

Multiscale Modeling of the Human Arterial Tree

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The human arterial tree is a fascinating adaptive flow system with 5 quarts of blood flowing through 60,000 miles of vessels in just one minute. The range of length and time scales that needs to be considered in modeling spans several orders of magnitude; it can be roughly divided into (1) a Macrovascular network (MaN) with hundreds of relatively large arteries; (2) a Mesovascular network (MeN) with millions of arterioles; and (3) a Microvascular network (MiN) consisting of billions of capillaries. Modeling of these multiscale networks requires different type of mathematical and computational techniques both of the continuum and atomistic type. The particular focus in this talk is the intracranial tree for which we will present simulation results from the entire circle of Willis (MaN) to the spectrin-level models of red blood cells in the capillary bed (MiN). The simulations of the MaN scale are image-based and are required to study three-dimensional blood flow dynamics while the MeN and the MiN scale problems serve as a closure for the MaN simulations by providing proper boundary conditions. This approach is appropriate for modeling pathologies such as hydrocephalus, aneurysms or the moyamoya syndrome. However, for diseases like malaria and sickle cell anemia the emphasis is on modeling the dynamics and rheology of individual's red blood cells at the molecular scale using coarse-grained molecular dynamics simulation methods. Examples of large scale simulations requiring high performance computing will be presented for patient-specific geometries for diseases associated with either the MaN or the MiN/MeN systems.

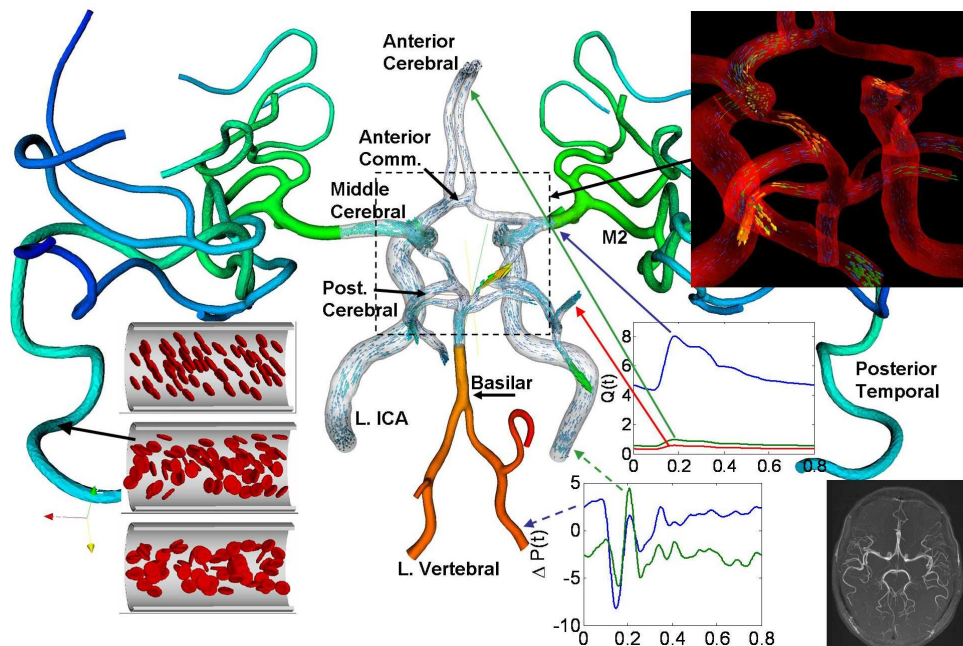


Figure 1: Multiscale Flow Phenomena in the Brain