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Particle-Based Simulation of RBC, WBC, and Platelet Dynamics in Microchannel Blood Flow

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Abstract

Understanding blood cell transport and spatial organization in confined microfluidic environments is essential for developing biomedical diagnostic systems and lab-on-a-chip technologies. This study developed a computational model to investigate the spatiotemporal dynamics of red blood cells (RBCs), white blood cells (WBCs), and platelets within a microfluidic channel. The model simulated cell motion and interactions under confined flow conditions. Cell trajectories and spatial distributions were analyzed over time, with particular emphasis on changes in the maximum vertical positions of RBCs and WBCs. The simulations revealed heterogeneous transport behavior, with distinct temporal patterns in the vertical distributions of RBCs and WBCs and localized platelet motion within the flow domain. Cell–cell interactions and channel confinement influenced spatial migration, while the evolution of maximum vertical position provided insight into transient cell redistribution and spatial organization. These findings characterize differences in the transport dynamics of blood components within microchannels. The computational framework provides a tool for investigating microscale blood flow and may support the design and optimization of microfluidic devices for blood analysis, cell sorting, and biomedical diagnostics.

Keywords: Blood Cell Dynamics; Microfluidic Channels; Computational Modeling; Cell Migration; Lab-on-a-Chip Technologies

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Introduction

The transport and spatial distribution of blood cells in confined microfluidic environments have attracted significant attention in recent years due to their importance in biomedical engineering, diagnostic tech The transport and spatial distribution of blood cells in confined microfluidic environments have attracted significant attention in recent years due to their critical importance in biomedical engineering, diagnostic technologies, and lab-on-a-chip systems. Blood is a complex multiphase suspension composed primarily of red blood cells (RBCs), white blood cells (WBCs), and platelets, each possessing distinct mechanical properties, sizes, and biological functions. The collective interactions between these cellular components strongly influence blood rheology and flow behavior, particularly in small vessels and microfluidic channels [1].

Red blood cells, which constitute approximately 45% of blood volume (hematocrit), are highly deformable biconcave discs that play a dominant role in determining blood viscosity and flow characteristics [1,2]. Their ability to deform allows them to migrate toward the center of the channel (axial migration), leading to the formation of a cell-free layer near the channel walls, a phenomenon known as the Fahraeus–Lindqvist effect [7]. This effect reduces flow resistance in microvessels and significantly alters apparent viscosity at small scales [1].

White blood cells, in contrast, are larger and less deformable than RBCs. Their mechanical rigidity and adhesive properties promote margination, a process by which WBCs migrate toward the vessel walls [3]. This behavior is crucial for immune response, as it facilitates interactions with the endothelium during inflammation. Similarly, platelets—being the smallest cellular components—also exhibit margination tendencies, especially in the presence of flowing RBCs, which enhance their lateral displacement toward the walls through hydrodynamic interactions [4].

In confined microfluidic systems, geometric constraints such as channel width, curvature, and surface properties further influence cell distribution and transport dynamics. Factors including shear rate, hematocrit level, and cell deformability govern the emergence of complex flow phenomena such as cell clustering, segregation, and non-Newtonian viscosity behavior [4,5]. These microscale interactions are essential for the design and optimization of biomedical devices, including cell sorting platforms, disease diagnostics, and drug delivery systems [5].

Recent advances in experimental techniques and computational modeling, such as micro-particle image velocimetry (μPIV) and dissipative particle dynamics (DPD), have enabled detailed investigation of blood flow at the cellular level [2,8]. These tools have provided valuable insights into the underlying mechanisms of cell-cell and cell-wall interactions in confined geometries. Understanding these processes is essential for improving the performance of microfluidic devices and for gaining deeper insight into microcirculatory physiology and related pathological conditions such as thrombosis, malaria, and sickle cell disease [6].

