Partitioned Parallel Processing Approach for Predicting Multi-Million Neuron Interconnectivity in the Brain : Involving Soma-Axon-Dendrites-Synapse

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Abstract- **This paper presents a simulation model based on partitioned parallel processing approach to predict Multi-Million Neuron Interconnections in the various brain regions involving soma, axon, dendrites and synapse. This is an attempt to develop a methodology for predicting such massive neural inter-connectivity to analyze the spatio-temporal information processing and synaptic based learning in its lowest level. The paper presents the importance of such massive prediction and opens up avenues for developing fault simulation techniques for modeling various brain diseases and disorders. The prediction of multi-million neuron interconnectivity involves awesome computations. To tackle this massive computational complexity a partitioned parallel approach employing the randomized algorithm namely the simulated annealing is evolved. The computational complexity is derived and is shown to be in hundreds of petaflop years. Heuristics are presented to drastically reduce this complexity. However, the high computational complexity necessitates the evolution of a novel super-supercomputer. This paper strongly suggests the need for evolving a DNA based computing paradigm for brain modeling in its total reality.**

Index terms

biological neural networks, inter-neural connectivity or neuron interconnections, algorithms, simulated annealing algorithm, supercomputer, fault simulation, computational and memory complexities

1 Introduction

Connectivity among neurons in the brain via their somas, axon, dendrites, telodendria and synapses is the crux that governs the functionality of various brain regions [rr2003] [shep98]. The inter-neural connectivity is the major factor that influences temporal, spatial and spatio-temporal information processing and the learning by the brain. In this regard, the knowledge of multi-million neuron interconnectivity involving complex dendritic arborescence, axons, billions of synapse and millions of soma is highly imperative.

The existing population models [wgwk2002] cannot provide connectivity details with regard to the dendritic arborescence, millions of soma, axons and billions of synaptic contacts. To develop an analytical (mathematical) model to deal with such massiveness to track the complex, intricate and finer neural connectivity will be highly intractable and impossible. Simulation models are powerful in dealing with such complex and massive systems.

This paper presents a partitioned parallel processing [dj99] approach to predict **M**ulti-**M**illion **I**nterconnected **N**eurons **i**nvolving the **D**endrites, **A**xon, **S**oma and **S**ynapse (**MMINi-DASS** Interconnectivity).

1.1 Importance of MMINi-DASS Interconnectivity

Once the MMINi-DASS interconnectivty is obtained a great deal of investigation can be performed with regard to simulation of the learning process, simulation of the information processing and the fault simulation of various brain regions.

With the help of the MMINi-DASS Interconnectivity either temporal or spatial or spatio-temporal information processing can be analyzed.

A deeper look at synaptic connectivity and the associated learning process is extremely feasible. The MMINi-DASS Interconnectivity prediction would be a powerful tool in evolving a simulation mechanism for the learning process [ejt95]. This MMINi-DASS interconnectivity would give the learning matrices that corresponds to the strength of each pre- and post-synaptic contact.

The predicted MMINi-DASS interconnectivity can be adopted straight away for fault simulating the corresponding brain region of interest. This fault simulation could be for electrical misbehaviour, physical damages or abnormal chemical activities and disequilibrium. Simulation of faults concerning dendrites, soma, axon, telodendria and synapse may be performed and the results can be analyzed.

For instance, in a given MMINi-DASS interconnectivity either millions of synaptic connectivity could be totally removed or ionic imbalances may be introduced in these synaptic contact affecting the neurotransmission. The impact of this on the information processing capabilities can then be studied. Similarly, faults like snapping off the axon or introduction of a graceful degradation to myelin sheath of the axon can be introduced in the predicted MMINi-DASS interconnectivity and its impact can be analyzed. In reality such an axonal fault occurring in scores of axons will greatly affect the information processing of million of neurons. Further the learning process can also get badly af-

fected due to such faults. Fault simulation on a predicted MMINi-DASS interconnectivity can help study the various brain diseases to discover new medicines.

However, there is neither experimental techniques nor theoretical approaches available currently that would determine the MMINi-DASS Interconnectivity.

Currently imaging techniques are widely used for diagnostic purposes. Structural Imaging Techniques like Magnetic Resonance Imaging (MRI) and Computer Aided Tomography (CAT) give details regarding the physical and chemical composition of various brain regions and are helpful in medical diagnosis of tumors etc. Functional Imaging techniques like Functional Magnetic Resonance Imaging (fMRI) gives details regarding the location of various brain centers and the corresponding Blood Oxygen Level Dependent (BOLD) response. Electroencephalograph, another functional imaging technique gives the temporal electrical activity of brain surface regions.

Massive edge detection can be employed using image processing techniques to the brain images obtained from MRI. There is a sea of difference between the capabilities of the simulation model to predict the MMINi-DASS Interconnectivity and even the enhanced images obtained from MRI. Moreover, the quality of MRI images are yet to reach a mark so that powerful image processing techniques could be efficiently applied for detecting the edges (soma, axon, dendrites, synapse) in the image. Even then the analysis that can be performed using these images can in no way match the capabilities of the predicted MMINi-DASS Interconnectivity using the proposed methodology. The simulation model based on partitioned parallel processing presented in the paper could be implemented as a research tool for deep brain analysis concerning spatio-temporal information processing, individual synaptic connectivity and associated learning, fault simulations concerning soma, axon, dendrites and synapse.

It is further discussed in detail in this paper, the limitations of the silicon supercomputer in handling the simulation model of the MMINi-DASS Interconnectivity prediction. A DNA computing paradigm needs to be evolved for the proposed prediction methodology.

Section 2 explores the application of the Simulated Annealing (SA) algorithm [kigv83] to predict MMINi-DASS interconnectivity. The generation of biologically realistic random MMINi-DASS interconnect structure as a initial state for the prediction algorithm (section 4.2) is discussed in section 3. The proposed partitioned parallel processing approach is given in section 4. The summary of the overall MMINi-DASS interconnectivity prediction approach is presented in table 3 in the form of a flowchart. The complexity of the proposed MMINi-DASS interconnectivity methodology is discussed in section 5.

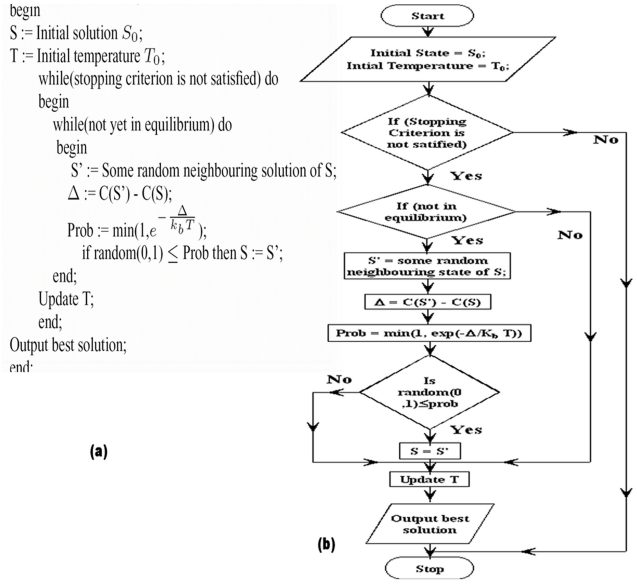

Figure 1: (a) shows the Generic Simulated Annealing Algorithm, (b) is the corresponding flowchart for the Generic Simulated Annealing Algorithm

