

# REALTIME NEOCORTICAL COLUMN VISUALIZATION

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**Abstract:** This paper presents a method for real-time rendering of a neocortical column in the mouse brain with 10000 individually simulated neurons, as implemented in the software GabrielStudio (TM). It also presents how the same system is used to create movie sequences of scripted camera keyframes for high resolution outputs. The current system is running on an SGI Altix Prism Extreme with 16 parallel graphics cards and a shared memory of 300 GB. Gabrielstudio works as a virtual microscope for computational neuroscientists to analyze their simulations of neurons.

## 1 INTRODUCTION

In the field of computational neuroscience simulations of neurons arranged in circuits like the neocortex in the rat brain, are quite complex in the amount of data that is created for each simulation step. The simulation computes the electrical membrane potential of the neurons, at a detail level of each individual branch in its morphology (Carnevale and Hines, 2006). A typical neuron morphology consists of a spherical soma of 20 micro meters (see Figure 1), a tubular axon and tubular dendrites which in turn can be branched down to very fine segments of tissue and usually contribute 300 sections (Al-Kofahi et al., 2002), (Can et al., 1999), (Kuss et al., 2007). Each of these three basic morphological parts are also sub-partitioned into electrical compartments, which on average are five per section depending on the length of the section. In order to analyze the fully detailed simulation at electrical compartment level on average 10000 neurons, times 300 sections, times five data points are inspected, which is 15 million data points in total per 10 millisecond simulation step. One real second of activity in the brain is quantized into steps of 10 milliseconds, so that there are 100 steps per real second of activity. Each such step can take minutes to compute even on an IBM Blue Gene (TM) super computer (BlueBrain, 2007).

Analyzing 15 million data points individually per time step is not reasonable, to simplify this, computational neuroscientists generally only have a look at

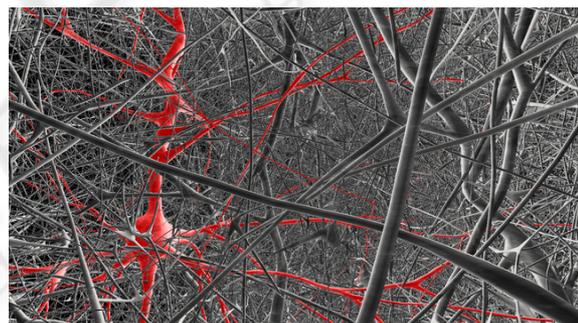


Figure 1: One neuron is highlighted as red in the column.

the membrane potential at the soma level of the neurons. If a normal color map view is used (see Figure 2) the scientist analyzes the data where each column of data is one time step and each row is the voltage value for the soma of that neuron. In visualization terms the flat 2D view, maps data from four dimensions into two dimensions since the original neuronal data is in three physical dimensions (position) and one time dimension (the time step). Data loss is inevitable if one data point is supposed to represent on average 1500 points. One can argue that only the somas are important in neuronal research. As simulations get more complex and include dendrite and synapse details, debugging the simulation itself becomes next to impossible, if one cannot access all levels of importance (Westerhoff, 2003).

Using a 3D real-time view the user can explore the circuit without any simulation knowledge neces-

sary in the viewer itself. As an operator of this virtual microscope it is possible to stand in all positions and view the neocortical circuit from any angle or perspective. The amount of information is as overwhelming as before (15 million data points) but it is rendered in the positions where it belongs, so that electrical potentials for axons innervating nearby dendrites are close and visually connected. In this virtual microscope it is also possible to do virtual clamping in the full circuit enabling the user to follow and record the electrical history for a specific clamping point.

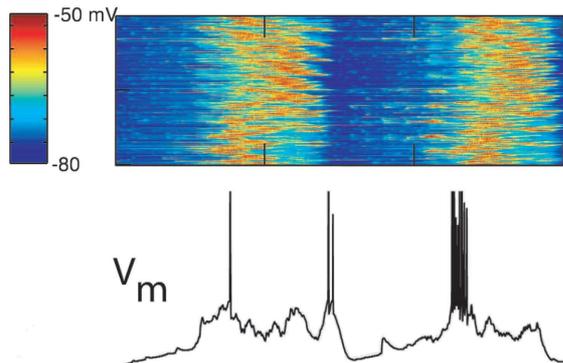


Figure 2: Each column is a time step and each row is the membrane potentials for the soma of one neuron. (Hill and TONI, 2004).