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Microfluidic devices have emerged as powerful tools for studying microscale blood flow phenomena and for developing biomedical applications such as cell sorting, disease diagnostics, and drug screening. In such confined geometries, the dynamics of blood cells become highly complex due to hydrodynamic interactions, particle collisions, and spatial confinement. These effects lead to non-uniform distributions of cells within the channel, which may significantly affect transport efficiency and separation mechanisms.

Red blood cells, being the most abundant component of blood, largely determine the bulk rheological properties of blood Microfluidic devices have emerged as powerful tools for studying microscale blood flow phenomena and for developing biomedical applications such as cell sorting, disease diagnostics, and drug screening [9]. In such confined geometries, the dynamics of blood cells become highly complex due to hydrodynamic interactions, particle collisions, and spatial confinement. These effects lead to non-uniform distributions of cells within the channel, which may significantly affect transport efficiency and separation mechanisms [4,9].

Red blood cells, being the most abundant component of blood, largely determine the bulk rheological properties of blood flow [1,2]. Their collective motion and deformability dominate flow resistance and influence the distribution of other cellular components. In contrast, white blood cells and platelets exhibit different migration behaviors due to their larger size, reduced deformability, and distinct mechanical characteristics [3,4]. Understanding

how these different cell types move and distribute themselves within microchannels is therefore crucial for improving the design and performance of microfluidic biomedical systems [5,9].

Computational modeling has become an effective approach for investigating blood flow behavior at the microscale [2,8]. Numerical simulations allow researchers to analyze complex cell interactions, track particle trajectories, and study the spatiotemporal evolution of cell distributions under controlled conditions. These models provide valuable insights that are difficult to obtain experimentally, particularly when examining transient dynamics, rare events, and detailed cell-cell interactions [8,10].

In this study, a computational framework is developed to simulate the motion of multiple blood cell types within a microfluidic channel. The model captures the dynamic transport of RBCs, WBCs, and platelets and analyzes their spatial distribution over time. Particular attention is given to the temporal evolution of the maximum vertical position of cells within the channel, which provides insight into migration patterns and vertical stratification of cellular components. Such analysis is essential for understanding margination, segregation, and layering phenomena in confined blood flow [4,10]. The results contribute to a better understanding of multicellular blood flow behavior in confined geometries and may support the development of more efficient microfluidic devices for biomedical and diagnostic applications [5,9].

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Particular attention is given to the temporal evolution of the maximum vertical position of cells within the channel, which provides insight into migration patterns and vertical stratification of cellular components. The results contribute to a better understanding of multicellular blood flow behavior in confined geometries and may support the development of more efficient microfluidic devices for biomedical and diagnostic applications.

Methodology (Nu1. Methodology (Numerical Model)

This study employs a computational framework to simulate the transport and interaction of multiple blood cell types within a confined microfluidic channel. The model considers three primary blood components: red blood cells (RBCs), white blood cells (WBCs), and platelets, which are represented as discrete particles with different physical and mechanical characteristics. Such particle-based approaches have been widely used to capture microscale blood flow behavior and cellular interactions in confined geometries [11].

The microfluidic domain is modeled as a two-dimensional rectangular channel with specified length and height, representing a simplified approximation of microvascular or lab-on-a-chip systems. Initially, RBCs, WBCs, and platelets are randomly distributed within the channel to mimic a homogeneous suspension at the بداية التدفق. Each cell type is assigned distinct properties reflecting its relative size and mechanical behavior: RBCs are modeled as deformable or moderately sized particles, WBCs as larger and less deformable particles, and platelets as smaller particles with higher lateral mobility [2,3,12]. This differentiation is essential to reproduce realistic margination and segregation phenomena observed in microcirculation.

The motion of cells within the channel is governed by time-dependent particle dynamics that incorporate hydrodynamic interactions, short-range repulsive forces to prevent overlap, and boundary effects imposed by the channel walls. At each simulation step, the positions and velocities of all particles are updated according to the governing equations of motion. Numerical schemes commonly used in mesoscale simulations, such as dissipative particle dynamics (DPD) or related particle-based methods, provide a suitable framework for resolving such complex interactions [8,11].

