The 18th International Conference on Finite Elements in Flow Problems (FEF2015)
16-18 March 2015, Taipei, Taiwan

# Multi-scale Modelling and Simulation of Thrombus Formation

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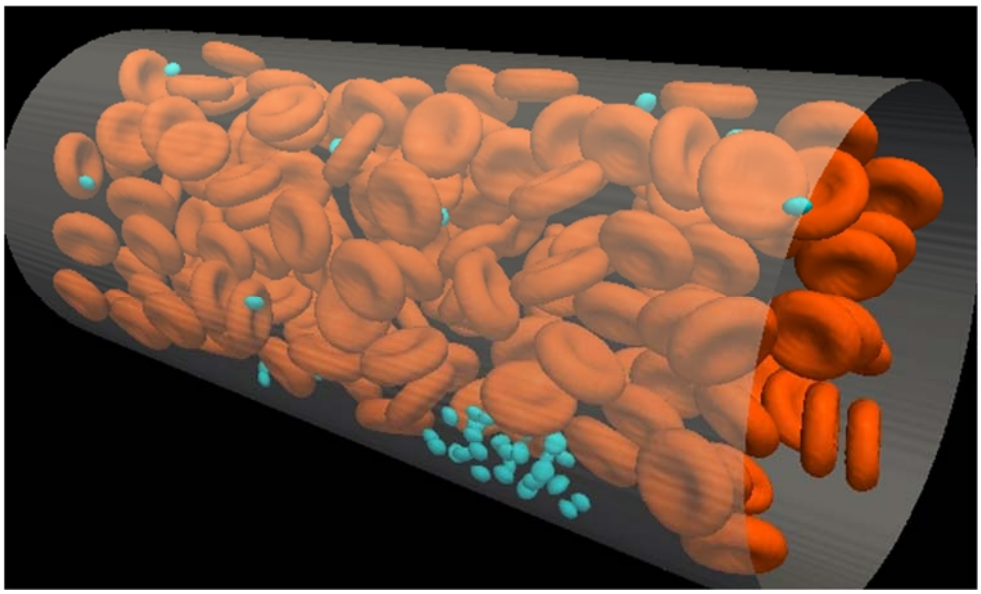
**Key Words:** *Multi-scale Simulation, Full Eulerian Approach, Kinetic Monte Carlo Method, Platelet Adhesion, Thrombus Formation, Fluid-structure Interaction.*

We are developing the multi-scale simulator for a living human body. Basic strategy of the simulator is to utilize the medical image data taken by MRI, X-ray CT, or ultrasound diagnostics for the prediction of disease and planning of therapy. For this purpose, we have developed the Eulerian numerical approach applicable for both fluid-structure and fluid-membrane interaction problems [1, 2, 3]. The method facilitates the treatment of a time-dependent complex geometry. We applied the method to the vesicle deformation subjected to the shearing fluid motion, and the blood flow in the capillary vessel. It should be noticed that the Eulerian method makes it easily possible to realize a massively parallel computation and to attain excellent scalability on state-of-the-art scalar-type supercomputers [4]. The integrated dynamics in e.g. a brain arteriole of 100 μm or larger vessel is expected to be covered using thousands compute nodes of the super computer like K-computer. A novel method is developed for fluid-membrane interaction problems, which is suitable for the numerical simulation of blood flows containing a large number of red blood cells.

Challenging tasks that should be tackled are improvements of the thrombosis simulator to capture the later stages of the thrombus formation involving more complicated phenomena such as the platelet activation, the change in the hemo rheology and the fibrin network formation / breakage. We demonstrate the preliminary results using the thrombosis simulator, in which the stochastic Monte Carlo method in consideration of the ligand-receptor interaction between the proteins is incorporated and initial stage of thrombosis is modelled [5]. The modelling of the bio-chemical reactions and the substance diffusions caused after the activation of platelet triggered by the glycoprotein Ibα (GPIbα) - von Willebrand factor (vWF) binding, and the implementation of a robust time advancement during the coupling are discussed. Platelet

adhesion is simulated by coupling the continuum scale simulation with the Monte Carlo simulation for the binding of GP1ba and vWF molecules.

Combining the adhesion of platelets onto the vessel wall, the blood flow with red blood cells and platelets is simulated. The results illustrate that platelets are much easier to aggregate on the wall in the presence of red blood cells. Experimental facts that adhesion of platelets do not occur without red blood cells are successfully reproduced in the present simulation.



Multiscale modelling of initial stage of thrombosis. The interaction between platelets and vessel walls in the primary aggregation of platelets was investigated using kinetic Monte Carlo simulation for the multiscale simulation of thrombus formation. The results show that platelets are much easier to aggregate on the vessel wall in the presence of red blood cells.

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