Multiscale Simulation of Blood Flow in the Coronary Arteries

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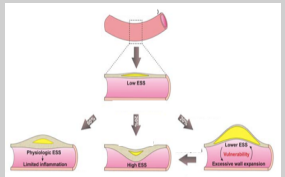
Summary

We present a large-scale simulation of the entire heart-circulation cardiovascular system, with a realistic description of the complex human arterial geometry, from centimeters down to the spatial resolution of red-blood cells. We discuss the scaling of the application to 294,912 cores, thus enabling the simulation of full heartbeats. We present a method for introducing the deformational forces exerted on the arterial flows from the movement of the heart by borrowing concepts from cosmodynamics. These additional forces have a great impact on the endothelial shear stress, a quantity associated with the localization and progression of heart diseases like atherosclerosis.

Cardiovascular Disease



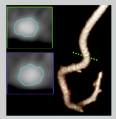
Plaque development in disease prone artery

- Leading cause of death in the Western countries
- 50% of these deaths occur without prior symptoms
- Low endothelial shear stress is a linked to heart disease progression

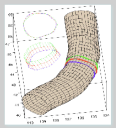
Currently, the only way to assess a patient's shear stress is through simulation

Hemodynamics Pipeline

CT Patient



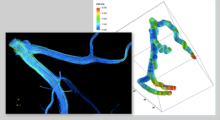
Data Segmentation



HPC Data Preparation

MUPHY

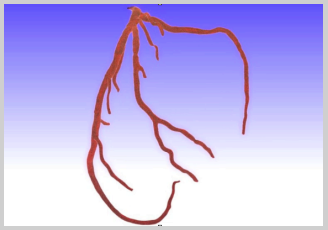
Output visualization



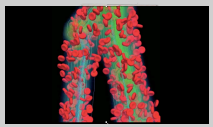
In collaboration with radiologists and cardiologists at the Brigham Women's Hospital in Boston, we retrieve patient specific coronary artery trees from MDCT data at a resolution of .1mm.

Multiscale Model

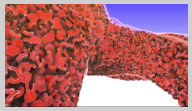
The model used in our multiphysics code, MUPHY, couples a Lattice Boltzmann kinetic representation for the fluid flow and a Molecular Dynamics treatment of the suspended bodies. We use a D3Q19 lattice of discrete velocities in order to recover the physics of the fluid dynamics.



1 billion fluid voxels are used to represent the left coronary tree



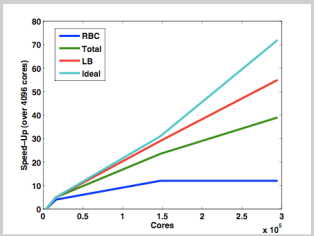
The red blood cells disrupt the fluid movement



300 million red blood cells are modeled

Scalability

In order optimally scale MUPHY, we had to handle the irregular geometries via topology driven graph partitioning for the domain decomposition. Traditional graph partitioning tools, such as *METIS*, cannot handle 294,912 domains to do memory constraints. We used *PT-Scotch* with a pruned graph to overcome memory errors.



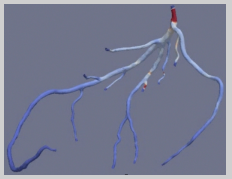
- 1 billion mesh nodes
- 10 million RBCs
- 294,912 domains
- Mesh resolution = 10 μm
- Time resolution:
  - 1μs
  - 10^4 time steps
- 72 racks of Blue Gene/P

Full Heartbeat

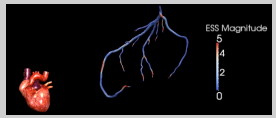
A human heartbeat is approximately .7 seconds and a realistic level of hematocrit would be 45%, or 300 million red blood cells. To model the realistic blood flow in 12 coronary arteries at 10 μm resolution for one heartbeat it took **6 hours** on 40 racks of Blue Gene/P.

Deformational Forces

In modeling multiple heartbeats, the effect of the pulsating heart on the coronary arteries must be taken into account. Concepts from cosmodynamics help estimate the deformational forces exerted on the arterial flows from the movement of the heart and cast them into a kinetic formalism by using a Gauss-Hermite projection procedure. From this we can assess the impact these forces have on the endothelial sheer stress.

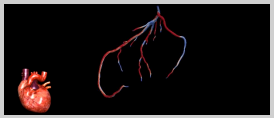


ESS with static geometry



0 seconds

.15 seconds



.35 seconds

Conclusions and Future Work

By successfully scaling to 72 racks of Blue Gene/P, we were able to simulate the cardiovascular flow of unprecedented scale in a geometry from real patient date and with blood flow at physiological hematocrit values for the length of a full heartbeat. We further introduced a method to introduce the deformational forces acting on the flow across heartbeats and demonstrated the impact these forces can have on endothelial shear stress. In the future, we intend to study the impact of these changes on disease progression.

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