Interactive 3D Gene Expression Viewer

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Abstract

Gene expression can be visualized in three dimensions using volume data generated through confocal microscopy. The Interactive Gene Expression viewer provides a way to view spatial relationships between different gene expression patterns and anatomic features. Web based 3D enabled technologies such as the Interactive Gene Expression viewer help to facilitate the analysis of 3D gene expression patterns and the creation of bioinformatics databases that can use this data to predict gene interaction and function.

Keywords: gene expression, scientific visualization, volume data, surface reconstruction

1 Introduction

The Interactive 3D Gene Expression Viewer manipulates surface reconstructions of volume data, allowing a user to interactively rotate and move their viewpoint or the model using our specially tailored interface. Most surface reconstructions (or models) are separated into several objects. Some surface reconstructions contain two channels of information. Currently, all models in our collection have been obtained through confocal microscopy or micro CT scans. Our 3D Gene Expression Viewer utilizes the Java 1.1 compliant IDX3D API [Walser 2000] to create 3D projections of surface models. Since, all projections are created through software rendering the viewer maintains usability across many different computing platforms and only requires a JAVA enabled web browser. Current revisions to the Interactive 3D Gene Expression Viewer are maintained at http://cbrbio.ucalgary.ca/3Dmodels/.

2 Exposition

The interface for the Interactive 3D Gene Expression Viewer was designed to allow data stored on separate channels to be easily adjusted by channel association or independently. Currently, the viewer allows for individual objects, which compose the overall model, to have independent color, opacity, and wire frame attributes. Channel modification supports opacity and visibility. Color and opacity are controlled by user adjustable sliders. The viewer application tracks the last object the user selected, and in this manner users can adjust the appearance and presence of an object in the scene by adjusting the sliders, buttons, and checkboxes listed under the model name.

Distances can be measured between the minutest of surface definitions by activating the interaction type to "measure" in the provided list box, then dragging the cursor between the two desired points. Each end point is highlighted and a solid line depicting the measured region is displayed, along with the calculated distance.

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In "manipulate" mode the viewer can rotate and move the scene or objects by clicking and dragging in the model view port. Rotation occurs when the navigation list box is set to rotation, and the user clicks and drags in the desired direction of rotation. Likewise, the user can control positioning with the move setting in the navigation list box. Positional information towards and away from the user is controlled through the arc "zoom" slider. By clicking and dragging on the "Arc" zoom slider in a vertical motion the user can increase and decrease positional increments towards or away from the user.

Within the navigation feature a targeting mode exists. The targeting list box determines whether the viewpoint or the currently selected element will be manipulated through navigation interactions. The element setting for targeting allows the user to alter how elements are assembled in data sets.

Typing in the desired data set filename into the text field provided can access 3D data sets stored on the web server. Clicking on the "load file" or "merge file" button allows the user to either completely replace or merge the currently viewed data set with another data set.

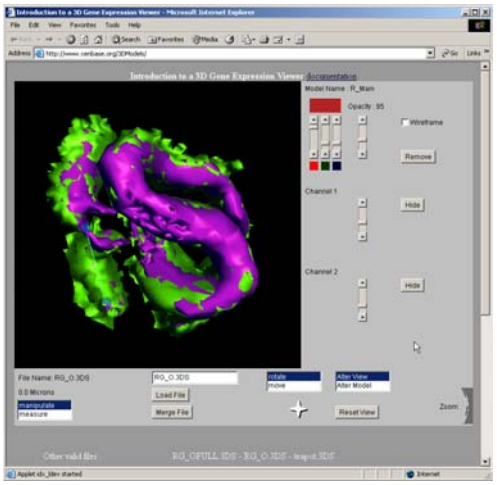

Figure 1. The Interactive 3D Gene Expression Viewer.

3 Conclusion

By providing an interface for visualizing and comparing 3D structures relating to gene expression and anatomy, the Internet based nature of the 3D Gene Expression Viewer allows a network friendly method for visualizing 3D anatomical and gene expression databases. Ultimately our tool addresses the need for a manner of sharing and comparing spatial relations existing within developing organisms.

References

WALSER, PETER . http://www.idx3d.ch/idx3d/idx3d.html