To ensure physical consistency, collision avoidance between particles is enforced through interaction potentials, while wall boundaries are treated using no-penetration and no-

slip conditions. These boundary conditions play a crucial role in reproducing near-wall effects such as the formation of the cell-free layer and margination of larger particles [4,7]. Additionally, the influence of shear flow is implicitly captured through the imposed flow conditions, which drive particle motion along the channel.

The simulation tracks the trajectory of each cell over time and records the spatial coordinates of all cellular components. Particular emphasis is placed on monitoring the maximum vertical position (Y-direction) reached by RBCs and WBCs during the flow. This parameter provides a quantitative measure of vertical migration patterns and reveals the extent of cell stratification and margination within the channel [3,4].

The simulation is performed over a specified time interval using sufficiently small time steps to accurately resolve transient dynamics and cell-cell interactions. The resulting dataset enables detailed analysis of spatiotemporal changes in cell distribution, including clustering, segregation, and near-wall accumulation phenomena. Such analyses are essential for understanding the collective behavior of multicellular blood flow and for optimizing microfluidic device performance in biomedical applications [5,10].

Furthermore, model validation is supported by qualitative comparison with well-established microcirculatory phenomena reported in the literature, such as axial accumulation of RBCs and wall-directed migration of WBCs and platelets. This ensures that the numerical framework captures the essential physics governing blood flow in confined environments [1,3].

Methodology (Numerical Model)

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The microfluidic domain is modeled as a two-dimensional rectangular channel with specified length and height. Initially, RBCs, WBCs, and platelets are randomly distributed within the channel to represent a simplified blood suspension. Each cell type is assigned distinct properties reflecting its relative size and mechanical behavior. RBCs are modeled as moderately sized particles, WBCs as larger particles, and platelets as smaller particles.

The motion of cells within the channel is governed by time-dependent particle dynamics that account for cell movement, interactions between neighboring cells, and boundary effects. At each simulation step, the positions of all cells are updated according to the governing motion equations while ensuring that overlapping between particles is prevented.

The simulation tracks the trajectory of each cell over time and records the spatial coordinates of all cellular components. Particular emphasis is placed on monitoring the maximum vertical position (Y-direction) reached by RBCs and WBCs during the flow. This parameter provides an indication of vertical migration patterns and the evolving spatial organization of cells within the channel.

The simulation is performed over a specified time interval with small time steps to capture transient dynamics accurately. The resulting dataset allows the analysis of spatiotemporal changes in cell distribution and provides insight into the collective behavior of multicellular blood flow in confined microfluidic environments.

Mathematical Model

To investigate the dynamics of blood cells in a confined microfluidic environment, a computational mathematical model was developed to simulate the motion and interaction of multiple blood cell types within a rectangular microchannel. The system consists of three primary cellular components: red blood cells (RBCs), white blood cells (WBCs), and platelets, each exhibiting distinct mechanical and transport characteristics that influence their behavior under flow conditions [1,4].

The microfluidic channel is modeled as a two-dimensional domain with specified length LLL and height HHH, representing a simplified geometry commonly used in microfluidic studies. Although real blood flow is inherently three-dimensional, two-dimensional approximations have been widely adopted to reduce computational cost while still capturing essential features of cell transport and distribution [11,13]. Initially, blood cells are randomly distributed throughout the domain to represent a homogeneous suspension at the onset of flow. Each cell is treated as a discrete particle characterized by its position (xi,yi)(x_i, y_i)(xi,yi), velocity (ui,vi)(u_i, v_i)(ui,vi), and an effective diameter did_idi, which varies depending on the cell type.

The motion of each particle is governed by a system of time-dependent equations derived from Newtonian mechanics, where the net force acting on each particle determines its acceleration and subsequent motion. [8,11].

