Computational feasibility of simulating radiation induced changes in vasculature and blood flow rates in the entire human body

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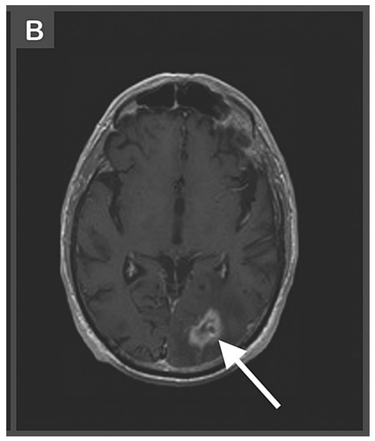
Motivation

Radiation therapy is used widely for the treatment of cancers. However, healthy tissues are often exposed to radiation during treatment, damaging the vasculature and leading to secondary health problems. As the long-term survivability of cancer increases, it is important to understand the systemic effects of the treatments. Radiation-induced blood vessel injury can lead to, for example, white-matter necrosis, atherosclerotic heart disease, or cerebral aneurysms[1]. Computational simulations can be used to analyze the effects of radiation in the vascular system.



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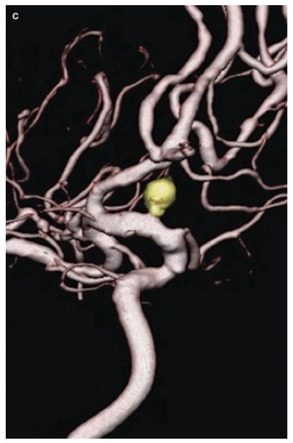


Matsumoto, Hiroaki, et al. "Radiation-induced cerebral aneurysm treated with endovascular coil embolization: A case report." *Interventional Neuroradiology* 20.4 (2014): 448-453.

Introduction

The human body has over 60,000 miles of blood vessels[2]. When analyzing the systemic effects of radiation on the vasculature of the entire body, it is necessary to consider each vessel, the dose it receives, and the blood flow through it. In vivo and epidemiological studies often neglect to analyze blood flow in the pathogenesis of radiation-induced vasculopathy. Recently, several groups have performed computational blood flow simulations. However, these simulations do not include radiation injury, and are often limited in scale[3]. Therefore, the goal of this study is to model the radiation damage and analyze the changes to blood flow in a vascular network the size of the entire human body, approximately 34 billion vessels.

Methods

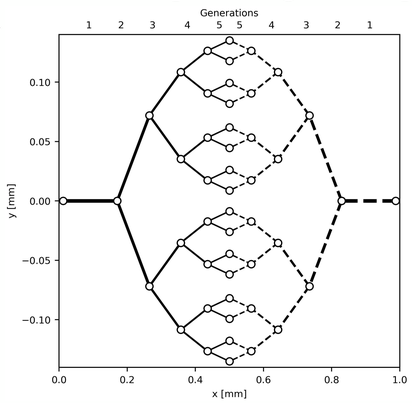
Vascular Geometry

We use a fractal algorithm to create 2 or 3-dimensional vascular networks that are scalable by number of generations (N_G):

$$N_v = 2^{N_G+1} - 2$$

N_v is number of vessels

Vessels are represented by rigid cylinders connected at junctions to form a closed loop. With each succeeding generation, each parent vessel creates two daughters in which the angle of bifurcation, length, and radius are scaled down to anatomical data. The network generates symmetrically comprising of arterial and venous halves, with the smallest levels representing the capillary beds.



Fluid Dynamics

The fluid dynamics follow from assumptions of steady-state, laminar, and fully developed flow. The volumetric flow rate (Q) in each vessel is calculated using a specialized case of the Navier-Stokes equation, known as the Poiseuille equation:

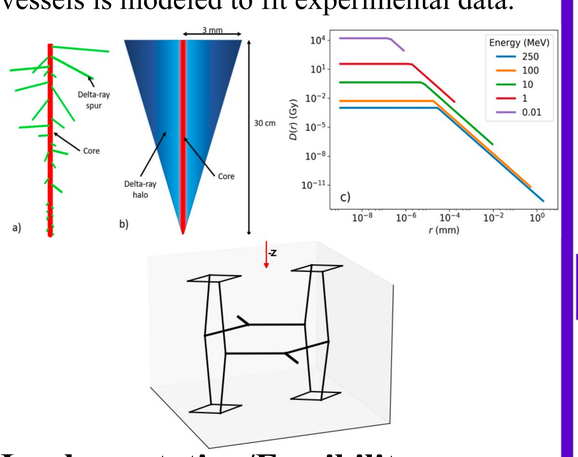
$$Q = \frac{\pi r^4}{8\eta L}(P_{in} - P_{out})$$

L is length, r is radius, η is viscosity, and P_{in} and P_{out} are the pressures at the vessel inlet and outlet, respectively

Because blood is incompressible, the net flow at each junction must be zero. The network can then be cast as system of linear equations, with appropriate anatomical boundary conditions. The system is solved by iterative Krylov methods.

Radiation Transport

We simulate a beam of protons propagating in the –z direction with stochastically sampled starting energy, position and direction. Dose deposition is modeled using an amorphous track-structure model, in which the dose is deposited radially symmetrically from protons and secondary ionized electrons, or δ-rays, with an energy dependent radius. We use a position dependent space-partitioning data structure to determine if a track radius intersects a vessel boundary, then score the dose accordingly. The biological response of vessels is modeled to fit experimental data.



Implementation/Feasibility

We implemented the algorithms in the C++ language. We utilize distributed memory parallelization on HPC clusters. Persistent storage is handled with the Hierarchical Data Format library. To assess the speed of the algorithm, we created networks ranging from 3 to 30 generations. We assessed the strong scaling by calculating the Speedup Factor (S):

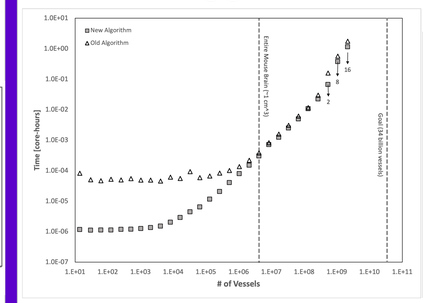
$$S = \frac{T_q}{q \cdot T_n}$$

T_q is execution time for reference number of compute nodes, q, and T_n is execution time for the same task on n compute nodes

The task was to create a 27-generation network. We will be integrating High Performance ParalleX (HPX) C++ library developed by the STE||AR Group.

Preliminary Results

Previous results from our laboratory have shown the computational feasibility of calculating blood flow in 17 billion vessels[4]. We have also shown the feasibility of demonstrating vascular injury from radiation in a network of 9 billion vessels from 2 million protons[5]. We have streamlined the previous algorithm by removing costly processes, thus decreasing execution time and improving scalability, as shown below for vessel network generation and export data. Execution time was improved by an average of 17.12 times, while speedup increased by an average of 58.3%. Further preliminary results are being generated at the CCT's Rostam cluster.



Challenges

1. **Size:** One instance of the vessel class is 80 bytes, meaning the construction of the entire human body requires nearly three terabytes of memory. This can be accomplished on 256 compute nodes with at least 64 GB of memory each.
2. **Anatomy:** To achieve greater anatomical accuracy, we must first include more biophysical mechanisms of blood flow. This includes pulsatile flow, vessel wall elasticity, and fluid momentum at junctions. We must also consider the stochastic geometry of vascular networks and the arrangement of organs in the body. We plan to implement these changes in future works.

References

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