2 Application of Simulated Annealing to MMINi-DASS Interconnectivity Prediction

The generic simulated annealing (SA) algorithm [kigv83] is given in figure 1(a). The corresponding flowchart is discussed in figure 1(b). Application of the Simulated Annealing (SA) algorithm to a system (here in our case it is the MMINi-DASS Interconnectivity) for optimizing its system parameters to obtain the near optimal solution (the desired MMINi-DASS interconnectivity) involves identification of the system parameters both variables and constants. It involves establishing a correspondence between the parameters of the SA algorithm namely the State of the system S, Temperature T, the energy difference Δ, Initial state S_0 and the Initial temperatures T_0 to that of the parameters of the MMINi-DASS interconnectivity (refer table 3). The system parameters correspond to the temperature parameters in the Generic Simulated Annealing algorithm, excluding the system parameters that are constant. The SA algorithm can also involve multiple temperature parameters corresponding to several system parameters. In that case the parameters of the SA algorithm would be the State of the system S, Temperature set (T-set) $\{T_1, T_2..., T_n\}$, the Energy difference Δ, Initial state S_0 and the Initial temperature set $\{T_{01}, T_{02}, ..., T_{0n}\}$.

The near-optimal solution from the SA algorithm is the State S of the system which corresponds to a minimum energy configuration. In our case the minimum energy state (near optimal solution) corresponds to the MMINi-DASS interconnectivity whose calculated temporal electrical ac-

tivity has maximum correlation with the experimental temporal activity of the desired brain region. The energy difference, Δ is the difference in energy of the current state and that of the previous state (Δ = C($S^{'}$) - C(S)). The T-set is heuristically scheduled in such a way that this energy difference is minimized over subsequent iterations. The intermediate state ($S^{'}$) is accepted or rejected during the iterations based on whether calculated probability is $\geq$ or $\leq$ random(0,1) (refer algorithm in figure 1(a)). This continues until we land up with the desired or the near optimal solution.

2.1 MMINi-DASS System Parameters, the $\{S - set\}$

MMINi-DASS system parameters (the S-set) characterize the electrical, chemical, physical and geometrical properties of the MMINi-DASS Interconnectivity. Currently, 35 MMINi-DASS system parameters (the S-set = $\{S_1, S_2, ..., S_{35}\}$) are thought-out for the proposed prediction methodology. These parameters are characterized under dendrites, soma, axon, telodendria and synapse. All the system parameters thought-out with respect to dendrites (electrical parameters, arborescence,...), soma (cell body shape, electrical parameters,...), axon (length, number of nodes of ranvier,...), telodendria (electrical parameters, arborescence,...) and synapse (contact sites, strength, number,...) are discussed in detail in table 1.

System parameters like threshold voltage and other electrical parameters of the soma of the MMINi-DASS Interconnectivity are treated as constants and are assumed to be available to predict the interconnectivity. The remaining system parameters are variables and are associated with the temperature parameters, the T-set.

2.1.1 Identification of $\{T - set\}$ with MMINi-DASS System Parameters

The variable and constant MMINi-DASS system parameters (S-set) are listed in table 2. These variable system parameters are identified with the temperature parameter set (T-set) as shown in table 2. Currently 24 such parameters are taken into account in the $\{T - set\}$ of the proposed prediction methodology i.e. $\{T - set\}$ = $\{T_1, T_2, ..., T_{24}\}$.

2.1.2 Correspondence between SA algorithm and the MMINi-DASS Interconnectivity System

The correspondence between generic SA algorithm and the MMINi-DASS Interconnectivity system is established in table 3. This correspondence shown in table 3 establishes the link between SA algorithm parameters and that of the MMINi-DASS interconnect structure.

2.2 $\{T - set\}$ Scheduling Heuristics for MMINi-DASS Interconnectivity Prediction

As discussed earlier, SA can involve multiple temperature parameters. Currently as mentioned in section 2.1.1, 24 temperature parameters have been identified that constitute the so-called T-set. To attain near optimal state one needs to schedule these temperature parameters listed in table 2 efficiently. In our case, the T-set (refer table 2) of the MMINi-DASS interconnectivity has to be so scheduled that the energy difference between the intermediate and the current MMINi-DASS interconnectivity is reduced over subsequent iterations to obtain the interconnect structure with minimum energy. The T-set heuristics will decide the time to convergence which means how fast *Prob* (refer algorithm in figure 1(a)) tends to 1 (or Δ tends to 0) i.e. how fast we obtain the state with minimum energy. These heuristics (T-set heuristics) correspond to the so called Temperature Scheduling mechanism of the SA algorithm.

In the current phase of this prediction methodology, a part of the WARF[1] project, ***The Deep Brain***[2], the following system parameters (that includes some temperature parameters as well) have not been included : S_3, S_{21} = T_{15}, S_{22} = T_{16}, S_{26} = T_{20}, S_{27} = T_{21} (refer table 2). However the electrical parameters associated with soma are taken into account. These electrical parameters are definitely influenced by the shape or geometry of the soma(S_3). The orientation of the dendrites and the telodendria neither influence the interconnectivity nor the spatio-temporal activities. However they influence the overall volume occupied by the MMINi-DASS interconnectivity.

On heuristically deciding the scheduling of the temperature parameters (refer table 2), either one or more to be scheduled, fixing up a suitable functional variations for these temperature(s) through some mathematical functions is called the temperature updating. One can work out several subsets from the T-set, $\{T_1, T_2..., T_n\}$ for the scheduling process. All temperatures in each of the subsets of the T-set can be scheduled by maintaining other temperatures constant. Table 4 lists all the possible temperature scheduling subsets (of T-set). The total number of possible subsets of the T-set adds up to 16777215 (=2^{24}-1). Corresponding to each of these temperature scheduling subsets, billions of computations are associated. This computational complexity depends on the complexity of the mathematical models of the soma-axon, dendrites, telodendria and the synapse, number of soma-axon, number of dendrites and branches, number of telodendria and branches and number of pre- and post-synaptic contacts. In all the computations is of the order of $O(N^k)$ with N varying in multi-millions and k being a few multiples of ten.

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[2] http://www.warfindia.org

2.2.1 Heuristics to Reduce the Massive Computational Complexity

The computational complexity can be very drastically reduced if the following well-thought out heuristics are applied. One is by considering certain temperature parameters as constants. In fact the temperature parameters associated with the dendrites and telodendria namely the number of branches and length of individual branches need not be scheduled for each iteration in the SA algorithm. Instead the initial random generation of this dendritic and telodendria tree can be so formed such that the number of branches and the branch length fall within a minimum and a maximum range that are biologically realistic. These heuristics are justified due to the fact that the dendrite and the telodendria trees and neuron interconnectivity may differ very widely across millions of people for every brain region. Hence the random generation of dendritic and neuron interconnectivity can be resorted to. However this random generation should be biologically realistic. More on the generation of the initial MMINi-DASS interconnectivity and their biologically realistic random generation is discussed in section 3.

