Journal of Neuroscience Methods 257 (2016) 17–25

Contents lists available at ScienceDirect

Journal of Neuroscience Methods

journal homepage: www.elsevier.com/locate/jneumeth

Computational neuroscience

A fully parallel in time and space algorithm for simulating the electrical activity of a neural tissue

Mathieu Bedez[a,b,c,*], Zakaria Belhachmi[b], Olivier Haeberlé[c], Renaud Greget[a], Saliha Moussaoui[d], Jean-Marie Bouteiller[a,e], Serge Bischoff[a]

[a] Rhenovia Pharma SA, Mulhouse, France
[b] Laboratoire LMIA, EA3993, Université de Haute Alsace, Mulhouse, France
[c] Laboratoire MIPS, EA2332, Université de Haute Alsace, Mulhouse, France
[d] Firalis SAS, Huningue, France
[e] Department of Biomedical Engineering, University of Southern California, Los Angeles, CA, USA

HIGHLIGHTS

- Description of a method coupling parallelization in time and space on the GPU.
- Resolution of a model describing the propagation of the electrical signal in a neural tissue using the parallel algorithm on GPUs.
- Significant reduction in the calculation time to obtain an accurate solution.

ARTICLE INFO

Article history:
Received 29 June 2015
Received in revised form
10 September 2015
Accepted 16 September 2015
Available online 28 September 2015

Keywords:
GPU
Neural activity
Parareal algorithm
MPI
Partial differential equations

ABSTRACT

Background: The resolution of a model describing the electrical activity of neural tissue and its propagation within this tissue is highly consuming in term of computing time and requires strong computing power to achieve good results.
New method: In this study, we present a method to solve a model describing the electrical propagation in neuronal tissue, using parareal algorithm, coupling with parallelization space using CUDA in graphical processing unit (GPU).
Results: We applied the method of resolution to different dimensions of the geometry of our model (1-D, 2-D and 3-D). The GPU results are compared with simulations from a multi-core processor cluster, using message-passing interface (MPI), where the spatial scale was parallelized in order to reach a comparable calculation time than that of the presented method using GPU. A gain of a factor 100 in term of computational time between sequential results and those obtained using the GPU has been obtained, in the case of 3-D geometry. Given the structure of the GPU, this factor increases according to the fineness of the geometry used in the computation.
Comparison with existing method(s): To the best of our knowledge, it is the first time such a method is used, even in the case of neuroscience.
Conclusion: Parallelization time coupled with GPU parallelization space allows for drastically reducing computational time with a fine resolution of the model describing the propagation of the electrical signal in a neuronal tissue.

1. Introduction

Brain activity results from electro-chemical reactions leading to the creation of an electric field propagating in all areas of the brain, as well as in the cranium. This electrical field, called electroencephalogram (EEG), can be measured by placing electrodes at specific locations of the skull. The EEG is used as potential biomarker in the diagnosis of some central nervous system diseases (CNS), such as epilepsy.

The main purpose of simulating EEG is to provide a better understanding of the connection between this global electrophysiological signal and the electrophysiological activity of subgroups of brain cells under physiological and/or pathological conditions.

* Corresponding author at: Rhenovia Pharma, 20C Rue de Chemnitz, Mulhouse, France. Tel.: +33 674403058.
E-mail address: bedez.mathieu@gmail.com (M. Bedez).

http://dx.doi.org/10.1016/j.jneumeth.2015.09.017
0165-0270/

This electrical activity can be modeled using the bidomain model, now widely used in the simulation of the electrical signal during the heart activity, which constitutes the electrocardiogram. This model was introduced for the first time in the 1970s (Schmitt, 1969; Tung, 1978).

Determining an analytical solution of this model, described via partial differential equations (PDEs), is not possible because the highly complex geometry. The digital resolution requests some simplifications in order to obtain a usable result within a reasonable computation time. These sacrifices are made, depending on the choice of the model, the precision of the mesh in time and space, or by fixing the problem within a portion of the definition of space. To avoid making concessions on the results' accuracy, specific tools, which enable massively parallel computing, may be useful, distributing equitably the involved work, and thus reducing the computation time, while at the same time increasing the quality of results.

In this study, we present a fully parallelization technique in time and space, and apply it to the monodomain model case (Keener and Sneyd, 2009), which constitutes a simplification of the bidomain model. This method will help us to determine the results quickly, and with an acceptable resolution in time and space. With this method, it is possible to run longer simulations within reasonable computation time, and also to perform simulations using very fine discretization grids, both in space and time. All this is not applicable in sequential methods, because calculation time would become excessively large. We used GPU computation, an approach already used in neuroscience: in 2013, Hoang has developed a CPU/GPU simulation environment for large-scale biological networks: NeoCortical Simulator. The possibility of simulating spiking neural networks on one or several GPUs was investigated by developers (Igarashi et al., 2011; Wang et al., 2011; Brette and Goodman, 2012). The use of GPUs yielded significant improvements compared to CPUs (Baladron et al., 2012). Such implementations perform a parallelization at the neuron model level, whereas our study aims at performing a parallelization of the solving methods, at the global problem level. We performed several simulations to validate the different algorithms and the computational setups.