The software library capable of rendering the neocortical column is called GabrielStudio. It is generic in terms of visualization for different areas of computational biology, and is the basis of the virtual microscope. Since this software is commercial only an older version of the software and the underlying algorithms are presented here, as the newest version is confidential. Nevertheless the authors are sharing some of the design decisions, rendering optimizations, adaptations to the SGI multi-pipe toolkit (MPK) and general interface decisions. The rendering engine is based on a target centric design where a target can be a set of neurons represented as triangle meshes, lines, segments (Melek et al., 2006), (Stoll et al., 2005) or soma billboards (Tarini et al., 2006), (Holm et al., 2005). Individual neurons can at all times be visible, invisible, colored independently and have simulation applied to them or not. The system is described in more detail in the following sections of the paper.

## 2 GABRIELSTUDIO

The rendering engine is based on the notion of targets where the total possible neurons to render is a set called the universe target. Each neuron has morphol-

ogy which is a hierarchical description of a neuron in a directed acyclic graph manner (DAG), see Section 2.2.1. Several neurons share the same morphology where a circuit of 10 000 neurons usually contains 700 different morphologies of 100 000 or more triangles. To visualize the column using a brute force rendering method, a total of one billion triangles per frame would have to be rendered. Given that a normal graphics card of 2007 can render 25 million triangles per second, this would take 40 seconds to render. Since the system is real-time an acceptable speed is 25 updates per second, which is 1000 times faster than one update every 40 seconds. Using the multiple pipes of an SGI Prism Extreme one can leverage this speed ten times, which gives us having to speed up the brute force method by a factor of 100. A factor of ten is always welcome. The solution proposed in this paper is the use of a regular grid, which is common in ray tracing and is a voxelization process on the triangle data.

### 2.1 Rendering Pipeline

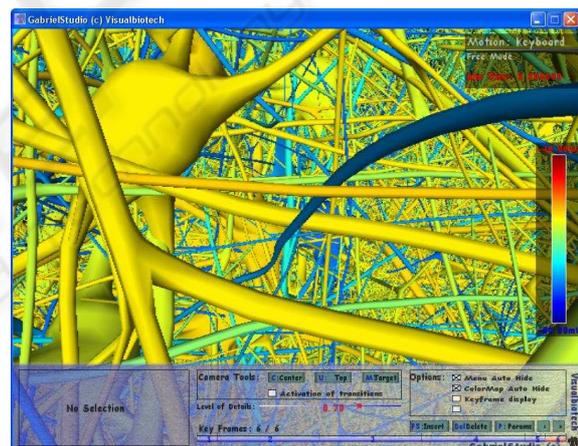


Figure 3: Action potential on neurons in the exploratory mode of GabrielStudio.

The neurons are inserted one by one, triangle by triangle, into the grid so that each grid cell contains a list of pointers to triangle data (3 vertices, uvs, normals and simulation information). Then the cells are re-allocated so that each cell contains an offset into a large continuous array of geometrical data. Depending on which neurons are part of the visible targets and level of detail (LOD), the index tables of the cell are appropriately called. Each cell has three LODs for each representation which is either triangle or mesh surface, diameter thick segments and one pixel wide lines. Two independent modes are rendered separately namely, the soma view using billboarded spheres and the synaptic view also using bill-

boards. The synapses are rendered connected to the hierarchy of the lines or branches that are visible.

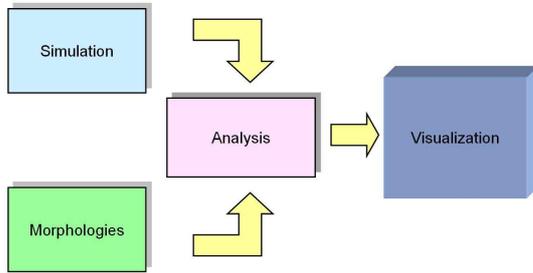


Figure 4: The visualization pipeline.

## 2.2 Regular Grid

The world of computer graphics consists mainly in tradeoffs between complexity and performance: level of detail (LOD) is a method offering such compromises and is explained in detail in the book (Luebke et al., 2002). Several examples of usage of this technique can also be seen in the papers (Gumhold et al., 2003) and (Schauffer and Stürzlinger, 1995) and Section 4 of this paper.

LODs are used to group branches in a priority order, going from always visible (LOD 0) to less important branches (LOD 2). Those LODs are computed when the neuron data is integrated into the regular grid with the help of a recursive algorithm which will be discussed later. This computation need to be done once, in an initialization phase at the launching of the program. During this phase, each neuron is inserted into the grid and its branches are distributed among the buffers of each LOD. Before going more in depth into the procedure, it is necessary to recall how a neuron is defined. It contains one root, from which several branches reach out, that in turn can be sub-branched. They are organized in sections which allow representing the whole hierarchy of the neuron easily. More precisely, those sections indicate the linkage of each node going from the root to the extremities.

