



Massively Parallel Model of Cardiovascular Hemodynamics



Amanda Randles^{1,2}, Erik Draeger¹, Efthimios Kaxiras³, and Franziska Michor²

¹Lawrence Livermore National Laboratory ²Department of Biostatistics and Computational Biology, Dana-Farber Cancer Institute ³School of Engineering and Applied Sciences, Harvard University

Summary



Cardiovascular disease is currently one of the leading causes of death in the western world.

Despite advances in CT and MRI technology, 50% of these deaths occur suddenly and with no prior symptoms.

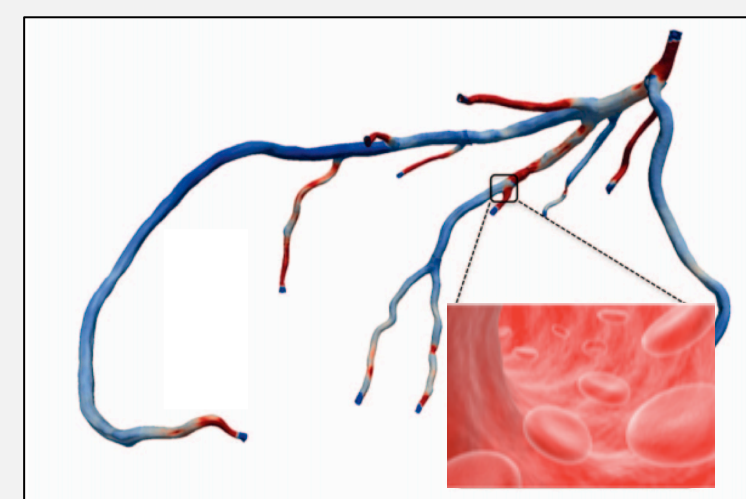
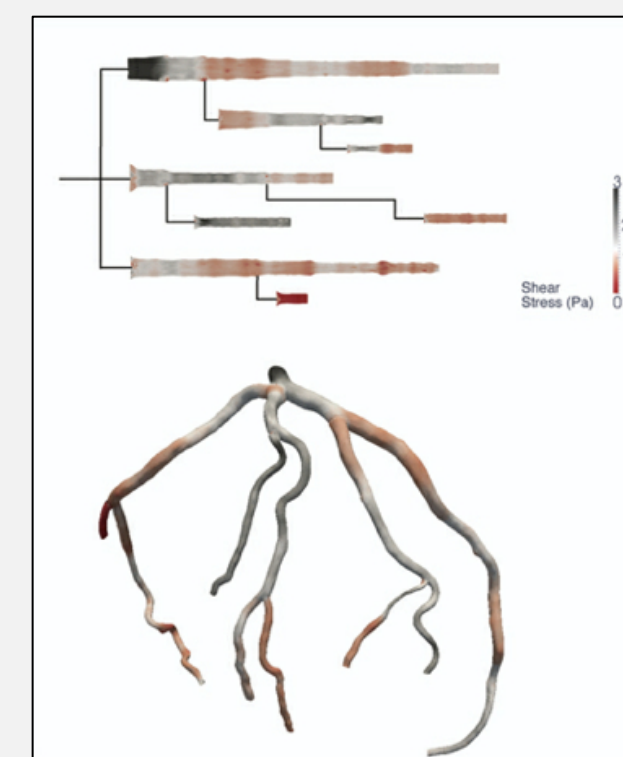
In collaboration with cardiologists, radiologists, mathematicians, visualization experts, and computer scientists, we are working to create a detailed, realistic model of human blood flow from which we can start

to elucidate trends and aid prognosis based on high-resolution patient specific data. The simulation must combine the motion of the fluid, the intricate geometry of the blood vessels, continual changes in flow and pressure driven by the heartbeat, and the behavior of suspended bodies such as red blood cells.

Such models can provide insight into factors like endothelial shear stress that can act as triggers for the complex biomechanical events that can lead to atherosclerotic pathologies. The scale of these simulations requires the use of large-scale supercomputers. We present a massively parallel simulation of hemodynamics in a patient-specific coronary tree as well as demonstrate a variety of other targets.

