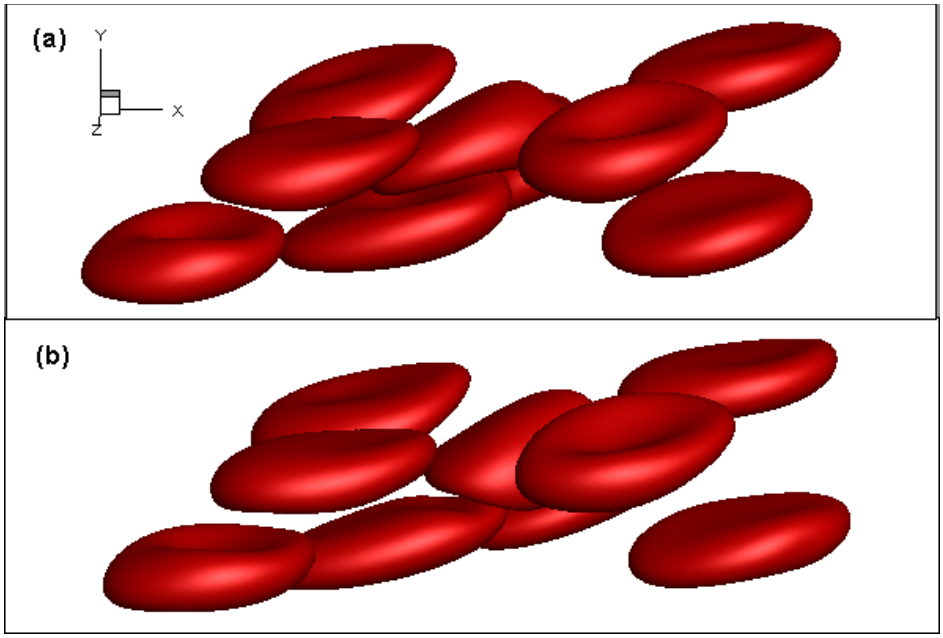
Supplementary Materials

"Platelet Dynamics in Three-Dimensional Simulation of Whole Blood"

Koohyar Vahidkhah, Scott L. Diamond, Prosenjit Bagchi

A. Accuracy and Grid-Independence of the Numerical Methodology

The numerical methodology has been developed in our group over the past few years, and has been validated extensively for capsule, cell and vesicle deformation in flow in our prior publications (1-7) against experimental, theoretical and other numerical studies. Since we use front-tracking/immersed-boundary method, the accuracy is between first and second order. A detail study of the Eulerian resolution requirement for capsule deformation can be found in reference 1. There, and in our subsequent studies on red blood cell dynamics (e.g., references 4 and 6), we have used about 55 Eulerian points across one cell diameter based on our resolution test. We find this resolution quite accurate when compared with theoretical and other numerical (e.g. spectral and boundary integral simulations) results for capsules (references 1, 5 and 7), theoretical and experimental results for vesicles (reference 3), and experimental studies with red blood cells (references 4 and 6). In the present study of many cells, we retain the same amount of Eulerian resolution inside each red blood cell. In addition, we check posteriori that there is about four Eulerian mesh points between two adjacent cells. We have performed two simulations in a domain of 27X13X18 μm^3 by doubling the resolution from 180X81X120 to 360X161X240, and the results are shown in Fig S1. As evident, the cell shapes in the two simulations remain similar. We also compare cell-averaged quantities, namely, the cell half-length (L) along its longest axis, the Taylor deformation parameter (D) defined as (L-B)/(L+B) where B is the shortest distance of the cell membrane from the center-of-mass, and the inclination angle (θ) of the cell major axis. These quantities agree well for the two simulations. We also compare these quantities for a specific cell, where again agreement is observed.