2. Material and methods

2.1. Bidomain model

As for the cardiac tissue, the neuronal tissue, defined by the domain B (see Fig. 1), can be modeled by decomposition into three distinct domains: the cells, called intracellular domain, the extracellular domain representing the outside of the cells, and the cellular membrane separating them. Each zone has an intracellular, an extracellular and a membrane potential (ϕ_i, ϕ_e and V_m, respectively) and the voltage across the membrane is defined by their difference:

$$V_m = \phi_i - \phi_e \tag{1}$$

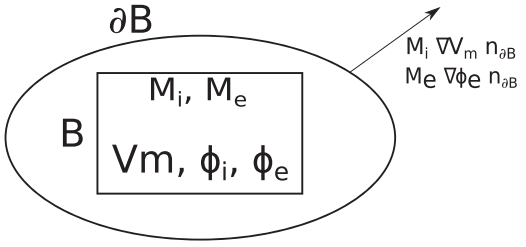

Fig. 1. Definition set of bidomain model.

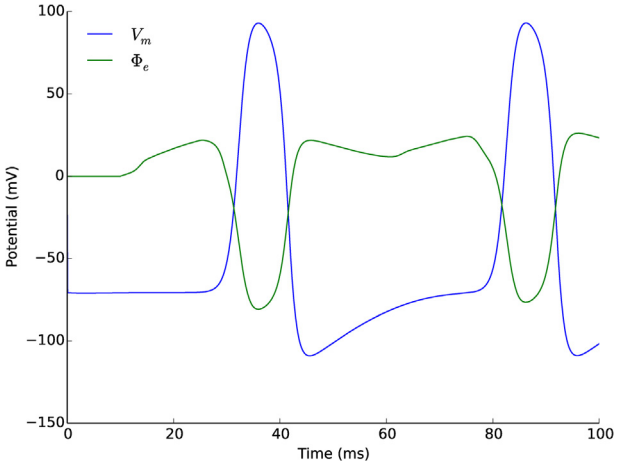

Fig. 2. Membrane (V_m) and extracellular (ϕ_e) potential after bidomain simulation.

The intracellular, extracellular and membrane potentials are functions defined in B by

$$\phi_i, \phi_e, V_m : B \to \mathbb{R}$$

In the absence of any stimulus, all cells remain in resting state, ranging between −60 and −70 mV. When a cell is excited, a depolarization phase is initiated reaching a threshold value. At a given potential, sodium channels close spontaneously, terminating the depolarization phase. At the same time, potassium channels open, causing repolarization of the plasma membrane. Then the potassium channel closure period causes a transient hyperpolarization (or relative refractory period) of the membrane potential and reach its resting potential.

Cell behavior has been described using models formulated from ordinary differential equations (see Section 2.3). Fig. 2 shows the variations of ϕ_e and V_m to a position over time.

The bidomain model might be used to describe the propagation of electrical signals along an axon, but also in the cells surrounding space. This model consists in two different types of equations: an evolution equation and an elliptic equation that describes the evolution of three potentials over time. Using a neuron model, and an appropriate conductivity tensor, these formulas can also be applied to neuronal tissue.

Throughout this research, the following assumption was made: in the intracellular and extracellular regions, current flow is resistive, resulting in a proportional relationship between the current density J and the potential gradient ϕ (Fick's law), where the matrix M is the conductivity tensor:

$$J = M\nabla\phi. \tag{2}$$

According to the current conservation law, the outflow from a domain must be equal to the inflow into the surrounding areas, which is described by the following equation:

$$\nabla \cdot J_i = -\nabla \cdot J_e. \tag{3}$$

The membrane current I_m is defined with respect to the flow of the potential, by combining Eqs. (2) and (3):

$$I_m = -M_i\nabla\phi_i \cdot n_i = M_e\nabla\phi_e \cdot n_i \tag{4}$$

where M_i and M_e are conductivity tensors representing the intracellular and extracellular area, respectively, and n_i is the unit outward normal vector of the intracellular domain.

The behavior of the membrane is both resistive and capacitive. The perceived capacitive behavior of the membrane is due to an insulating bilipidic layer that separates the extra-cellular environment from the intra-cellular medium. The resistive part