Multi-scale Model

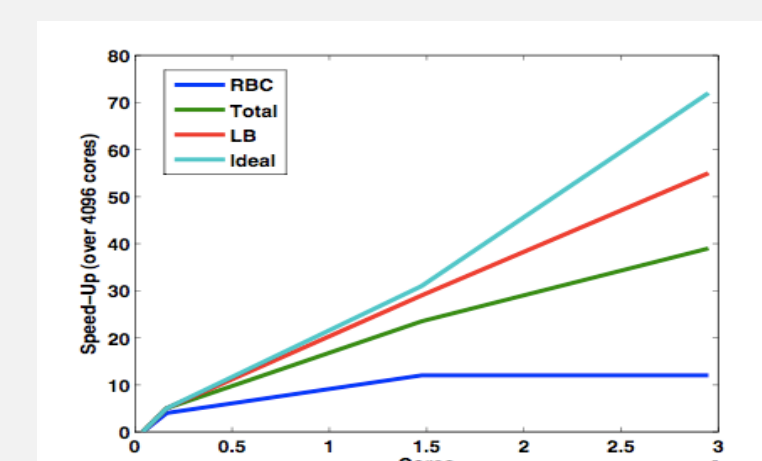
The approach combines different levels of the description of matter, continuum fluids for the dynamics of blood plasma and individual particles for the representation of red blood cells and other minority suspended species. The method is also multi-scale, since fluid and particles are advanced concurrently and the exchange of information is computed dynamically.



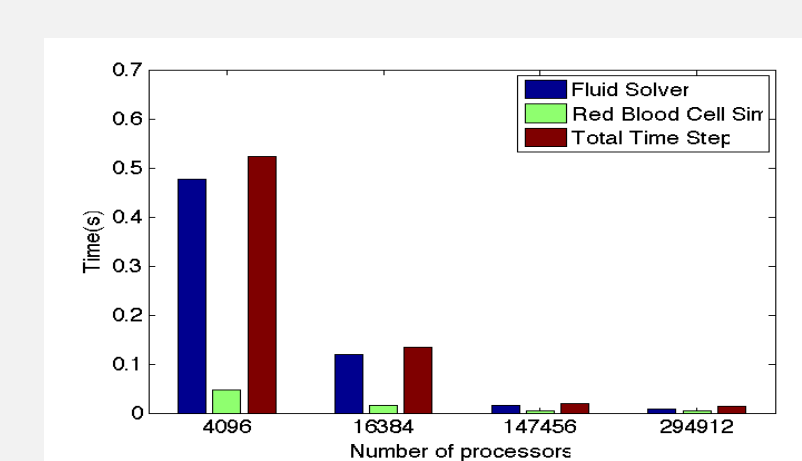
Scaling to Full Heartbeat

This simulation, involving one-billion fluid nodes, embedded in a bounding space of one trillion and coupled with the concurrent motion of ten million red-blood cells, achieves over 60 Teraflops performance on the full 294,912 Blue Gene/P processor configuration, with a parallel efficiency in excess of 60%, performing about 100 billion lattice updates per seconds.

1 billion mesh nodes + 300 million RBCs + 294,912 domains:



Scalability to 294,912 cores



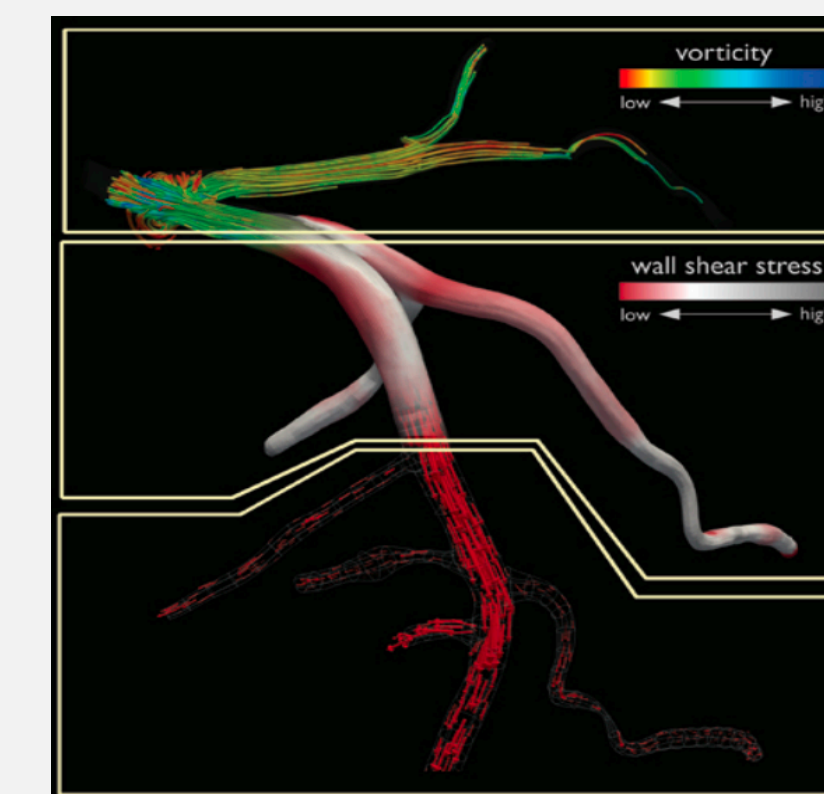
Runtime breakdown

Human heartbeat:

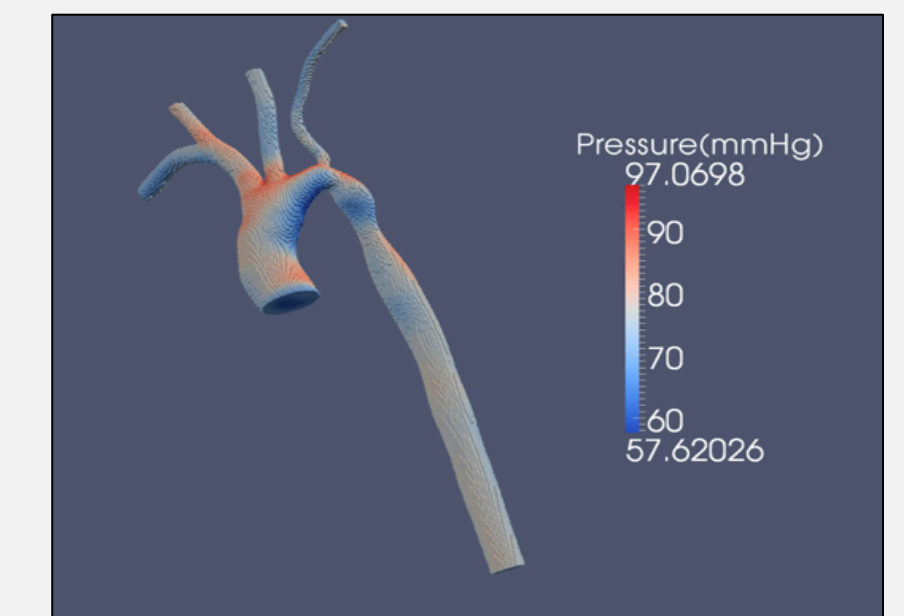
~.7 seconds, 300 million red blood cells,
12 coronary arteries at 10 μ m resolution,
40 racks of Blue Gene/P, 6 hours.