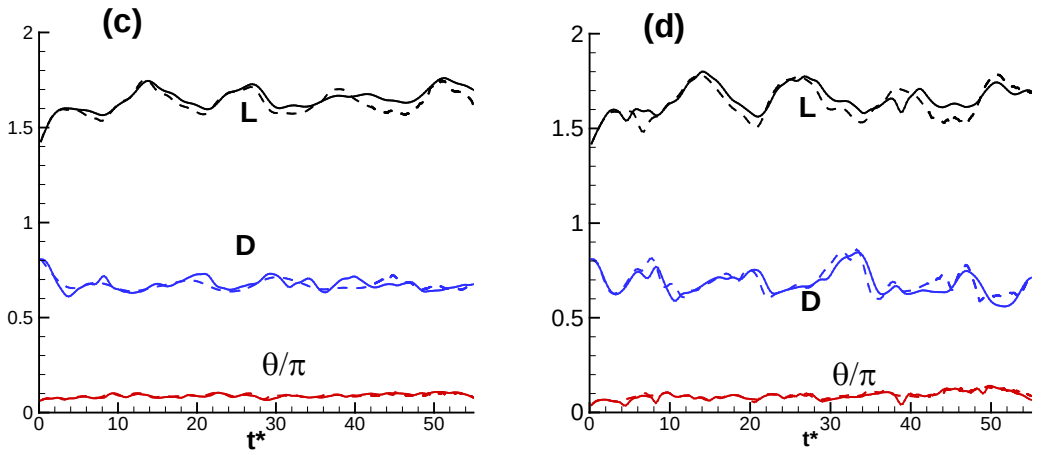
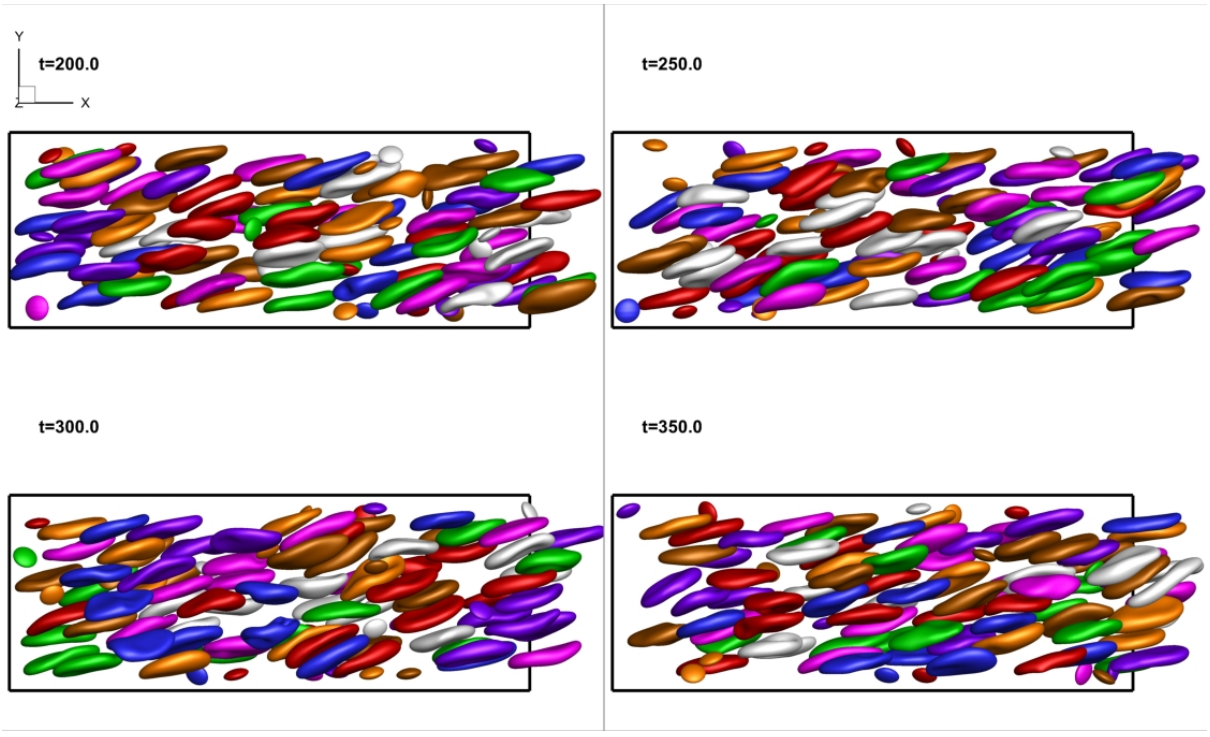


Figure S1. (a) and (b) show cell shapes at Eulerian resolution 81X160X120 and 161X360X240, respectively. (c) shows the cell-averaged semi-major axis (L), Taylor deformation parameter (D) and inclination angle (θ), while (d) shows the same quantities for a specific cell. The solid lines are for coarser resolution, and dashed lines for finer resolution.

B. Evolution of cell distribution

Evolution of cell distribution over time is shown in Fig S2 for the simulation corresponding to Figure 1 in the main text. As evident, the distribution is random, and forgotten over time.



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