# Digital Blood in Massively Parallel CPU/GPU Systems for the Study of Platelets deposition

Kotsalos, C.[1], Beny, J.[1], Latt, J.[1], Chopard, B.[1]

[1]Computer Science Department, Scientific and Parallel Computing Group, University of Geneva

We propose a novel high-performance computational framework for the simulation of fully resolved whole blood flow. The framework models blood constituents like red blood cells (RBCs) and platelets individually, including their detailed non-linear elastic properties and the complex interactions among them. This kind of simulations are particularly challenging because the large number of blood cells (up to billions) stand in contrast with the high computational requirement of individual constituents. While classical approaches address this challenge through simplified structural modelling of the deformable bodies (e.g., through mass-spring systems), the present framework guarantees accurate physics, desirable numerical properties through a fully featured FEM model and computational efficiency at the same order as the more simplified state-of-the-art models. The required numerical performance is achieved through a hybrid implementation, using CPUs for the blood plasma and GPUs for the blood cells.

Blood flow is involved in most of the fundamental functions of living organisms regarding health and disease. It is essential for the transport of oxygen, nutrients, waste products, as well as of infectious parasites and metastasizing tumour cells to tissues and organs. Blood is a complex suspension of RBCs, white blood cells and platelets, submerged in a Newtonian fluid, the plasma. The accurate modelling of the collective transport of the cells in the plasma is of paramount importance since it can help us decipher not well-understood in vivo phenomena, e.g., formation of blood clots and margination of platelets. RBCs are disk-shaped cells, made of a deformable membrane containing a Newtonian solution of haemoglobin, whose role is to transport oxygen in the organism. They account for about 35-45% of the blood volume (this fraction is called the haematocrit), corresponding to roughly $10^6$ RBCs per $mm^3$. The deformability of RBCs is strongly linked to some pathological conditions, e.g., hereditary disorders (like spherocytosis, elliptocytosis, and stomatocytosis), metabolic disorders (like diabetes, hypercholesterolemia, and obesity), malaria, or sickle anaemia. Platelets are small blood cells, with a concentration between $250x10^3$ and $500x10^3$ per $mm^3$, at a ratio about 1 platelet to 10 RBCs.

Most of the simulations at the spatial scale of millimetres ignore the particulate nature of blood because of the tremendous computational cost. On the other hand, in the state-of-the-art fully resolved whole blood simulations, the spatial scale remains very small, of the order of a few tens of micrometres. The suggested HPC framework is built toward the direction of simulating macroscopic flows, of the order of $mm^3$ of whole blood, and offers to the user the possibility to address a large range of problems with clinical relevance. The constituents of this framework are the fluid solver, the solid body solver and the fluid-structure interaction (FSI) module. Our software is designed to be modular, in the sense that the components above can accommodate any state-of-the-art numerical technique to solve the fluid or solid phase.

As far as the simulation of the blood plasma is concerned, there exists a plethora of mature CFD approaches. For our simulations, we make use of the lattice Boltzmann method (LBM) which indirectly solves the Navier-Stokes equations. LBM uses a static, homogeneous lattice and the advancement of the fluid in time happens through collision and streaming operations. The above two processes alter the fluid populations which reside at every lattice site and constitute the degrees of freedom of the LBM.

The coupling of the fluid with the solid phase is a critical point for accurate and stable simulations. Peskin developed the immersed boundary method (IBM) to model blood flow in combination with moving heart valves. The strength of the IBM is that the fluid solver does not have to be modified except for the addition of a forcing term, and the fluid mesh does not need to be adjusted dynamically. Moreover, the deformable body and its discrete representation do not need to conform to the discrete fluid mesh, which leads to a very efficient fluid-solid coupling.