Short-range repulsive interaction forces are incorporated to prevent particle overlap and to mimic excluded volume effects arising from physical cell-cell contact. These forces are typically modeled using soft repulsive potentials that become significant when particles approach each other within a critical distance [11]. This approach enables the simulation of collision-like behavior and local rearrangement of cells without explicitly resolving detailed membrane mechanics.

Boundary conditions are imposed along the channel walls to confine particle motion within the domain. The top and bottom walls are treated as impermeable, enforcing no-penetration conditions (v=0v = 0v=0 at the walls), while tangential motion may be influenced by no-slip or partial-slip assumptions depending on the flow configuration. These boundary effects are essential for reproducing near-wall phenomena such as cell-free layer formation and margination [7,12].

The temporal evolution of the system is computed using an explicit time-stepping scheme, such as the Euler or Verlet integration method, where particle positions and velocities are updated iteratively based on the net forces acting on them. The choice of sufficiently small time steps ensures numerical stability and accurate resolution of transient interactions between particles [8].

This mathematical framework enables detailed tracking of individual cell trajectories and facilitates quantitative analysis of the spatiotemporal distribution of RBCs, WBCs, and platelets within the microchannel. Key observables, such as cell concentration profiles, vertical displacement, and migration trends, can be extracted to better understand mechanisms of segregation, margination, and collective flow behavior. Such modeling approaches have proven effective in reproducing experimentally observed phenomena and providing insights into microscale hemodynamics that are otherwise difficult to measure directly [10,13].

Governing Equations

The motion of each cell in the simulation is governed by a simplified particle dynamics formulation. The position of each particle is updated using the following equation:

$$X_i(t+\Delta t)=x_i(t)+v_{x,i}\Delta t \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots(1)$$

$$y_i(t+\Delta t)=y_i(t)+v_{y,i}\Delta t \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots(2)$$

Where :

$x_{i,yi}$ represent the spatial coordinates of particle i

$v_{x,i}$,$v_{y,i}$ represent velocity components

Δt is the simulation time step

To prevent overlapping between cells , a short –range repulsive interaction force is applied when the distance between time particles becomes smaller than the sum of their radii .

$$F_{ij} = \begin{cases} k(d_{ij} - r_{ij}) & d_{ij} < r_{ij} \\ 0 & d_{ij} \geq r_{ij} \end{cases} \ldots\ldots\ldots\ldots\ldots\ldots (3)$$

Where

d_{ij} is the distance between particles i and d_{ij}

r_{ij} is the sum of their radii r_{ij}

k is a repulsion coefficient

The maximum vertical position of cells inside the channel is commuted as

$$Y_{max.}(t) = \max(y_i(t)) \ldots\ldots\ldots\ldots..(4)$$

This parameter is evaluated separately for RBCs and WBCs to analyze their vertical migration behavior over time.

Results and Discussion

The simulation results reveal the dynamic behavior and spatial redistribution of blood cells within the microfluidic channel. The instantaneous distributions of RBCs, WBCs, and platelets illustrate the heterogeneous arrangement of cellular components and the continuous movement of particles within the confined domain.

At the initial stages of the simulation, the cells are randomly distributed throughout the channel. As time progresses, interactions between cells lead to noticeable rearrangements in their spatial positions. RBCs, due to their relatively large number, dominate the flow field and form clusters in certain regions of the channel. In contrast, WBCs exhibit more dispersed movement patterns due to their larger size and lower concentration.

Platelets, being the smallest particles in the system, display localized motion and tend to occupy regions between larger cells. Their trajectories appear more irregular, reflecting the influence of interactions with surrounding RBCs and WBCs.

The temporal analysis of the maximum vertical position of cells provides further insight into the migration behavior of different blood components. The results indicate that both RBCs and WBCs experience slight variations in their vertical positions during the simulation. However, WBCs occasionally reach higher vertical positions due to their larger size and stronger interaction effects.

