

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 the 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 physiology based on individual patient data is now achievable. Improving the quality, resolution and scope of these is the focus of significant ongoing research. Whilst the virtual human is developing on all levels, we are particularly considering blood flow in our work. Vascular simulations are a good candidate for modelling at the human-scale as they can be built upon mature methods for studying fluid mechanics in complex systems. Furthermore, the integration of the vascular network with all other physiological structures means that a full virtual human will also need coupling between the computational models developed for them.

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. The development of the code over the last decade has encompassed various aspects of blood flow, from resolving cellular transport to vascular modelling of full human arterial and venous networks. HemeLB's strong scaling performance has also been demonstrated to over 300,000 CPU cores, demonstrating its capacity to efficiently solve human-scale challenges. Further developments are being made for deployment on the next-generation exascale supercomputers including on accelerated architectures. 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. In particular, we will highlight our work linking arterial and venous geometries and demonstrate HemeLB capturing realistic flow through an arteriovenous fistula in the vessels of the left forearm. We will also provide an outlook for current and future work that is being conducted to further efforts towards the creation of the virtual human.