

COMPUTATIONAL MODELLING OF BLOOD CLOTTING: A COUPLED LATTICE BOLTZMANN AND DISCRETE ELEMENT APPROACH

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ABSTRACT

Blood clotting generally involves two interacting processes known as blood *platelet aggregation* and *coagulation*. The aggregation of blood platelets is normally initiated by the release of chemicals to blood plasma from damaged tissues in an injured blood vessel. This biochemical reaction can induce platelets to adhere to the damaged tissue and to undergo an activation process that causes the surface of the platelet membrane to become highly adhesive. Activated platelets are able to cohere to one another and to those that already adhere to the subendothelial layer. The injured vessel also triggers a series of enzymatic reactions, leading to the process of blood coagulation. It is believed that the injured vessel first releases a tissue factor VIIa on the surface, and the subsequent involvement/activation of other enzymes finally leads to the formation of activation thrombin, which cleaves the plasma protein fibrinogen into fibrin monomers. The polymerization and cross-linkage of these fibrin monomers form a fibrous matrix that mechanically binds and stabilises the aggregates. The predominated platelet aggregate and fibrin strands, together with the entrapped red and white blood cells, constitute the blood clot. Platelet aggregation plays a major role in normal hemostasis as well as pathological thrombosis that may occlude partly or completely the blood vessel.

In addition to a very complex biochemical mechanism involved, hemodynamic conditions also play an active role in the formation, growth and lysis of blood clots, and in fact, both biochemical and hemodynamic factors are interrelated. The process of blood clotting may be further complicated by the presence of possible pathological conditions that may be originated in both hemodynamics and biochemical disorders.

Consequently, understanding all the processes involved in blood clotting and how they are regulated is of major medical importance. Over the last decade or so, some researches have been conducted ranging from experiments to mathematically modelling [1-3]. Due to the inherent difficulty associated with *in vivo* experiments, mathematical modelling aided with advanced computational techniques appears to be an attractive approach [1-3]. The continuous based modelling strategy [1, 2] however inevitably encounters the problem that many biochemical/rheological factors involved have to be either significantly simplified or arbitrarily assumed. The recent work [3] in which each platelet is individually represented provides a more promising approach to the model of

blood clotting.

The current work presents a coupled lattice Boltzmann and discrete element approach [4] for the numerical modelling of the blood clot formation, with blood plasma flows being simulated by the lattice Boltzmann method while thrombi formation due to platelet aggregation/coagulation being modelled by the discrete elements. Blood plasma can be assumed as non-Newtonian flow and the interaction between platelets and platelet/blood vessel wall is modelled by a simplified piecewise linear distance-force function, mainly following the work of [3], although more complex and realistic interaction models can be readily incorporated.

Figure 1 demonstrates the numerical simulation of the formation of two aggregates in a blood flow. The two large red particles are ‘seed’ platelets initially placed as active. Inactive platelets (in black) are randomly introduced in the upstream of the blood plasma flow. When a platelet is close to an active platelet, it becomes triggered (shown in blue). After a randomly prescribed delay time, it further becomes active (shown in red), and can adhere to existing active platelets to form aggregations. A triggered/active platelet will return back to inactive if it does not adhere to an active platelet after a given period of time. The influence of the aggregations on the blood plasma flow is also clearly shown in the figure.

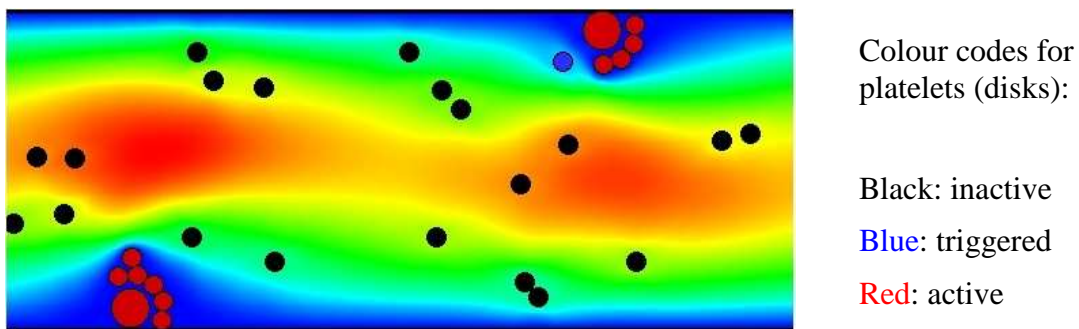


Fig.1 - Formation of platelet aggregations: contour plot of total flow velocity

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