What is of great importance is the pre- and post-synaptic connectivity and the associated learning process [ejt95]. The synaptic connectivity in general could be similar across people. On the other hand the strength of each synaptic contact will differ widely based on specialized learning that a person would receive. Hence the variations associated with pre- and post-synaptic contacts i.e. their corresponding temperature parameters and hence their scheduling are of importance. However, if on scheduling the change in energy of the system is not appreciable then the temperature parameters associated with the dendrites and telodendria is also considered for scheduling during that iteration.

Another heuristics considered to reduce computational complexity is that only those T-set subsets having more than 10 elements (or temperatures) are considered for scheduling. This is justified since only on a change in sufficient temperature parameters would the energy of the MMINi-DASS interconnectivity change by an appreciable amount.

Also, by applying SA algorithm [kigv83] to these temperature themselves, computations can be reduced and convergence can be speeded up. (SA is applied among these temperature subsets to choose the near optimal subset among the 16777215 temperature subsets and those temperatures in that subset is updated. SA is applied to choose the near-optimal temperature subset to be scheduled, along the similar line as explained in this section 2).

These heuristics reduce the computational complexity drastically. The order of the computational complexity comes down to $O(N^{\frac{k}{x}})$ with N varying in multi-millions and k varying as a few multiple of ten and $3 \leq x \leq 3.5$.

Another important factor to be considered in obtaining the near optimal solution is the selection of models for dendrites, soma-axon and the synapse.

As in the SA, the initial state of the system (in our case the initial MMINi-DASS interconnectivity) affects the near-optimality (in our case the predicted MMINi-DASS interconnectivity) of the solution to be obtained. To arrive at the inter-neural connectivity of the given brain region, we have to begin with an arbitrary and realistic MMINi-DASS interconnectivity which is the initial state. So another major factor of this approach is to develop an efficient methodology to generate a realistic MMINi-DASS interconnectivity. Obviously one has to resort to random generation of this MMINi-DASS interconnectivity with the extent of randomness being restricted by the statistical properties (refer table 5) of the MMINi-DASS interconnect structure to be predicted, like the average number of pre- and post- synaptic contacts in each neuron and the average dendritic tree configuration etc. More statistical properties of a MMINi-DASS Interconnectivity is listed in table 5.

2.3 MMINi-DASS Interconnectivity Simulation Model

A simulation model is made up of several algorithmic sequences comprised of generation of initial MMINi-DASS Interconnectivity, MMINi-DASS partitioning, application of SA algorithm for prediction which also includes the temperature scheduling is developed. This simulation model is discussed over the subsequent sections.

3 Phase I : Biologically Realistic Generation for an Initial MMINi-DASS Interconnectivity (Initial State)

As discussed under section 2 forming the initial state for the MMINi-DASS interconnectivity prediction is of paramount importance due to its complexity and impact on convergence to a near-optimal solution. The generation of a realistic initial state for MMINi-DASS Interconnectivity Prediction demands a randomized approach to mimic the natural formation of the neural interconnectivity in the brain. The randomness of initial state is constrained by the statistical properties (refer table 5) of the neural interconnections depending on the brain region whose interconnectivity is to be predicted. The statistical properties are listed in table 5. This random structure is used as the initial state for the simulated annealing based prediction algorithm (refer section 4.2).

The generation of a random and biologically realistic MMINi-DASS interconnectivity requires a model of representation for the interconnect structure. A matrix based

S_n	System Parameters $\{S-set\}$ of the MMINi-DASS interconnect structure Prediction
S_1	number of neurons, N
S_2	threshold (V_{th}) of the neuron
S_3	neuron cell body shape (soma shape)or geometry
S_4	relative cell body (soma) coordinates as (x,y,z)
S_5	nature of the neuron - inhibitory or excitatory
S_6	neuron level association i.e. which neurons are presynaptic to neuron n_i and which neurons are post-synaptic to neuron n_i
S_7	length of axon of each neuron n_i
S_8	conductance of axon of each neuron n_i
S_9	number and location of nodes of ranvier in each neuron n_i
S_{10}	length and thickness of each myelin sheath on axon of each neuron n_i
S_{11}	number and location of recurrent collateral of neuron n_i
S_{12}	with which neurons is the recurrent collateral from neuron n_i is associated and type of association (inhibitory or excitatory)
S_{13}	the location of the recurrent collateral terminal of neuron n_i on the incident neurons n_j
S_{14}	number of pre-synaptic and post-synaptic contact to each neuron n_i
S_{15}	which pre-synaptic contacts of neuron, n_i are provided by its presynaptic neuron, n_j
S_{16}	which post-synaptic contacts of neuron, n_i are provided by its post-synaptic neuron, n_j
S_{17}	nature of synaptic contact - inhibitory or excitatory
S_{18}	dendritic tree set d_i associated with each neuron n_i
S_{19}	number of dendritic branches in each dendrite d_i associated with each neuron n_i and their branching structure
S_{20}	length of each dendritic branch d_l in each of the dendritic tree, d_i associated with each neuron n_i
S_{21}	dendritic tree orientation in 3-D or 2-D space of each neuron n_i
S_{22}	dendritic tree tapering coefficient of each neuron n_i
S_{23}	telodendria tree set t_i associated with each neuron n_i
S_{24}	number of telodendria branches in each telodendria t_i associated with neuron n_i and their branching structure
S_{25}	length of each telodendria branch t_l in each of the telodendria, t_i associated with each neuron n_i
S_{26}	telodendria orientation in 3-D or 2-D space of each neuron n_i
S_{27}	telodendria tapering coefficient of each neuron n_i
S_{28}	location of pre-synaptic sites corresponding to each pre-synaptic neuron n_j on the dendritic tree, d_i associated with each neuron, n_i
S_{29}	location of post-synaptic sites corresponding to each post-synaptic neuron, n_j on the telodendria,t_i associated with each neuron, n_i
S_{30}	the strength or the learning weight associated with each synaptic contact on the dendritic spine of each dendrite d_i associated with each neuron n_i
S_{31}	resistance of the membrane in the dendritic trees
S_{32}	resistance of the membrane in the soma-axon portion in the cable theory model
S_{33}	capacitance of the membrane in the dendritic trees
S_{34}	capacitance of the membrane in the soma-axon portion in the cable theory model
S_{35}	EEG or fMRI of the MMINi-DASS structure to be predicted

Table 1: System Parameters of the MMINi-DASS interconnect structure prediction corresponding to that in the SA algorithm (S_n). Out of all these system parameters in the MMINi-DASS interconnect structure, some are taken as the system's temperature parameters (refer table.(2)) while others are assumed to be a constant being the statistical property of the MMINi-DASS structure to be predicted

System Parameters $\{S-set\}$ of MMINi-DASS that are **constants** for the MMINi-DASS Interconnect Structure Prediction	System Parameters $\{S-set\}$ of the MMINi-DASS that are **variables** and are considered as the Temperature Parameters $\{T-set\}$ for the MMINi-DASS Interconnect Structure Prediction, $\{T_1, T_2, T_3, ..., T_{23}, T_{24}\}$
$S_1, S_2, S_3, S_4, S_8, S_{14}, S_{31}, S_{32}$ S_{33}, S_{34}, S_{35}	$S_5, S_6, S_7, S_9, S_{10}, S_{11}$, $S_{12}, S_{13}, S_{15}, S_{16}, S_{17}$, $S_{18}, S_{19}, S_{20}, S_{21}, S_{22}$, $S_{23}, S_{24}, S_{25}, S_{26}, S_{27}$, S_{28},S_{29}, S_{30}

Table 2: Characterization of each System Parameter as a Constant or a Temperature Parameters. The table shows that out of the 35 system parameters, 24 are temperature parameters and 11 are constant parameters.