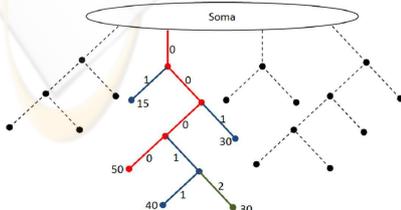


Figure 5: Neuron morphology branching numbering. Notice how at each branching only one section keeps the father number.

### 2.2.1 Insertion Into Lods

The insertion into LOD buffers is done according to a certain branch priority. The branching computation is done for each neuron morphology independently. It is made by going through each existing branch of a neuron, using the corresponding section map, and then attributing an index to each segment corresponding to the actual priority of its branch. To define this priority, a recursive algorithm is used, which looks at the depth of each branching and gives higher priorities to the longer ones. For a better understanding of this, it is possible to represent this scheme as a tree, where the nodes represent the splitting points between two branches taking as value the actual distance from the root (the neuron soma). Assuming the aim of the algorithm is to compute the sorting of one of the branches starting from the root; the path with the highest priority is going from the root to the extremity children with the largest distance; denoted as the longest branch of the tree (see Figure 5). Once this main branch is known, it starts from the root and goes through all the nodes of the tree. At intersection  $i$  (node  $i$ ) it keeps the current priority for the longest branch of the sub-tree with node  $i$  as root and the other branch gets this priority increased by 1. Like that we will have branching index from 0 to a maximum of 255 (fixed limit). From those indices we can enter each vertices inside the corresponding LOD array respecting some ranges defined by the user (e.g. Lod-0: 0,1 / Lod-1: 2,3 / Lod-2: 4,...,255). Then each branch of a neuron will be rendered or not by comparing its LOD with the current LOD of the cell. In a similar manner synapses also need to be rendered conditionally to the LOD level.

### 2.2.2 Usage of the Lods

Employing a LOD system, allows splitting the rendering into several levels of detail yielding better performance. Those levels are defined by cells accordingly to the distance to the camera position, such that the closer cell to the viewer the better its definition is.

### 2.2.3 Update Function

Another particularity regarding the implementation of the regular grid is the use of an update target function which allows to have a per branch visibility capacity and a per cell representation mode. Each time a neuron state is changed (visibility or representation), the data is checked once and the right indices of the visible neurons are entered into the grid. The line buffer and the mesh buffer are used depending on the current cell representation. Since drawing is done using

arrays, it allows having the correct indices always directly for the rendering phase reducing the real-time computational expense.

### 2.3 Stylized Rendering

The implementation seen in the last section allows the use of different data representations. This is a necessary functionality since sometimes it is preferable to have a more simple representation using less details for a better global view. This is possible with the use of billboarding techniques which allows rendering neurons as spheres (using quadrilaterals always in front of the camera, see Figure 6) and more somas are visible since no extra branches are occluding each other.

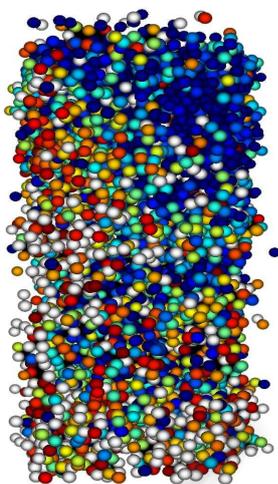


Figure 6: GabrielStudio also renders using billboards of somas.

### 2.4 User Interface

In order to interact dynamically with the rendering, a user interface was created. It offers several possibilities from camera centering to key frame editing. A lot of useful options are given to the user and allows having a good feeling about what is happening on the screen. There is an indication about the current selection, neuron or synapse and the simulation color mapping allowing to distinguish the current electrical value of each entity as well as the number of key frames kept for the movie creation, as depicted in Figure 9.

### 2.5 Scalable Rendering Architecture

The major difference between rendering on a single graphics card architecture available on most PCs and

a parallel graphics pipeline, as the SGI Prism, is that several graphics contexts need to be tracked and updated simultaneously. Since the library uses GLEW to handle OpenGL extensions, it also keeps a separate MX GLEW context per graphics card. However recompiling such a library including a multi-pipe version of a helper library is not sufficient. This comes as the result that each function in the rendering engine that uses shaders, textures, vertex buffer objects, display lists or any other context specific data has a special structure sent to it containing the necessary data for that context. Each graphics card is assigned this context upon entry into that threads rendering loop.