In a typical numerical framework for blood flow, the computational time is dominated by the structural solver for the deformable blood cells. We proposed a novel approach for deformable viscoelastic bodies based on the nodal projective finite elements method (npFEM) [1]. The expression "nodal" refers to the mass lumping technique, in which both the masses and the forces are lumped on the vertices of the discretized body, and therefore the finite elements act like generalized viscoelastic springs. The term "projective" stands for the use of specially designed potential energies that help us build a fast solver based on quasi-Newton optimization techniques. Our solver inherits the versatility and robustness of FEM and is almost as fast as plain mass-spring systems (current state-of-the-art solvers). It is characterized by strong mesh independence and just one set of parameters, for any mesh resolution, can successfully describe the behaviour of blood cells.

For the LB and IBM parts, we use the open source library Palabos (http://www.palabos.org/), which stands for Parallel Lattice Boltzmann Solver. Palabos is a powerful open source high-performance LB solver that utilises modern C++ and advanced Message Passing Interface (MPI) techniques. The npFEM part is written in C++/ CUDA in order to leverage the massive parallelism offered by the general-purpose GPUs.

The developed numerical framework is intended to grow to be a general-purpose tool for first-principle investigation of blood properties. The focus of this research work is the study of platelet margination [2]. This is a very complex transport phenomenon, where the platelets are pushed toward the vessel walls while the RBCs form a denser structure away from them. While this is a well reported phenomenon, there is no clear understanding of the real mechanisms behind it. Deciphering this property of blood could help design efficient drugs that prevent clot formation and help doctors detect various cardiovascular diseases at more ease. Our analysis is not only focused on healthy subjects but also on patients with various pathological conditions, e.g., diabetes, obesity and various other hereditary disorders (linked with the RBC/ platelet deformability and shapes). Figures 1 & 2 present a pure shear flow (opposite velocities on top

and bottom walls) for healthy and diabetic subjects, respectively, as produced using our HPC framework. In the latter case, the RBCs are more swollen and less deformable, leading to a faster deposition of platelets toward the vessel walls.

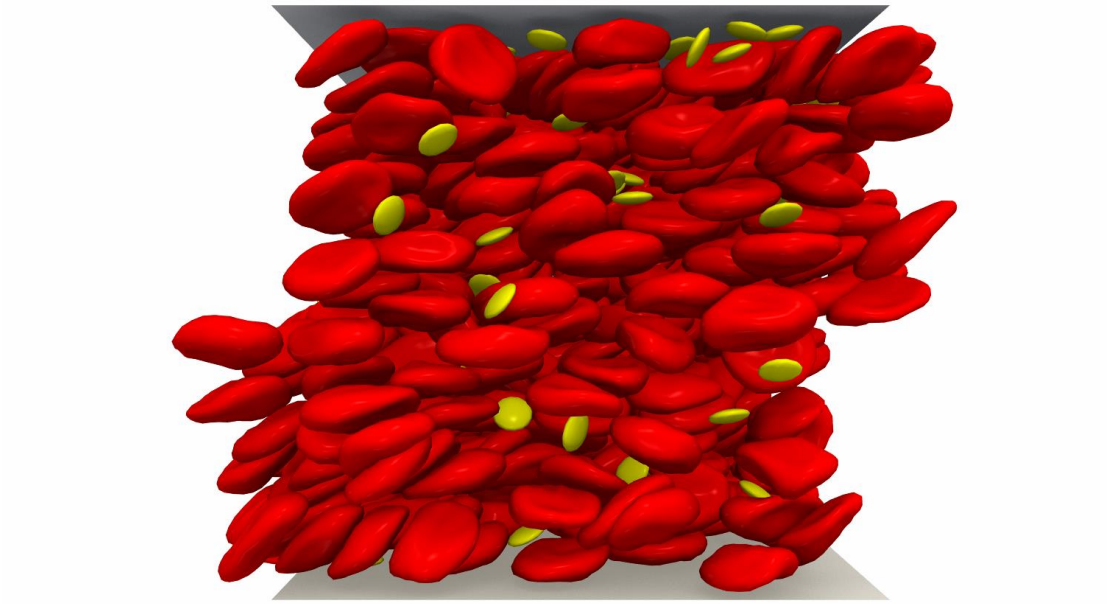

***Figure 1*** *Shear flow with healthy RBCs (in red) and platelets (in yellow) in a domain of 50 $\mu m^3$ at 35% haematocrit.*