Terminologies in Generic Simulated Annealing Algorithm	Corresponding Parameters in MMINi-DASS
State	MMINi-DASS Interconnectivity configuration
Initial Solution S_0	Arbitrary MMINi-DASS interconnectivity
Initial Temperature T_0	The values of all the system parameters mentioned in table.1
Stopping Criteria	Degree of accuracy of the MMINi-DASS Interconectivity produced to that of the actual MMINi-DASS structure sought
Current State, S	Current MMINI-DASS interconnectivity
Intermediate State, $S^{'}$	Updated MMINI-DASS interconnectivity obtained due to the scheduling mechanism
Equilibrium Condition	The updated MMINi-DASS configuration ($S^{'}$) is better than the previous MMINi-DASS configuration (S) in terms of accuracy with respect to the actual MMINi-DASS configuration
Energy	degree of correlation of the temporal activity of a MMINi-DASS interconnectivity with that of the experimental temporal activity of the MMINi-DASS interconnectivity
Energy Difference, Δ	the difference between degree of correlation of the temporal activity of the updated interconnectivity with the experimental temporal activity of the interconnectivity and temporal of the previous interconnectivity with the experimental temporal activity of the interconnectivity to be predicted
Temperature (T)	$\{T-set\}$ listed in table 1
Update Temperature (T)	Some pre-determined mathematical function to update temperature or $\{T-set\}$ values
Near-optimal Solution (or) Best Solution	The MMINi-DASS Interconnect structure with least Energy

Table 3: The table illustrates what parameters of the generic simulated annealing algorithm is mapped onto the parameters in the MMINi-DASS Interconnectivity

Number of Temperatures Involved in the Scheduling	Subsets of Possible Temperature Scheduling Schemes and the Number of possible scheduling subsets (All the Temperatures of one Subset are simultaneously updated during one scheduling cycle)
One	$\{T_1\}$, $\{T_2\}$, ... $\{T_{24}\}$. Number of Possible Temperature Schedulings = $24C_1$ = 24.
Two	$\{T_1, T_2\}$, $\{T_1, T_3\}$ etc. Number of Possible Temperature Schedulings = $24C_2$ = 276.
Three	$\{T_1, T_2, T_3\}$, $\{T_1, T_2, T_4\}$, etc Number of Possible Temperature Schedulings = $24C_3$ = 2024.
Four	$\{T_1, T_2, T_3, T_4\}$, $\{T_1, T_2, T_3, T_5\}$, etc Number of Possible Temperature Schedulings = $24C_4$ = 10626.
Five	$\{T_1, T_2, T_3, T_4, T_5\}$, $\{T_1, T_2, T_3, T_4, T_6\}$ etc Number of Possible Temperature Schedulings = $24C_5$ = 42504.
Six	$\{T_1, T_2, T_3, T_4, T_5, T_6\}$, $\{T_1, T_2, T_3, T_4, T_5, T_7\}$, etc Number of Possible Temperature Schedulings = $24C_6$ = 134596.
Seven	$\{T_1, T_2, T_3, T_4, T_5, T_6, T_7\}$, $\{T_1, T_2, T_3, T_4, T_5, T_6, T_8\}$, etc Number of Possible Temperature Schedulings = $24C_7$ = 346104.
..	..
..	..
Twenty Four	$\{T_1, T_2, T_3, T_4, T_5, T_6, T_7, T_8, T_9, T_{10}$, $T_{11}, T_{12}, T_{13}, T_{14}, T_{15}, T_{16}, T_{17}, T_{18}, T_{19}$, $T_{20}, T_{21}, T_{22}, T_{23}, T_{24}\}$ Number of Possible Temperature Schedulings = $24C_24$ = 1.

Table 4: The table shows all the possible temperature scheduling subsets. The temperature parameters $\{T_1, T_2, T_3, ..., T_{23}, T_{24}\}$ are shown in table (2). The total number of scheduling subsets are (2^{24}-1=) 16777215. Thus there are 16777215 possible temperature scheduling mechanisms for the MMINi-DASS interconnect structure prediction. In each cycle the best possible scheduling subset is chosen through a probabilistic process that is inherent in the Generic Simulated Annealing Algorithm. **Note:** $xC_y = \frac{x!}{y!(x-y)!}$.

model has been evolved which would represent the complete connectivity details of a neural interconnectivity involving soma, axon, dendrites and synapse. The connectivity model has been so evolved that it would address all the intricate neural interconnectivity details.

Moreover an algorithm for generation of random and biologically realistic MMINi-DASS interconnectivity for any brain region given its statistical properties (refer table 5) has been evolved and is presented in section 3.1.2.

The general connectivity model for a MMINi-DASS interconnectivity is presented in the subsequent section.

3.1 Connectivity Representation for MMINi-DASS

3.1.1 The 2-D and 3-D Representation

Neuron-Neuron Connectivity Matrix (NNC) Matrix This matrix depicts the neuron level connectivity in the MMINi-DASS i.e. which neurons are pre-synaptic to neurons, n_i and which neurons are post-synaptic to neurons, n_i. It is an adjacency matrix [nar74] where 01 corresponds to a pre-synaptic neuron and 11 corresponds to a post-synaptic neuron while 0 represents no association.

Neuron Excitatory or Inhibitory (NEI) Matrix This matrix depicts which neurons are excitatory and which are inhibitory neurons. It a column matrix. It is matrix where 0 corresponds to excitatory neuron and 1 denotes a inhibitory neuron.

Neuron Coordinate (NC) Matrix This matrix contains the (x,y) or (x,y,z) coordinates of the neurons. This the only matrix where there is difference between a 2-D MMINi-DASS interconnectivity or a 3-D MMINi-DASS interconnectivity. All the other matrices would be of the same for both 2-D and 3-D MMINi-DASS interconnectivity.

Neuron pre-Synapse Association (NpSA) Matrix This matrix depicts the association of each of the pre-synaptic contact of neuron, n_i with the pre-synaptic neurons of the neuron, n_i. There would be a NpSA matrix for each neuron, n_i in the MMINi-DASS interconnectivity. It is an incidence matrix [nar74] where 01 and 11 represents excitatory and inhibitory pre-synapse association with the corresponding pre-synaptic neuron. A 0 represents no association.

Neuron post-Synapse Association (NpoSA) Matrix This matrix depicts the association of each of the post-synaptic contact of neuron, n_i with the post-synaptic neurons of the neuron, n_i. There would be a NpoSA matrix for each neuron, n_i in the MMINi-DASS interconnectivity. It is an incidence matrix [nar74] where 01 and 11 represents excitatory and inhibitory post-synapse association with the corresponding post-synaptic neuron. A 0 represents no association.

Dendrite Structure (DS) Matrix This matrix portrays the structural arborescence of the dendritic tree including its individual branch lengths. There would be a DS matrix for each dendrite for each neuron, n_i in the MMINi-DASS interconnectivity. It is a incidence matrix [nar74] whose elements are branch lengths.