## 3 CREATING MOVIES

Science needs to reach out and touch more interested minds through marketing, which is possible to do through the movie creation pipeline of GabrielStudio. Using such a software tool the user has the possibility to navigate through the scene, using the virtual microscope view and sample the interesting locations. A set of sampled view points or camera key frames are interpolated and rendered using a non-interactive mode for high resolution and detail as shown in Figure 7. Standard digital movie production pipelines are used for editing. In the off-line mode it is also possible to output stereo images for passive stereo outputs as displayed in Figure 1. These movies are shown to various visitors of our clients projects to give them a better picture of what neuroscience entails and reveal some of its mysteries. Movies are also shown at conferences for scientific discourses and presentations. It is also possible to do individual snapshots in high resolution for posters that require greater details.

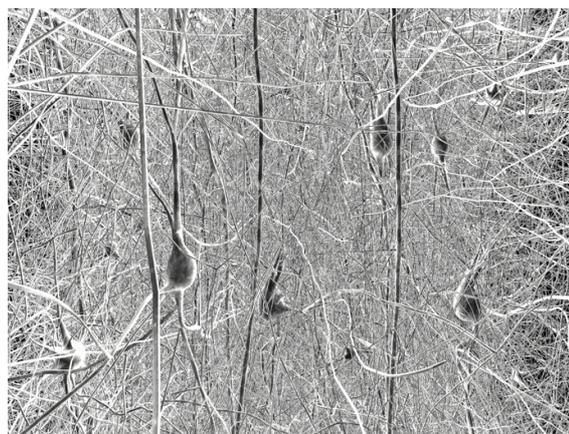


Figure 7: From a stereo flythrough sequence of the dendritic forest. The effect of having to dodge parts of neurons coming out of the screen is quite dramatic.

## 4 RESULTS

Rendering the neurons on a SGI Prism Extreme with 16 graphics cards, gives acceptable update rates of 15 frames per second with 5000 neurons in view. The viewer can observe the neurons from a distance or a closer range, while having the details preserved thanks to the employed LOD system.

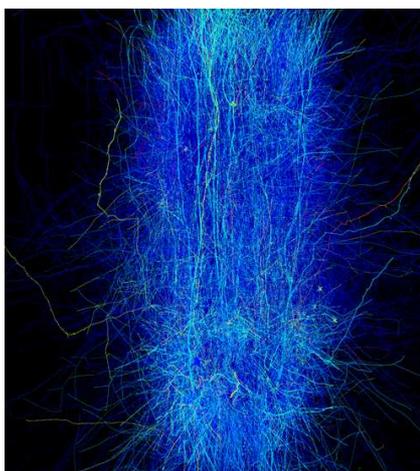


Figure 8: Simulation mapping applied.

When using the regular grid one must cope with some additional requirements. A typical example is the case when the viewer is far away from the column, such that the cells being just in front of the camera are rendered with a high level of detail i.e. all LODs are displayed. Those being near to the center of the column are represented using a lower definition, and some of the branches belonging to the LOD-2 are displayed in the front cells and not in the back ones. Since the branches appear not to be linked, the user gets a strange impression about the scene. One possible solution to such cases is to check for each branch whether one of its parts is drawn; if this is the case, this branch is rendered in each visible cell. In order to achieve such an implementation, a regular grid should be somehow replaced, since using the conditional tests increases the computational cost. Otherwise utilizing a regular grid leads to satisfying results even when employing the update target function since it is done only once per update and not per frame, at the rate of user interactions.

## 5 CONCLUSIONS

In this paper the software tool for real-time visualization of neurons has been presented. Acceptable rendering speeds are attained on large shared memory

machines, where geometry duplication is not a limiting factor due to 300 GB memory banks. However, this is not useful on ordinary PCs, which is the next challenge for the authors. Using a regular grid gives a memory bound problem that is comfortable to render on a parallel rendering architecture. The movie mode of the described software GabrielStudio allows movie creation with ease. Finally the possibility of interacting and exploring the data in real-time, offers new perspectives to neuroscientists to observe their own simulations. Besides being a powerful tool for neurological process monitoring, the proposed software has additional applications for marketing purposes.

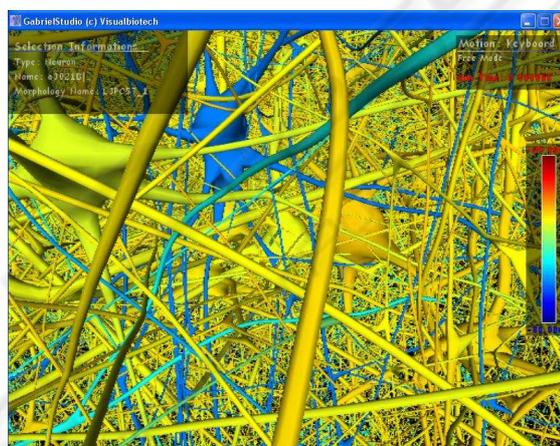


Figure 9: Selecting neurons in GabrielStudio.

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