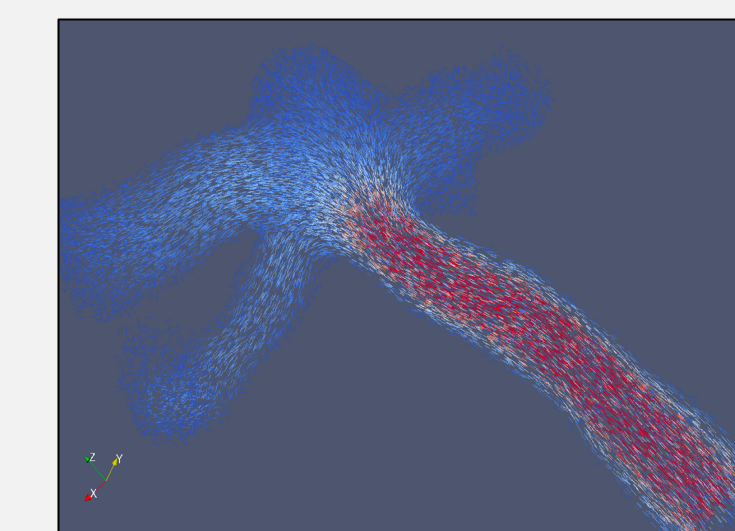
Results



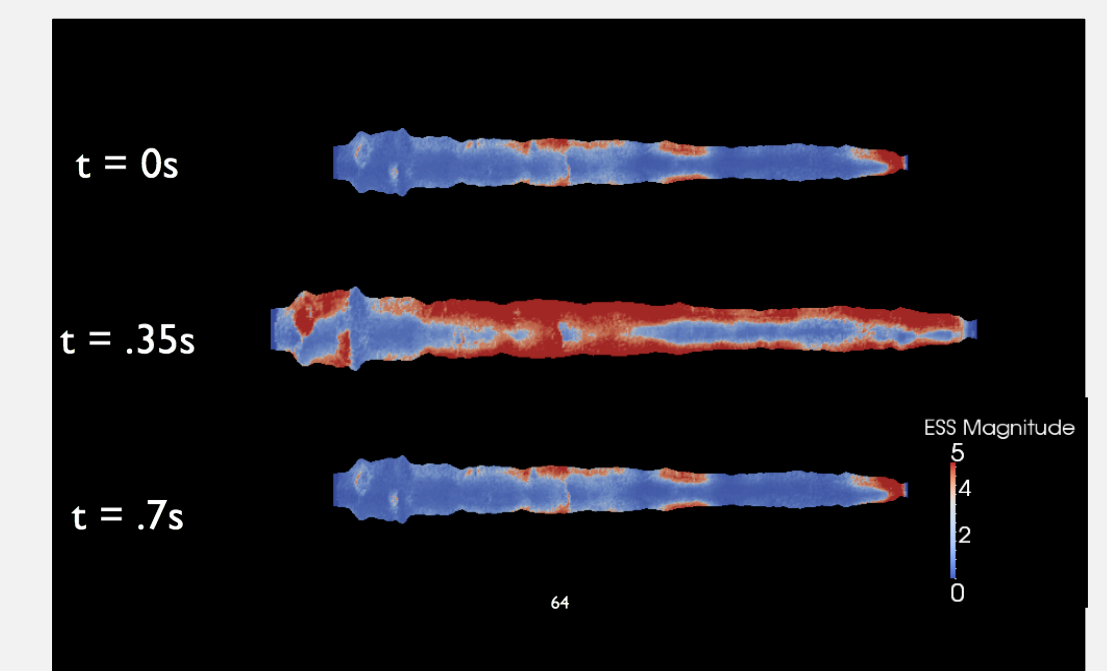
Coronary arteries



Pressure gradient across co-arcuation of the aorta

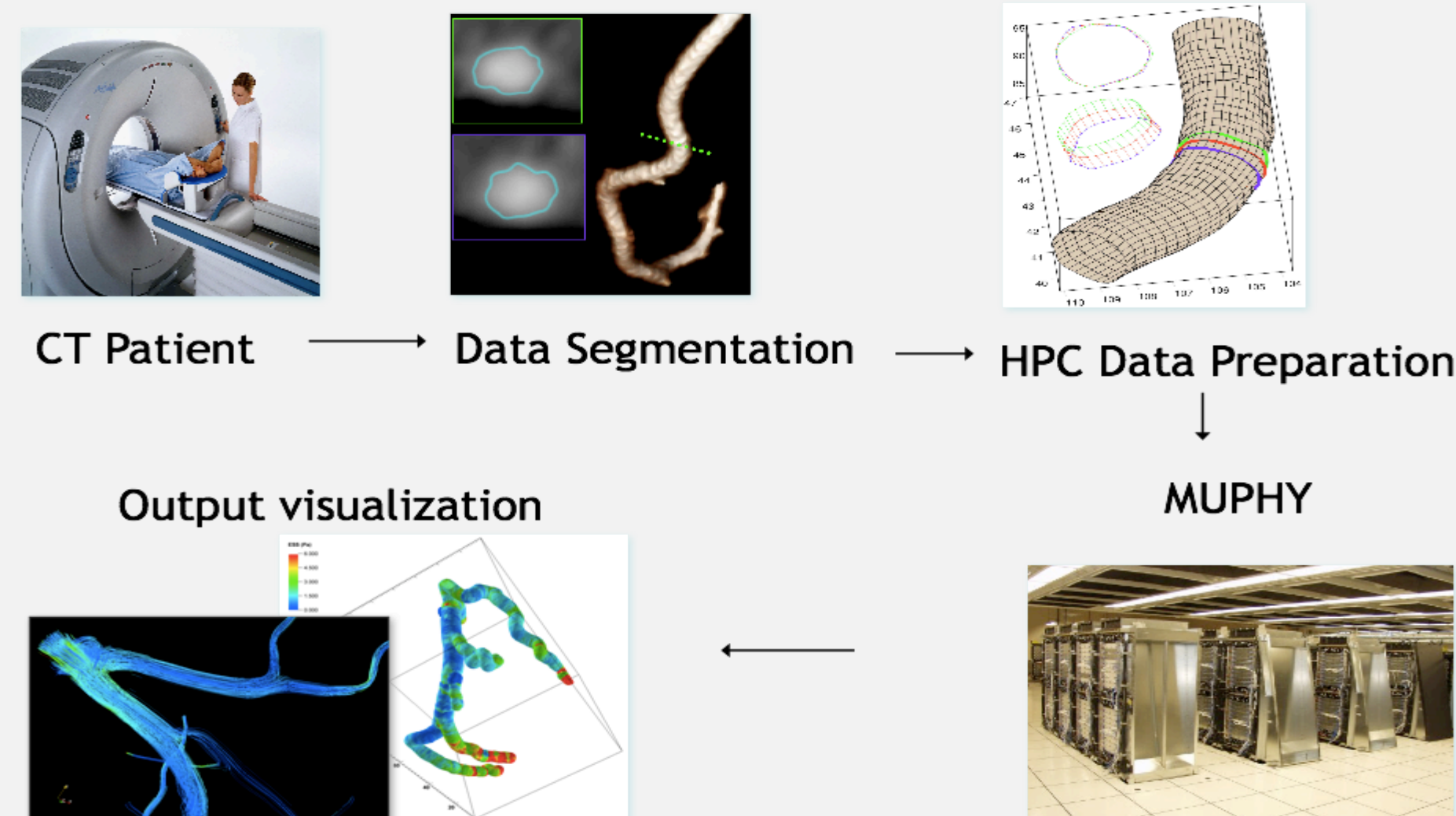


Flow through aneurysms



Shear stress throughout the cardiac cycle

Hemodynamics Pipeline



Working with physicians at the Brigham Women's Hospital in Boston, we retrieve patient-specific coronary arterial trees from MDCT data at a resolution of .1mm. This geometry is utilized for our multi-scale simulations.

Future Work

In the next phase of our research, we are extending the model to include the deformability of suspended bodies and extending the application's scalability to enable the modeling of larger regions of the arterial system. This will allow us to study phenomena such as the movement of circulating tumor cells through the arteries.

References

- A. Peters, S. Melchionna E. Kaxiras, J. Latt, J. Sircar, M. Bernaschi, M. Bisson, and S. Succi, "Multiscale simulation of cardiovascular flows on the IBM Blue Gene/P: full heart-circulation system at red-blood cell resolution." Proceedings of the 2010 ACM/IEEE International Conference for High Performance Computing, Networking, Storage, and Analysis (SC), Gordon Bell Finalist.
- S. Melchionna, M. Bernaschi, S. Succi et al, Hydrokinetic approach to large-scale cardiovascular flows, Comp. Phys. Comm., 181, 462, (2010).
- A. Peters Randles, V. Kale, J.R. Hammond, W. Gropp, and E. Kaxiras, "Performance analysis of the Lattice Boltzmann model beyond Navier-Stokes", Proceedings of the 27th IEEE International Parallel and Distributed Processing Symposium, IPDPS13.
- S. Succi, The Lattice Boltzmann Equation for Fluid Dynamics and Beyond, Oxford University Press, USA, 2001

Acknowledgements: We would like to thank both the Crimson Grid support team and the Juelich Jugene support team for continued hardware support and providing us with dedicated time and access. This work was performed under the auspices of the U.S. Department of Energy by Lawrence Livermore National Laboratory under Contract DE-AC52-07NA27344.