Telodendria Structure (TS) Matrix This matrix portrays the structural arborescence of the telodendria including its individual branch lengths. There would be a TS matrix for each telodendria of each neuron, n_i in the MMINi-DASS interconnectivity. It is a incidence matrix [nar74] whose elements are branch lengths.

Dendrite pre-Synapse Association (DpSA) Matrix This matrix depicts the connectivity of the pre-synapses of the neuron, n_i on its dendritic tree. It gives details regarding the point of pre-synaptic contact on the dendritic tree. There would be a DpSA matrix for each dendrite of each neuron, n_i in the MMINi-DASS interconnectivity. It is an incidence matrix [nar74] whose elements are the point of contact of the synapse on the dendritic branch.

Telodendria post-Synapse Association (TpoSA) Matrix This matrix depicts the connectivity of the post-synapses of the neuron, n_i on its telodendria. It gives details regarding the point of pre-synaptic contact on the telodendria. There would be a TpoSA matrix for telodendria of each neuron, n_i in the MMINi-DASS interconnectivity. It is an incidence matrix [nar74] whose elements are the point of contact of the synapse on the telodendria branch.

Axon Length (Ax) Matrix The axon length matrix contains the length of axon of each neuron, n_i. There would be single Ax matrix for the MMINi-DASS interconnectivity. It is a column matrix that contains the axon length of all neurons.

Recurrent Collateral Point (RCP) Matrix The recurrent collateral point matrix contains the location of the recurrent collateral on the axon of each neuron, n_i. There would be a RCP matrix for each neuron, n_i in the MMINi-DASS interconnectivity. It is a column matrix that contains the point of recurrent collateral in the axon.

Recurrent Collateral Association (RCA) Matrix The recurrent collateral association matrix contains association of the recurrent collateral of each neuron, n_i with other neurons. There would be a RCA matrix for each neuron, n_i in the MMINi-DASS interconnectivity. It is a column matrix that contains the neuron each collateral is associated with and the type of association (inhibitory or excitatory).

The above connectivity representation can be extended to 3-D as well by changing the NC matrix alone as discussed under the NC matrix representation.

An Example A couple of sample matrices (DpSA matrix of neuron 2, N_2, DS matrix of neuron 2, N_2) depicting the connectivity is given in figure 2.

It is cumbersome to access the elements of different matrices which are large in order and number. Particularly the number of access required to these matrices is huge. It is

\\The value of the following variables : NC, PrS, PoS, B, Pr, Po, PS_1, PS_2 are
\\pre-requisites for the Matrix Generation Algorithms
N_NEU = Number of neurons;
NC1 = Average number of neurons pre-synaptic to each neuron;
NC2 = Average number of neurons post-synaptic to each neuron;
PrS = Average number of pre-synaptic contacts for each neuron;
PoS = Average number of post-synaptic contacts for each neuron;
B = Average number of branches in each dendritic tree;
Pr = Out of PrS average pre-synaptic contacts for each neuron, on an average how many are associated with each pre-synaptic neuron of that neuron;
Po = Out of PoS average post-synaptic contacts for each neuron, on an average how many are associated with each post-synaptic neuron of that neuron;
PS_1 = Average number of pre-synaptic contact on each dendritic branch;
PS_2 = Average number of post-synaptic contact associated with each branch of the telodendria;
PEREI = Percentage of Neurons in the MMINi-DASS Interconnectivity that are excitatory;

Table 5: Statistical Properties of the MMINi-DASS, the Pre-requisite values required for the generating the random structure

\\NNC Matrix Generation algorithm
Declare a N_NEU$\times$N_NEU square matrix, NNC(i,j);
Fill NNC matrix with zeros;
\\pre-synaptic neuron connection;
ROW=random(1,N_NEU);
while (connection not complete)
begin
CHECK current ROW of NNC matrix for filled positions corresponding to pre-synaptic connections;
STORE filled positions in the current ROW of NNC matrix in FILLED array, FILLED(i) such that $0 \leq i \leq F$ where F = number of filled positions in current ROW of NNC matrix;
A array, A(j) = (NC1 - F) random numbers such that ROW$<$A(j)$\leq 10^6$ for $1 \leq j \leq$(NC1 - F) and for each A(j) $1 \leq j \leq$(NC1 - F), A(j)$\neq$FILLED(i) for $1 \leq i \leq F$;
flag=1;
while (flag$\leq$total number of entries in A array)
begin
TEMP=A(flag);
if (row number TEMP of NNC matrix has less than NC1 pre-synaptic entries) then
NNC(ROW, A(flag)) = 01;
NNC(A(flag), ROW) = 01;
flag=flag+1;
end
ROW=random(1,N_NEU);
end
\\post-synaptic neuron connection;
ROW=random(1,N_NEU);
while (connection not complete)
begin
CHECK current ROW of NNC matrix for filled positions corresponding to post-synaptic connections;
STORE filled positions in the current ROW of NNC matrix (including pre-synaptic and post-synaptic connection entries) in FILLED array, FILLED(i) such that $0 \leq i \leq F$ where F = number of filled positions in current ROW of NNC matrix;
A array, A(j) = (NC2 - F) random numbers such that ROW$<$A(j)$\leq 10^6$ for $1 \leq j \leq$(NC2 - F) and for each A(j) $1 \leq j \leq$(NC2 - F), A(j)$\neq$FILLED(i) for $1 \leq i \leq F$;
flag=1;
while (flag$\leq$total number of entries in A array)
begin
TEMP=A(flag);
if (row number TEMP of NNC matrix has less than NC2 post-synaptic entries) then
NNC(ROW, A(flag)) = 11;
NNC(A(flag), ROW) = 11;
flag=flag+1;
end
ROW=random(1,N_NEU);
end
\\NEI Matrix generation
begin
Declare a N_NEU column matrix, NEI;
Store Zeros in the matrix;
Fill ones in the matrix randomly so that PEREI (refer table 5) is satisfied;
end
\\NC Matrix generation
begin
Declare a N_NEU column matrix, NC;
Store Zeros in the matrix;
Calculate total area or volume that would occupied by N_NEU neurons using DENS;
Obtain the Boundary coordinates;
Generate random coordinates such that they fall within boundary coordinates;
end

Table 6: NNC, NEI, NC Matrix Generation algorithms

\\NpSA Matrix Generation algorithm
Declare a NC1$\times$PrS matrix, NpSA(i,j);
Fill NpSA matrix with zeros;
ROW=random(1,NC1);
while (connection not complete)
begin
CHECK current ROW of NpSA matrix for filled positions;
STORE filled positions in the all rows of NpSA matrix in FILLED array, FILLED(i) for $1 \leq i \leq$TOTAL, where TOTAL = total number of filled positions;
STORE F = number of filled positions in current ROW of NpSA matrix;
A array, A(j) = (P - F) random numbers such that for each A(j) $1 \leq j \leq$(P - F), A(j) $\neq$ FILLED(i) for $1 \leq i \leq$TOTAL;
flag=1;
while (flag$\leq$total number of entries in A array)
begin
NpSA(ROW, A(flag)) = 1;
flag=flag+1;
end
ROW=random(1,NC1);
Replace 1's in the matrix by 01 or 11 to denote inhibitory or excitatory synapse connectivity randomly satisfying PERSEI (refer table 5);
end