Overall, the simulation demonstrates that cell–cell interactions and spatial confinement play significant roles in determining the distribution patterns of blood cells in microfluidic channels. The observed behavior highlights the importance of considering multicellular interactions when modeling blood flow at the microscale.

The computational simulations provide insight into the complex transport mechanisms governing multicellular blood flow within a confined microfluidic channel. The instantaneous spatial distributions reveal that cell–cell interactions play a significant role in determining the evolving arrangement of RBCs, WBCs, and platelets.

At the early stage of the simulation, the cellular components are randomly distributed throughout the channel. As the simulation progresses, hydrodynamic-like interactions and particle collisions lead to a gradual restructuring of the cellular configuration. RBCs, which constitute the largest fraction of particles in the system, dominate the overall flow dynamics and form clusters in regions where local particle density increases.

The temporal evolution of the maximum vertical position of cells provides further insight into migration mechanisms. RBCs exhibit moderate fluctuations in vertical position due to repeated interactions with neighboring cells. In contrast, WBCs occasionally reach higher vertical positions within the channel because of their larger effective size and stronger interaction forces.

Another important observation is related to platelet transport behavior. Due to their smaller size, platelets demonstrate more irregular motion and tend to move through interstitial regions between larger RBCs. This phenomenon reflects the influence of particle-size disparity on the spatial organization of cells in confined flows.

The vertical distribution analysis indicates that RBCs preferentially occupy the central region of the channel, while smaller particles such as platelets display greater dispersion across the channel height. This behavior can be interpreted as a consequence of particle collisions and spatial constraints within the confined geometry.

Furthermore, the trajectory analysis highlights the highly dynamic nature of multicellular blood flow. Individual cells follow non-linear paths influenced by repeated interactions with surrounding particles. These interactions generate complex migration patterns that contribute to the heterogeneous distribution observed in the microchannel.

Overall, the results demonstrate that particle interactions, size differences, and confinement effects collectively determine the spatiotemporal organization of blood cells in microfluidic environments. Such insights are essential for improving the design of biomedical microdevices used for blood diagnostics, cell sorting, and microcirculation studies.

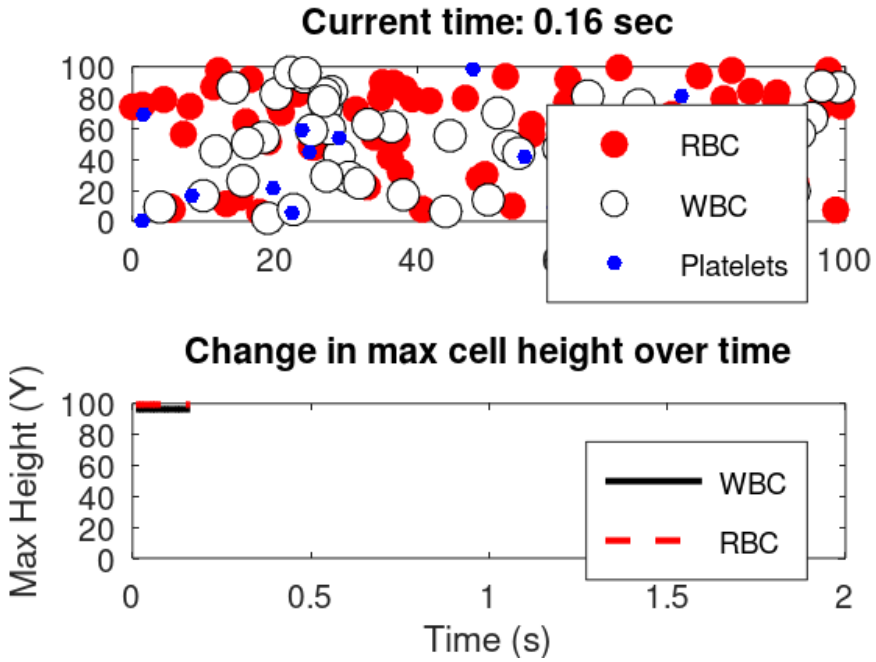


Figure 1. Instantaneous spatial distribution of blood cells inside the microfluidic channel at a representative simulation time

