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Implementing a Multi-Scale Model to Simulate Blood Flows in Circulatory Networks

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Using a multi-scale model, we simulated blood circulation in a global, closed-loop circulatory network including arterial and venous systems, with heart-pulmonary circulation, in addition to microcirculation, which includes blood flow in small blood vessels such as capillaries. Blood circulation in the human body includes all of the components above, with blood flowing simultaneously in different vessels, constituting a closed-loop network. Blood flow into the large vessels in arterial and venous systems is simulated using a one-dimensional (1D) model. This model can be used for analysis of the evolution of the cross-sectional area A, blood flow Q, and mean pressure P for each vessel in the temporal field and spatial field. The zero-dimensional (0D) model is applied to simulate the time-varying Q and P in each vascular subsystem corresponding to peripheral arteries. In computations, 1D and 0D models are solved respectively using the two-step Lax–Wendroff scheme and fourth-order Runge–Kutta method.

This constructed closed-loop circulatory network elucidates the induced changes of blood flow or blood pressure in a human system associated with vessel occlusion or organ lesion. Taking the circle of Willis (CoW) as an example, we simulated blood flow evolution under two conditions: normal flow with complete CoW, and one of its most frequent anatomical variations from which part of the posterior cerebral artery is absent.

Furthermore, a distinctive feature of our model is that it clarifies details of blood circulation in the portal vein system and its related organs: the liver, stomach, spleen, pancreas, and intestine. Along with the convection–diffusion equation system, it will be feasible to ascertain how different materials of interest, such as insulin, which is produced in the pancreas, will be transferred via blood vessels throughout the human body over time until a steady state is reached.

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