Table 7: NpSA Matrix Generation algorithm

\\DS Matrix Generation algorithm
Generate a random number I, the number of terminals to the dendritic tree;
Generate Partition matrix [nrrsm2004] for a I input dendritic tree;
while (generated partition matrix is not acceptable)
begin
Generate another Partition matrix [nrrsm2004] for a I input dendritic tree;
end
Convert the partition matrix into the corresponding incidence matrix [nar74], IM ;
T_ROWS = total number of rows in the incidence matrix IM;
ROW = 1;
while (ROW$\leq$T_ROWS)
begin
In row number ROW of the incidence matrix, IM replace all non-zero entries by random($\min_l$, $\max_l$);
\\$\min_l$ = average minimum length of a dendritic branch;
\\$\max_l$ = average maximum length of a dendritic branch;
end
\\Partition Matrix Generation for a I input terminal dendritic tree
COL = 1;
while (I $\neq$ 1)
begin
Generate a unrestricted partition sequence for I;
N_par = Number of unrestricted partition into which I has been broken into;
\\all ones partition must be excluded
STORE this sequence column number COL of the partition matrix;
I = N_par;
COL = COL +1;
end

Table 8: DS Matrix Generation algorithm

\\DpSA Matrix Generation algorithm
Declare a B$\times$PrS matrix, DpSA(i,j);
Fill DpSA matrix with zeros;
ROW=random(1,B);
while (connection not complete)
begin
CHECK current ROW of DpSA matrix for filled positions;
STORE filled positions in the all rows of NpSA matrix in FILLED array, FILLED(i) for $1 \leq i \leq$TOTAL, where TOTAL = total number of filled positions;
STORE F = number of filled positions in current ROW of DpSA matrix;
A array, A(j) = (PS_1 - F) random numbers such that for each A(j) $1 \leq j \leq$(PS_1 - F), A(j) $\neq$ FILLED(i) for $1 \leq i \leq$TOTAL;
flag=1;
while (flag$\leq$total number of entries in A array)
begin
DpSA(ROW, A(flag)) = random(0,length of corresponding branch from DS Matrix);
flag=flag+1;
end
ROW=random(1,B);
end

Table 9: DpSA Matrix Generation algorithm

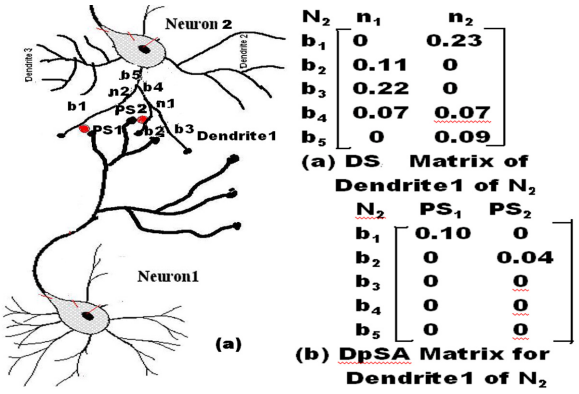

Figure 2: **Figure on the left**:2 Neuron Interconnect Structure. Key : s1 = pre-synapse for neuron 1, s2 = pre-synapse for neuron 2, b1 = branch 1 of dendrite 1, b2 = branch 2 of dendrite 1 etc, n 1 = node 1 of dendrite 1, n 2 = node 2 of dendrite 1, length b1=0.23, length of b2=0.11, length of b3=0.22, length of b4=0.07, length of b5=0.09, **Figure on the right:**DS and DpSA Matrix of Dendrite 1 of Neuron2, N_2

easier to integrate all the above matrices into a single matrix in which the elements become a vector. The given vector element of this integrated matrix corresponds to the elements of all other matrices. However this integration of all matrices to a single matrix should preserve the connectivity represented by the original individual sets of matrices.

3.1.2 Algorithms for Initial MMINi-DASS Interconnectivity Matrices Generation

The algorithms for generation of the MMINi-DASS Interconnectivity Matrices has been presented in tables 6, 7, 8, 9. The algorithm for the generation of other matrices are very similar to the matrices whose algorithms are presented.

4 Phase II : The Proposed Partitioned Parallel Processing Approach for Predicting the Biologically Realistic MMINi-DASS Interconnectivity

To tackle the computational complexity and to achieve very high performance, parallel processing [dj99] approach is essential. High degree of parallelism is achieved by proper partitioning of the MMINI-DASS Interconnectivity matrices. With this individual partitions can be executed simultaneously on a parallel machine [vaans2003] [spk96].

4.1 Application of Graph theory for Partitioning

The paper evolves a methodology for MMINi-DASS Interconnectivity Prediction using a graph theoretic approach (refer fig.3). The MMINi-DASS interconnectivity is modeled as a graph. The graph [nar74] is divided into a number of subgraphs. Each of these subgraphs represents a smaller neural interconnect structure in the bigger MMINi-DASS interconnect structure to be predicted.

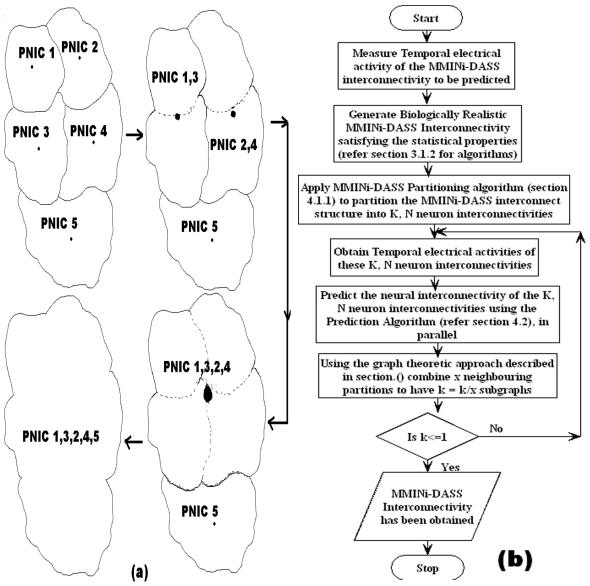

Figure 3: (a) shows the snapshot of the Graph theoretic approach, (b) shows the flowchart for the simulation model for the MMINi-DASS interconnectivity prediction

The MMINi-DASS Interconnectivity partitioning algorithm is given in the next section.

4.1.1 MMINi-DASS Interconnectivity Partitioning Algorithm

The design of the MMINi-DASS Interconnectivity Partitioning Algorithm first requires the enumeration of a set of well thought-out rules to partition the MMINi-DASS Interconnectivity. These rules are :

- the MMINi-DASS interconnectivity must be partitioned (or severed) only along its dendritic trees
- the pre-synaptic contact or the post-synaptic contact of the dendrite or telodendria along which partitioning is to be done must be grouped to be on the same of the partition
- the number of neuron in each partition must be such that their temporal electrical activity in the form of EEG or fMRI is obtainable or measurable. Also, the number of neurons in each partition must be similar

The algorithm for partitioning the MMINi-DASS interconnectivity is given in table 10.

