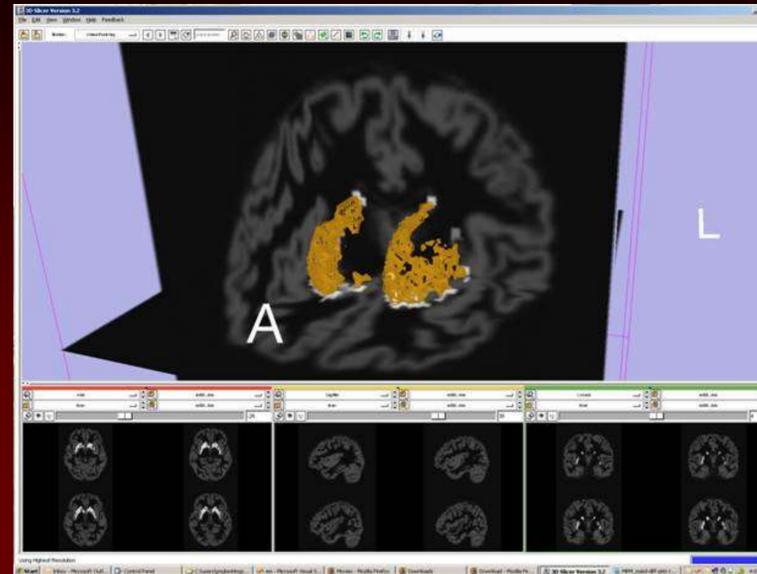


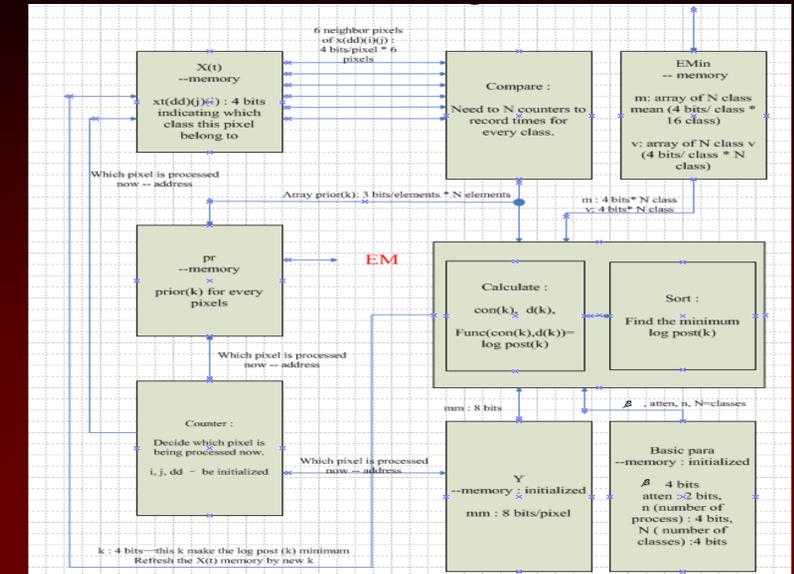
Abstract

Medical imaging technology is a valuable asset for healthcare providers in diagnosis and treatment of patients. Segmentation algorithms are key to visualization of volume and time data, and can estimate signals in the presence of random noise, as in PET brain activation images. The goals of this study are to analyze and improve the performance of the EM/MPM iterative segmentation algorithm in both software and hardware, and to improve the brain PET visualization. To improve the interface for the algorithm a graphical user interface was designed. To assess the software algorithm speed we first tested multiple platforms, processors and memory configurations. Samples of one hundred images or "slices", with a size of approximately 300 KB each, were input to the single-threaded algorithm. The fastest program completion was 2 hours on a 2GHz Intel quad-core personal computer. A parallel or multithreaded algorithm can take advantage of multiple processor systems and increase the execution speed by greater than 10 times. The algorithm is also designed in VHDL hardware language for use in a Xilinx FPGA and can increase throughput by greater than 100 times (from Master's student work). The test benches in VHDL were written for each block to verify speed improvement. We next apply the algorithm to a new type of functional image, derived from dynamic PET image data, to improve visualization. To do this we use segmentation as a clustering over image volume and peak activation time information. The results are viewed in 3D volume for clustered time data. The data are also shown as a movie, with the PET overlaid on MRI, showing activation over time. A key challenge of combining these data in MATLAB was to format the two image modes with similar arrays and similar scaling.

