Balthazar3D - A Simulation Invariant Geometrical Neuron Data Format

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Keywords: computer graphics, visualization, computational biology, neuroinformatics

Abstract: This paper presents a method for formatting three dimensional geometrical neuron and similar biological hierarchical representations. The format ensures that varying detail simulations of electrical surface potentionals, can be mapped and re-mapped on-line and displayed in real-time. Annotating each vertex with a normalized relative distance and a simulation section identifier, is the solution presented here.

1 INTRODUCTION

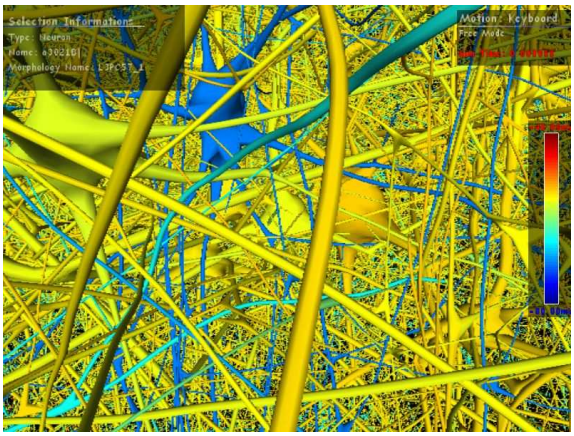

Figure 1: Selecting a neuron in GabrielStudio. Raw neuron data courtesy the Blue Brain Project. Copyright Visualbiotech 2006-2008, all rights reserved.

The hierarchical Balthazar3D biology format is part of the GabrielStudio and BioInspire software and was used already in the Blue Brain Project (Project, 2008) as a client of Visualbiotech starting in 2006. It is a file format storing morphological data about blood cells, dendritic lymphatic cells, neurons, protein, viruses, blood vessels and simulations thereof. A morphology is a shape description of a biological primitive, containing surface parameters, scale, behaviors and deformations and is necessary for visualization and interaction. In this white paper only neuronal meshes and surface potential simulations will be discussed. The source data for the neurons comes from microscope image stacks and (Al-Kofahi et al., 2002) describes this process, while it is assumed in this paper that the reconstruction (see (Westerhoff, 2003)) is already done. In Figure 1 you can see a screenshot from the analyst operating view of GabrielStudio, where the electrical potential of the surface is encoded with a color. A lower voltage of -80 mV is blue and red indicates -40 mV and these colors can be arbitrarily chosen. A deeper look into the rendering pipeline and the design decision of GabrielStudio in one if its earliest versions can be found in (de Heras Ciechomski and Mange, 2008). The user can load different kinds of simulations, computed for example by the NEURON system (Carnevale and Hines, 2006), to better understand and interpret the behavior and characteristics of the neurons and their relations. Since different precision simulations are used the mesh format must be flexible and independent of the simulations.

2 SURFACE COLORING

A neuron morphology is a tree structure starting in the soma body, which in the Balthazar3D format, is

also the first section with an index of zero. The morphology is branching into subsections and sub subsection and can be described as a directed acyclic graph (DAG), since branches are hierarchical and do not form loops. To have a three dimensional rendering of neurons, as seen in Figure 1 the surface of each morphology is triangulated. The surface of the morphology is continuous and has no holes, creating seamless transitions between branching sections of the neuron. Each triangle on this surface is linked to three vertices and in Figure 2 you can see a schematic of how the triangles stitch together.

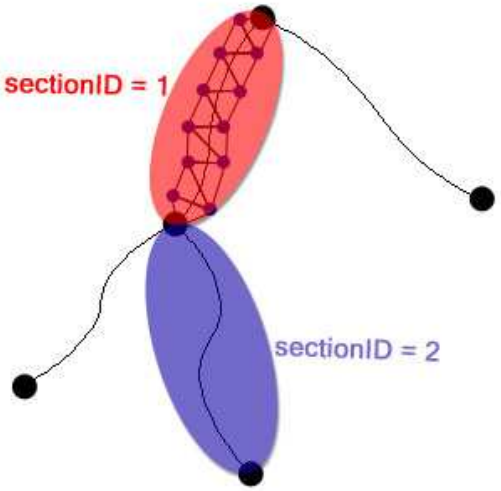

Figure 2: A neuron morphology is decomposed into sections with an increasing sectionID parameter. Copyright Visualbiotech 2006-2008, all rights reserved.