4.2 The Prediction Algorithm

Using the Initial State discussed in section 3, the temperature parameters discussed in section 2.1.1 and the temperature scheduling heuristics discussed in section 2.2, the prediction algorithm given in table 11 is applied to each partition. The prediction algorithm is applied iteratively as per the graph theoretic approach. Currently the temporal electrical activity of the EEG is being made use of in the prediction methodology.

The simulation model used to predict MMINi-DASS Interconnectivity of a brain region applying the graph theoretic approach is given in figure 3 in the form of a flowchart.

4.2.1 Dendrites, Telodendria, Synapse and Soma-Axon models

The models used for dendrites, soma-axon, telodendria and synapse has a great deal of influence on the predicted MINi-DASS Interconnectivity. The Hodgkin-Huxley model [tuckwell88] for soma-axon, cable theory models for dendrites and telodendria [tuckwell88] [nrrsm2004], Spike response model [jr99] model for the synapse are being made use for the prediction methodology.

These models are integrated with the state S and S' (refer table 3 elaboration) during each iteration of the prediction algorithm, to obtain the complete voltage depolarization across the neural interconnectivity represented by the states S and S' during that iteration. From these depolarization voltage, EEG is calculated and correlated with the experimental EEG of the neural interconnectivity.

5 MMINi-DASS Interconnectivity Prediction Challenges the Supercomputers

Application of parallel processing for solving highly complex problems has acquired great importance in recent times. This is due to two major factors, one is the Deep Sub-Micron (DSM) [itrs2002] technological advancement leading to multi-billion device fabrication and the other is emerging need for challenging applications like weather modeling, ocean modeling, n-body simulation, molecular dynamics, seismological predictions and many more applications.

The following excerpt from [lkqs93] gives the extent of computational complexity of galaxy structure prediction.

> If we want to determine the structure of a cluster of galaxies, how large must the survey volume be?..... The Sloan Digital Sky Survey will produce fluxes and sky positions for 5×10^7 galaxies with redshifts for the brightest 10^6. Our ambitious observational colleagues have cut steel and ground glass to survey a "fair volume" that we must simulate, bue we need N=10^{12} to do this. Direct summation of the gravitational forces using fixed timesteps would take 10^{10} Teraflop-years." [lkqs93]

IBM is involved in designing supercomputer named Blue

\\MMINi-DASS partitioning algorithm for 2 partitions;
Identify the Boundary Neurons in a such a way that the number of neurons is large enough and also number of neurons in all the partitions is the same;
Number of boundary neurons = nboun;
Identify all the neurons in each partition;
Form the Connectivity representation of each partition by retaining all the matrices associated with interior neurons;
\\The matrices associated with the boundary neurons are formed as follows
i=1;
partition = 1;
while (partition¡=2)
begin
  while (i¡=nboun)
  begin
    Assemble all the DpSA matrices and DS matrices of the neuron i in partition j;
    Identify the node in the each of the dendritic tree of neuron i in partition j such that there is no synapses after that node;
    Update the DpSA and DS matrices as it would be when the partition is made at that node in each of the dendritic trees;
    Update the connectivity matrices of partition j;
  end
end

Table 10: MMINi-DASS Interconnectivity Partitioning Algorithm

begin
N = Number of neurons involved in the population of neurons whose interconnectivity is to be predicted;
V = Experimental Temporal electrical activity of the N neuron population;
In_Struct = Generated Biologically Realistic Random Neural Interconnectivity of N neurons satisfying the statistical properties of the population of neurons to be predicted as discussed in section.3.1.2;
\\refer table.3 for correspondence of simulated annealing terminologies with that of the neural interconnectivity;
S := Initial solution S_0 := In_Struct = Biologically Realistic Random neural interconnectivity of N neurons generated using algorithms discussed in section.3.1.2;
T_0-set := Initial temperature set := Initial value of the temperature parameters generated for the Biologically Realistic Random N neuron interconnectivity i.e. Initial value of all temperature parameters in In_Struct;
  while(temporal electrical activity of state S is acceptably close to that of the experimentally determined temporal electrical activity (V) of the neural population whose interconnectivity is to be predicted) do
  begin
    while(the correlation of the temporal electrical activity of the intermediate state S' with V is worse than the correlation of the temporal electrical activity of the state S with V, i.e.$\Delta < 0$) do
    begin
      S' := Some random neighbouring solution of S;
      Δ := corr(S',V) - corr(S,V);
      Prob := min(1, $e^{-\frac{\Delta}{k_b T_1}}$, $e^{-\frac{\Delta}{k_b T_2}}$, $e^{-\frac{\Delta}{k_b T_3}}$,...., $e^{-\frac{\Delta}{k_b \{T_1,T_2\}}}$,...., $e^{-\frac{\Delta}{k_b \{T_1,T_2,T_3\}}}$,...., $e^{-\frac{\Delta}{k_b \{T_1,T_2,T_3,T_4\}}}$,...., $e^{-\frac{\Delta}{k_b \{T_1,T_2,T_3,T_4,\ldots,T_{10}\}}}$,...., $e^{-\frac{\Delta}{k_b \{T_1,T_2,T_3,T_4,\ldots,T_{10},\ldots,T_{15}\}}}$, $e^{-\frac{\Delta}{k_b \{T_1,T_2,T_3,T_4,\ldots,T_{10},\ldots,T_{15},\ldots,T_{20}\}}}$, $e^{-\frac{\Delta}{k_b \{T_1,T_2,T_3,T_4,\ldots,T_{10},\ldots,T_{15},\ldots,T_{20},\ldots,T_{24}\}}}$);
      \\refer table.1 and table.2 for details regarding the temperature parameters;
      if random(0,1) $\leq$ Prob then S := S';
    end;
    if (Prob = $e^{-\frac{\Delta}{k_b T_1}}$) then Update T_1; if (Prob = $e^{-\frac{\Delta}{k_b T_2}}$) then Update T_2;
    ..
    if (Prob = $e^{-\frac{\Delta}{k_b \{T_1,T_2\}}}$) then Update $\{T_1, T_2\}$;
    ..
    if (Prob = $e^{-\frac{\Delta}{k_b \{T_1,T_2,T_3\}}}$) then Update $\{T_1, T_2, T_3\}$;
    ..
    if (Prob = $e^{-\frac{\Delta}{k_b \{T_1,T_2,T_3,T_4,\ldots,T_{10}\}}}$) then Update $\{T_1, T_2, T_3, T_4, ..., T_{10}\}$;
    ..
    if (Prob = $e^{-\frac{\Delta}{k_b \{T_1,T_2,T_3,T_4,\ldots,T_{10},\ldots T_{15},\ldots,T_{20},\ldots,T_{24}\}}}$) then Update $\{T_1, T_2, T_3, T_4, ..., T_{10}, ..., T_{15}, ..., T_{20}, ..., T_{24}\}$;
  end;
Output best neural interconnectivity of N neurons;
end;
Currently temporal electrical activity being made use for the prediction is the \\EEG;

Table 11: Prediction algorithm based on the SA algorithm

Gene to be applied for the protein folding problem. This proposed supercomputer would contain a million nodes and would have a computational capability of a 10^15 computations per second (Petaflop) [blueg]. The following excerpt from "Blue Gene : A vision for protein science petaflop supercomputer" [protfold] is an indication of the computations required to identify a protein structure involving minimum number of atoms.