(Figure 1); Instantaneous spatial distribution of blood cells inside the microfluidic channel at a representative simulation time. Red markers represent red blood cells (RBCs), white markers correspond to white blood cells (WBCs), and blue markers indicate platelets. The figure illustrates the heterogeneous distribution of cellular components within the confined flow domain and highlights the dynamic interactions between different blood cell types.

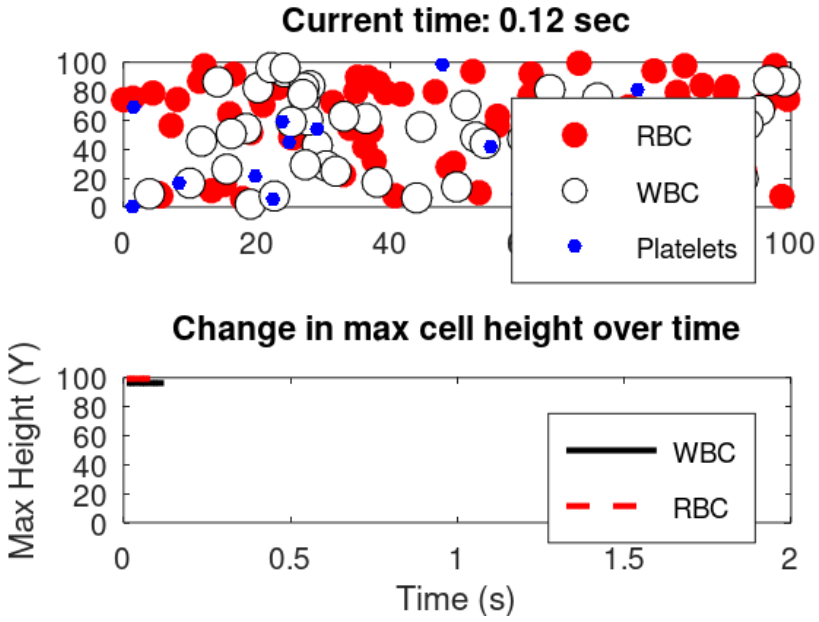


Figure 2. Temporal evolution of the maximum vertical position (Y-direction) of blood cells within the microfluidic channel

Figure(2) ;Temporal evolution of the maximum vertical position (Y-direction) of blood cells within the microfluidic channel. The black solid line represents the maximum height reached by white blood cells (WBCs), while the red dashed line corresponds to red blood cells (RBCs). The plot provides insight into the vertical migration behavior of cells and their spatial distribution during the flow process.

