

3D Blood Flow for the Virtual Human with HemeLB: Steps Towards the Exascale

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A fundamental tenet of humanity is that every person's health is a product of not just their unique physiology but also individual factors such as gender, age, weight, genetics and pre-existing conditions or ailments. The environment in which a person lives and the lifestyle they lead also strongly influences health outcomes. When a medical professional is called upon to advise and treat a patient they must consider all of these issues to provide the best outcome. In many situations, it may be difficult to ensure that the optimal course is selected.

The development of a virtual human is a holy grail for many scientific and medical researchers. The virtual human - a digital replica of an individual that captures their own unique characteristics - will allow cheap and repeated investigation of possible treatment options for a patient prior to the optimal course being recommended. Simulation of an individual's response to treatment also allows for examination of physical properties that may be difficult or expensive to study within a patient by conventional means. Insights provided by these may assist clinicians in making better informed treatment decisions for patients.

Advances in the size and performance of computers means that *in-silico* simulation of components of human anatomy based on individual patient data is now achievable. Improving the quality, resolution and scope of these is the focus of significant ongoing research. The development of HemeLB over the last decade has focussed on the study of various aspects of blood flow, from resolving cellular transport to vascular modelling of full human arterial and venous networks. Simulations of blood flow are a good candidate for modelling at the human-scale as they can be based upon mature methods for studying fluid mechanics in complex systems. The relative simplicity of the operation of the blood flow network compared to that of organs such as the brain or digestive tract means that it is an achievable system to target. The importance of the vascular network as a transport system throughout the body also means that the operation of all other physiological structures is dependent upon it. This will be reflected in the computational models developed for these other structures as they will all need to couple to the blood flow to some extent.

HemeLB is an open-source code that numerically solves fluid flow using the lattice Boltzmann method and has been optimised for large-scale performance on sparse geometries such as those found in vascular networks. Simulations have been performed on over 300,000 CPU cores and further developments are being made for deployment on the next-generation exascale supercomputers. Operation and performance on these machines is necessary for simulations to be conducted at the full human-scale.

In this presentation, we will discuss recent developments within HemeLB that have both improved its performance at scale and enhanced its capabilities for modelling full human-scale vascular geometries. We will also provide an outlook for current and future work that is being conducted to further these efforts towards the creation of the virtual human.