"The computational effort required to study protein folding is enormous. Using crude workload estimates for a petaflop/second capacity machine leads to an estimate of three years to simulate 100 microseconds.

Physical Time for Simulation : 10^{-4} seconds
Typical time step size : 10^{-15} seconds
Number of MD time steps : 10^{11}
Atoms in a typical protein and water simulation : 32000
Approximate number of interactions in force calculations : 10^9
Machine instructions per force calculation : 1000

Total number of machine instructions : 10^{23}". [protfold]

However, initiatives on application of Supercomputers for modeling the complex brain regions has not been much. Some initiatives has been taken by IBM to develop fastest super computers for tackling the complexity of brain modeling. In the subsequent sections we present the memory and the computational complexity of the proposed MMINi-DASS Interconnectivity prediction methodology.

5.1 Memory Complexity

The expression for memory complexity for representing a N neuron interconnectivity is given below.

Memory Complexity of representing N neuron Interconnectivity = $2 \times N^2 + \Sigma_{i=1}^{N}(PrN_i \times Pr_i) + \Sigma_{i=1}^{N}(Bd_i \times Pr_i \times 8) + \Sigma_{i=1}^{N}(Bd_i \times Dnodes_i \times 8) + \Sigma_{i=1}^{N}(PoN_i \times Po_i) + \Sigma_{i=1}^{N}(Bt_i \times Po_i \times 8) + \Sigma_{i=1}^{N}(Bt_i \times Tnodes_i \times 8) + N + \Sigma_{i=1}^{N}Pr_i + \Sigma_{i=1}^{N}(8 + (rc_i \times 8))$

where N = number of neurons, PrN_i = number of pre-synaptic neuron of neuron i, Pr_i = number of pre-synapses of neuron i, Bd_i = number of branches of dendritic trees of neuron i, $Dnodes_i$ = number of nodes in the dendritic tree of neuron i, PoN_i = number of post-synaptic neuron of neuron i, Po = number of post-synapses of neuron i, Bt_i = number of branches in the telodendria of neuron i, $Tnodes_i$ = number of nodes in the telodendria of neuron i, rc_i = number of recurrent collateral in the axon of neuron i.

5.2 Computational Complexity

The computational Complexity of predicting a N neuron Interconnectivity is given below.

Computational Complexity of predicting a N neuron Interconnectivity = $\alpha\beta\gamma\delta\theta$

where

$\alpha = \Sigma_{i=1}^{N}(\Sigma_{s=1}^{s_i}\frac{Bd_i!}{(Bd_i-s)!s!})$,

$\beta = \Sigma_{i=1}^{N}\frac{tot1_i!}{Pr_i!\times(tot1_i-Pr_i)!}(Bd_i\Sigma_{j=0}^{j=m}(Pr_i-j)+(\mathrm{Bd}_i-1)\,\Sigma_{j=m+1}^{2m+1}(Pr_i-j)+...+1(m+m-1+m-2+...+1))))$,

$\gamma = \Sigma_{i=1}^{N}(\Sigma_{s=1}^{s_i}\frac{Bt_i!}{(Bt_i-s)!s!})$,

$\delta = \Sigma_{i=1}^{N}\frac{tot2_i!}{Po_i!\times(tot2_i-Po_i)!}(Bt_i\Sigma_{j=0}^{j=l}(Po_i-j)+(\mathrm{Bt}_i-1)\,\Sigma_{j=l+1}^{2l+1}(Po_i-j)+...+1(l+l-1+l-2+...+1)))$

$\theta = O(N^n)$where n varies from n varies from 1 to 3 depending on the accuracy required.

The notations used in the computational complexity expression is the same as that used for memory complexity. However, $tot1_i$ = $PrN_i \times$Po$_i$ and $tot2_i$ = $PoN_i \times$Pr$_i$, s_i = subset size for scheduling.

The computational complexity for a Million Neuron Interconnectivity prediction is of the order of $O(N^k)$ where N is in Millions while k is a few multiples of 10. Thus the computations required for multi-million neuron interconnectivity prediction is about 10^{200}. By applying certain heuristics (refer section 2.2.1) the order of computations is reduced to $O(N^{\frac{k}{x}})$ where 3≤x≤3.5 depending on the number of heuristics employed. Thus the computations required for multi-million neuron interconnectivity prediction gets reduced to about 10^{60}.

The computational complexity throws a big challenge to the supercomputer and defies the computational power of the existing ones. This leads to 2 major research developments : one, evolution of an architecture for *super-supercomputers* [vaans2003] [ak2003] [as2003] [nk2003] and the other, design of libraries for mapping the MMINi-DASS Interconnectivity prediction methodology on the super-supercomputer. These libraries are for the prediction algorithm (refer section 4.2), Partial and differential equations, MMINi-DASS interconnectivity partitioning algorithm (refer section 4.1.1), sorting and searching algorithms, massive random number generation algorithms, initial MMINi-DASS interconnectivity generation algorithms (refer section 3).

6 Discussion

Some of the parameters like neuron cell body shape, impact of myelin sheath, dendritic tapering, dendritic and telodendria orientations need to be included to predict both the MMINi-DASS Interconnectivity realistically and its structure. However, inclusion of these parameters would increase the computational demand to several petaflop years.

The authors feel that the MMINi-DASS Interconnectivity prediction being fundamental in modeling brain functionality, new avenues of DNA based computing need to be evolved to tackle the awesome computations demanded. *It is our strong feeling that the problem and the solution presented in this paper is bound to open up massive research fronts on developing DNA computing for brain modeling involving neuroscientists, computer scientists, DNAscientists, computer architects and algorithm designers. Further, the prediction methodology presented should help fault simu-*

late the brain regions involving millions of neurons thereby leading to discovery of new medicines for brain diseases.

Instead of correlating the EEG obtained from the MMINi-DASS Interconnectivity and the experimental EEG, fMRI could be adopted. Our initial investigation shows there is a lot of scope for the electrical activities of the predicted MMINi-DASS interconnectivity to be converted to the corresponding Blood Oxygen Level Dependent (BOLD) response. This could be correlated with the experimental BOLD response of the MMINi-DASS interconnectivity of the concerned brain center. This would enable us to predict MMINi-DASS interconnectivity in the deep brain regions.

7 Conclusion

In this paper, an attempt is made to present an approach for predicting a Multi-Million Neuron Interconnection involving soma, axon, dendrites and synapse. Moreover the approach is a partitioned one enabling it to be executed on parallel machines. A simulation model has been developed involving randomized simulated annealing algorithm for MMINi-DASS Interconnectivity prediction. Besides cracking down the intricacies and complexities of the MMINi-DASS Interconnectivity, the identification of this interconnectivity in a particular brain center will be of great importance as a research opening in the field of neuroscience.

The paper clearly brings out the need for this MMINi-DASS Interconnectivity prediction in understanding the information processing, the spatio-temporal activities and learning in various brain regions. This simulation model is expected to be highly helpful in developing fault simulation techniques for modeling brain diseases. The computing power needed for the simulation model is presented and the necessity for, evolving super-supercomputer and investigation on DNA computing paradigm.

"DNA Computing Takes Up the Challenge of Brain Modeling"

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