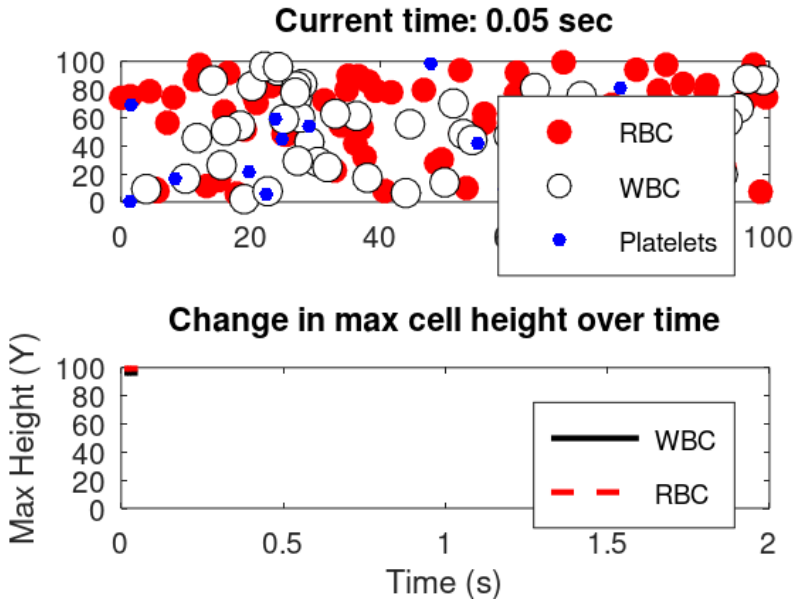


Figure 3. Time-resolved snapshots of the multicellular blood flow simulation at different time instances.

Figure(3) ;Time-resolved snapshots of the multicellular blood flow simulation at different time instances. The figures demonstrate the progressive motion and redistribution of RBCs, WBCs, and platelets within the microchannel. These snapshots highlight the transient dynamics of cell transport and the influence of intercellular interactions on spatial organization.

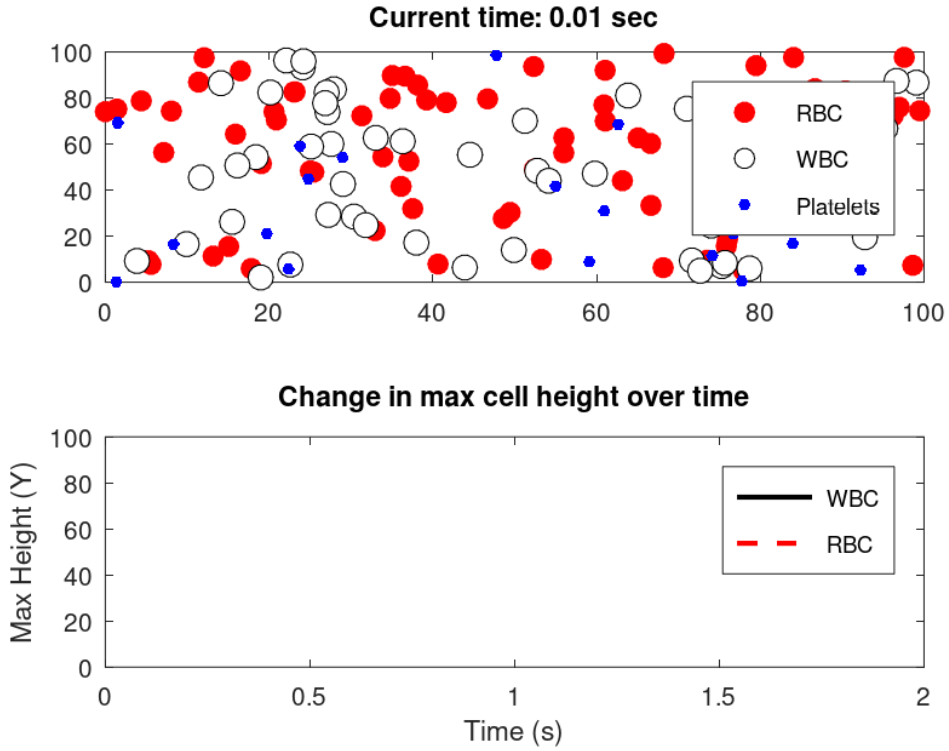


Figure 4. Vertical distribution of blood cells across the microchannel height

Figure (4) ; Vertical distribution of blood cells across the microchannel height. The plot illustrates the spatial concentration of RBCs, WBCs, and platelets along the vertical direction. The results show that RBCs tend to occupy central regions of the channel, while smaller particles such as platelets exhibit greater dispersion.