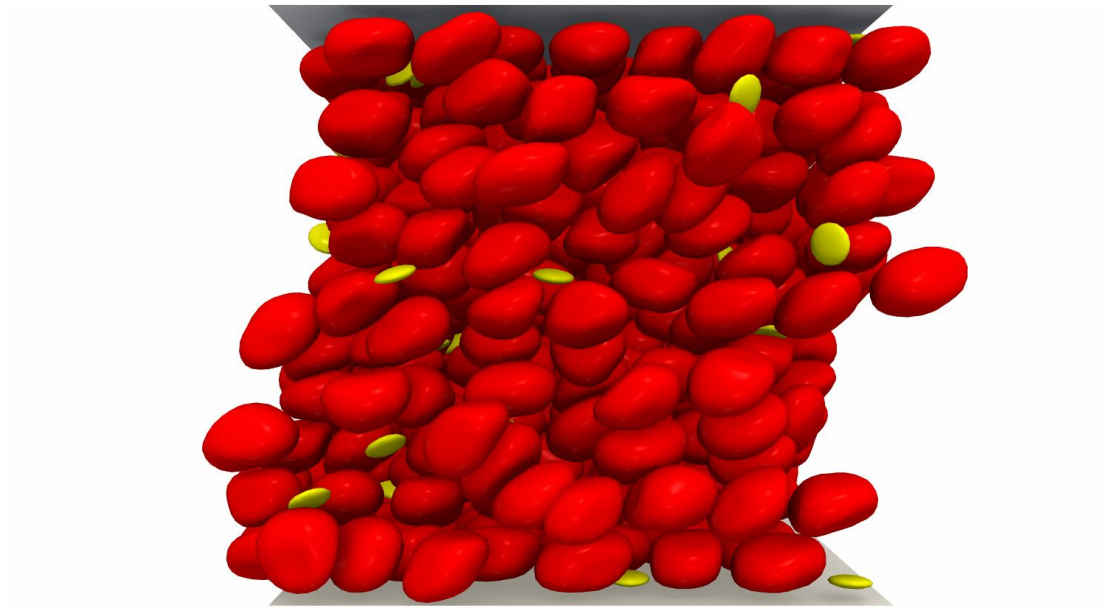

***Figure 2*** *Shear flow with diabetic RBCs (in red, more swollen and less deformable than healthy ones) and platelets (in yellow) in a domain of 50 $\mu m^3$ at 35% haematocrit.*

In the context of the current scientific goals (toward the simulation of macroscopic flows), the performance metrics of our parallel framework must be considered under the light of weak scaling. Indeed, the purpose of seeking more powerful computational resources is not to improve the resolution or increase the time span of the simulation, but to extend the physical volume of the blood considered in the model. Tests of the hybrid CPU/GPU code have shown that at a haematocrit of 35%, it is reasonable to assign each GPU approximately 500 blood cells, while the

CPU cores on the same node treat the corresponding volume of blood plasma. In this case, the computational cost of the different parts of the code are balanced (no single part constitutes a bottleneck), and a single global iteration of the solver is carried out in less than 0.5 seconds, allowing to cover a significant physical time span in a few days of computation. An increase of the number of compute nodes translates into a proportional increase of the number of RBCs and blood plasma volume.

To conclude, our research product delivers fully resolved whole blood simulations at unprecedented computational efficiency. Current state-of-the-art solvers report that the deformable blood cells solver constitutes over 95% of the total computational time, while our novel computational framework has dropped this time to about 15% of the total computational time. The proposed design deems suitable for the upcoming exascale supercomputers, allowing us to simulate physical domains and time spans that are yet to be explored.

## References


1. C. Kotsalos, J. Latt, B. Chopard, Bridging the computational gap between mesoscopic and continuum modeling of red blood cells for fully resolved blood flow, 2019, https://arxiv.org/abs/1903.06479.
2. B. Chopard et al. 2017, A physical description of the adhesion and aggregation of platelets, R. Soc. open sci. 4: 170219. http://dx.doi.org/10.1098/rsos.170219