SRC-6 Implementation of Contrast Agent Flow and Diffusion Model for Macromolecules in Tumors

David Meixner[1], Nicholas Szrama[2], Michael Aref[2,3,4], Volodymyr Kindratenko[1]
[1]National Center for Supercomputing Applications, UIUC; [2]Department of Nuclear, Plasma, and Radiological Engineering, UIUC
[3]College of Medicine, UIUC; [4]Biomedical Imaging Center, Beckman Institute, UIUC

Introduction

Dynamic contrast-enhanced (DCE) magnetic resonance imaging has the potential for greater diagnostic accuracy using high spatial resolution estimates of contrast agent pharmacokinetics. The heterogeneous microenvironment of the tumor exerts convective and diffusive forces on contrast agent molecules that are hypothesized to be related to histopathologically important features such as neovascularization. To better understand the transport of fluids and macromolecules inside tumors, a mathematical model has been developed and implemented on an SRC-6 reconfigurable computer.

Why SRC-6

- The SRC-6 is conveniently programmed in a C-like language
- The compiler translates the code into hardware description language (HDL) for implementation on an FPGA
- Compile time for debugging is short
- FPGAs provide performance improvement when running pipelined loops
- More efficient use of gates, power, and bandwidth
- Code can also be run on an Intel processor

Results

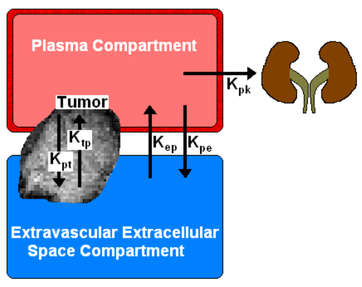
- Frame size of 100×100
- 3000 steps
- Step size of 10^{-5}

	MATLAB	C	SRC-6
Time (sec)	82.21	12.83	2.15

Model

A two compartment model based on the convection-diffusion equation was used to describe the macromolecule kinetics.

A central finite difference scheme was employed to discretize the equations.



$$\frac{\partial\, CA_p}{\partial t} + \vec{\nabla}\bullet\, \vec{v}_i\, CA_p = \vec{\nabla}\bullet\, D_i \vec{\nabla}\, CA_p + \frac{1}{V_p} K_{e\to p}\, CA_e - K_{p\to e}\, CA_p - K_{p\to k}\, CA_p$$

$$\frac{\partial\, CA_e}{\partial t} + \vec{\nabla}\bullet\, \vec{v}_j\, CA_e = \vec{\nabla}\bullet\, D_j \vec{\nabla}\, CA_e + \frac{1}{V_e} K_{p\to e}\, CA_p - K_{e\to p}\, CA_e$$

- $[CA]_i$ is the concentration of the contrast agent in the i^{th} compartment
- v_i is velocity of the contrast agent within the compartment of interest
- D_i is the diffusion coefficient in the i^{th} compartment
- $K_{p\leftrightarrow e}$ is the transfer rate coefficient between the plasma and EES compartments
- V_i is the tumor volume per unit mass in the i^{th} compartment

MATLAB → SRC-6

MATLAB

Rewrite

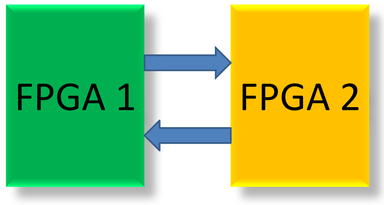
MAP-C

MAP Compiler

HDL

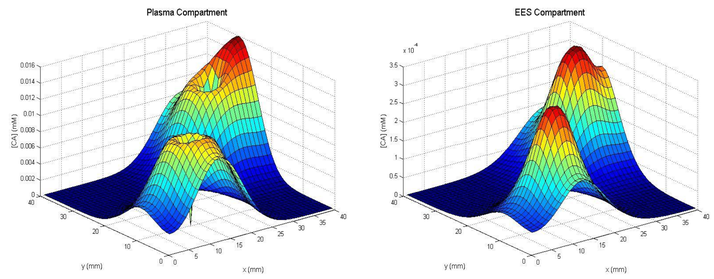
Loop Structure

```
for iterations = 1:steps
   compute boundary conditions at corners
   for x = 1:200
      compute some boundary conditions
      for y = 1:200                    } execute
         compute frames                } on second
      end                              } FPGA
   end
   store results for one out of 100,000 frames
end
```



Figures

Simulation of Contrast Agent Transport in a Simple Two Blood Vessel Isolated Tumor



Conclusions & Future Work

- Use frame size of 256×256
- 300,000,000 steps
- Time step of 10^{-6}
- Only 8 simultaneous read/writes → inner loop takes 4 clocks to complete
- Some of these problems will be solved with SRC-7
- 150 MHz clock vs. 100 MHz clock provides 1.5x speedup
- 16 read/write operations provides 4x speedup
- SRC-7 will also be used on a related parameter extraction problem using a similar model