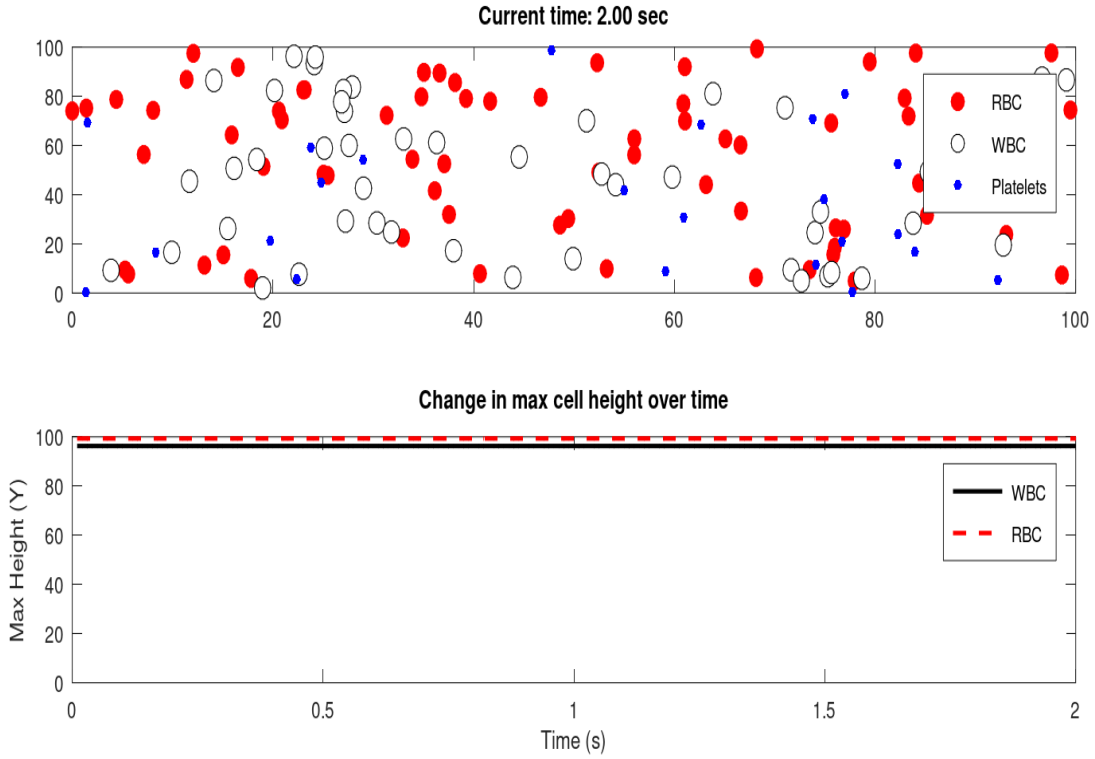


Figure 5. Temporal evolution of cell concentration within the microchannel

Figure(5) ; Temporal evolution of cell concentration within the microchannel. The figure shows the variation in the number density of RBCs, WBCs, and platelets during the simulation period, highlighting the dynamic redistribution of cells due to interparticle interactions.

Conclusion

In this study, a computational model was developed to investigate the spatiotemporal dynamics of multicellular blood flow within a microfluidic channel. The simulation considered three major blood components—red blood cells, white blood cells, and platelets—and tracked their movement and spatial distribution over time.

The results demonstrated that the interactions between different cell types lead to complex redistribution patterns within the confined channel environment. RBCs dominate the overall flow structure, while WBCs and platelets exhibit distinct migration behaviors influenced by their size and interaction characteristics.

The analysis of the maximum vertical position of cells provided additional insight into the transient migration and spatial organization of blood cells during the simulation. These findings contribute to a better understanding of microscale blood flow dynamics and may assist in the design and optimization of microfluidic biomedical devices used for blood analysis and cell separation.

Future work may focus on incorporating more detailed hydrodynamic interactions, deformable cell models, and realistic physiological parameters to further improve the accuracy and applicability of the simulation framework.

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