A simulation at a certain time step can be a single section value for the soma, a single simulation value for each section or a variable number of point samples along the interior of each section. Coloring the neuron surface depends on the colors in the individual vertices. The Balthazar3D format annotates each vertex in the mesh with a section identifier (sectionID, with a two byte value between 0 and number of sections-1) and a relative distance (relativeDist, with a normalized byte value of 0 to 255), as can be seen in Figure 3. The relative distance value is a geodisic distance along the central axis of the section (see Figure4) and is normalized so as to map to arbitrary number of simulation points. A geodesic distance differs from an Euclidean, in that it takes the path that the vertex has to walk into account, instead of just the direct distance to the starting point of the section. To calculate which potential to use, sectionID defines the section offset and relativeDist is multiplied with the number of points in the section. Using the electrical potential value a color is computed by a look up table (LUT) of 256 entries ranging from the minimum electrical potential to the maximum potential. Smoothly interpolating the vertex colors along the triangle surfaces results in a nice layout as in Figure 1.

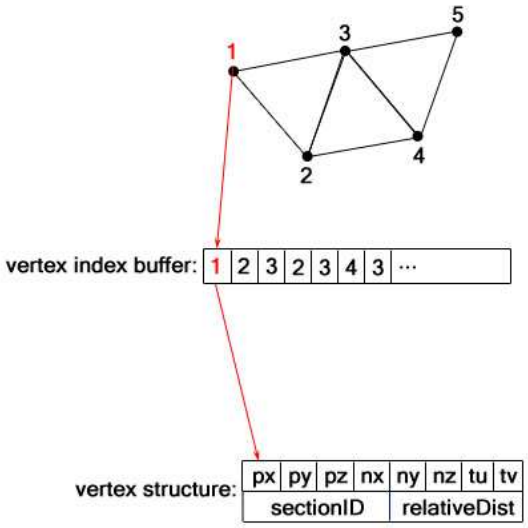

Figure 3: Each triangle indexes three vertices, which in turn consist of positional data (p), surface normal (n), texture coordinates (t), section identifier and relative distance. Copyright Visualbiotech 2006-2008, all rights reserved.

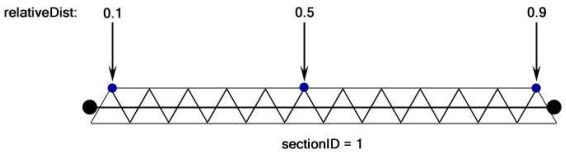

Figure 4: Each vertex inside a section has a relative distance from the start of the section. Copyright Visualbiotech 2006-2008, all rights reserved.

3 MAPPING AND REMAPPING SIMULATIONS

When a simulation is loaded GabrielStudio computes a temporary acceleration structure using the relative distance and the section identifier. The structure holds the offset memory addresses to the simulated electrical potentials for each vertex. Each vertex thus knows its precise offset into the simulation data buffer without having to compute the location on each update.

When a new simulation is loaded the acceleration structure is re-evaluated.

4 RESULTS

This simple dual data structure, with a pre-computed per vertex relative distance and section identifier and its on-line temporary offset address counterpart, is easy to implement and maintain. It has been used commercially since November 2006 in GabrielStudio and its successor BioInspire and did not yet change.

Calculating the geodesic distance of vertices is straightforward, by projecting the vertex onto the section line description, finding the intersection point and walking backwards to the start of the section along the medial axis.

5 CONCLUSION

The properties of the hierarchical biology Balthazar3D format are indeed efficiency and simplicity. A pre-computed relative distance factor in each geometrical representation, ensures a mapping of different simulation streams without a costly re-computation or re-loading.

ACKNOWLEDGEMENTS

Professor Henry Markram of the Blue Brain Project. Blue Brain Project for data. Sebastien Lasserre for the morphologies built in Maya and for his zen attitude.

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