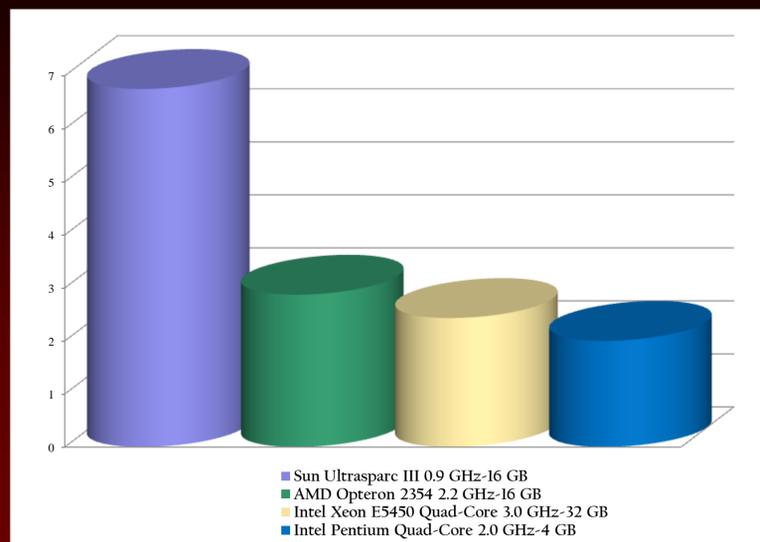
3D Slicer Image



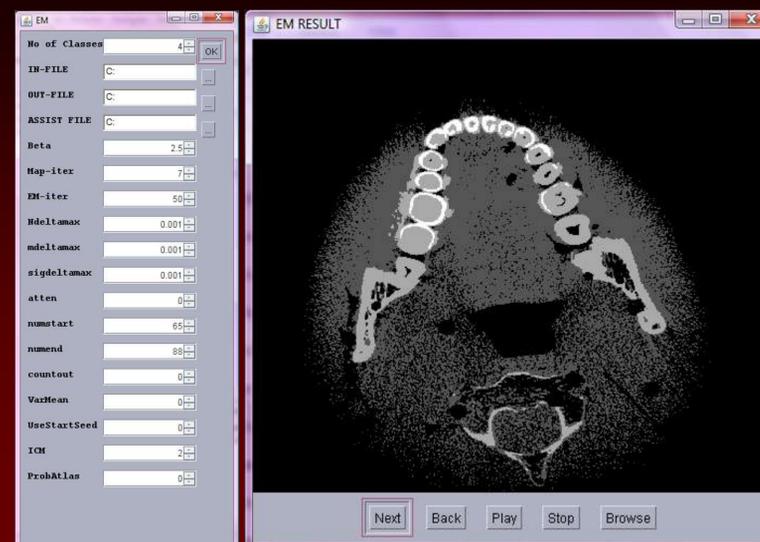
VLSI Block Diagram



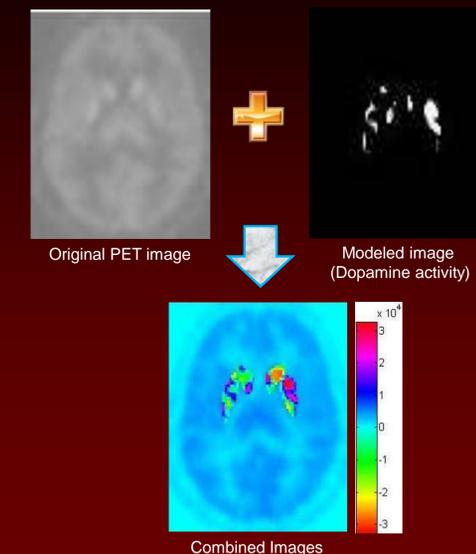
Single-Threaded Algorithm Runtime



Graphical User Interface



PET Visualization



PROBLEM: Give spatial context to derived image.

DATA: PET images were acquired with the tracer $[^{11}\text{C}]\text{raclopride}$. After kinetic modeling, an image of dopamine activity was produced.

PROCESSING: To combine the images they were (i) converted from a struct array to an array using `analyze75reader` in Matlab. (ii) The PET image was scaled much larger than the dopamine PET image. The PET image was multiplied by 19,286 to allow both images to be seen when combined. (iii) Each image (array) was multiplied by .5 and added together. (iv) The HSV color table was applied. The `imshow` command displays the combined image.