamics can be used to design congestion window control and rate control. But in the case the existing route fails, the above-mentioned algorithm will be applied.

VI. CONCLUSION

The basis and the framework of DMN are presented in this paper, and a brief picture of DMN is made in the eyes of network informatics. As one of the examples of biologically inspired networking, a DMN-inspired routing algorithm is proposed, from which robustness is expected to be obtained.

ACKNOWLEDGEMENT

J.-Q. Liu sincerely thanks Satoru Miyauchi, Shigeyuki Kan and Takahiko Koike on brain science, Masayuki Murata, Naoki Wakamiya and Kenji Leibnitz on advanced network architecture, Haruhiko Nishimura and Teruya Yamanishi on nonlinear dynamics, Kazuhiro Oiwa on molecular biology.

REFERENCES

[1] Raichle ME et al. (2001), A default mode of brain function. Proc. Natl Acad. Sci. USA 98:676-682

[2] Buckner RL, et al. (2008), The brain's default network: anatomy, function, and relevance to disease. Ann. N. Y. Acad. Sci. 1124:1-38

[3] Fox MD and Raichle ME (2007), Spontaneous fluctuation in brain activity observed with functional magnetic resonance imaging, Nature Reviews Neuroscience 8: 700-711.

[4] Greicius MD, et al. (2004), Default-mode network activity distinguishes Alzheimer's disease from healthy aging: evidence from functional fMRI, Proc. Natl Acad. Sci. USA 101 (13): 4637-4642.

[5] Gusnard DA et al. (2001), Medial prefrontal cortex and self-referential mental activity: relation to a default mode of brain function, Proc. Natl Acad. Sci. USA 98 (7): 4259-4264.