Microfluidic Simulation of a Separation System of *T.cruzi* from Blood Samples

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Introduction: In 2014, it was estimated that there are between 6 to 7 million people worldwide infected with Trypanosoma cruzi (the parasite responsible for Chagas disease), and approximately 25 million people are currently at risk. The disease develops in two stages and eventually leads to heart disease [1]. The first stage (acute) is asymptomatic and last for about 8 to 12 weeks. This is followed by a second stage (chronic) where the parasite invades tissues. Treatments are only effective during the acute stage but available detection methods require extensive blood testing and well-equipped laboratories, which in turn lead to additional costs [1].

Here we present the CFD simulation of a microfluidic device capable of separating the parasites from Red Blood Cells (RBCs). This represents an opportunity for the development of rapid and affordable diagnostics of Chagas during early stages of the disease via a portable and self-contained system.

Computational Methods: FEM-based modeling and simulations were implemented in the CFD module of COMSOL Multiphysics®. Figure 1 shows the computational domain, which was composed by 5 turns of a 0.5mm wide channel and 4 outlets downstream of a major opening with a 60° angle with respect to the X-axis. Incompressible, Newtonian fluid flow was modeled with the Navier-Stokes Equations (Eq.1) using a Reynolds number of 10. Atmospheric pressure was set as boundary condition for inlet and outlets. The non-slip condition was defined for the other boundaries. The Particle Tracing Module was used for the transport of parasites and RBCs, which were defined as spheres with a diameter of 30µm and 8µm, respectively (Eq.2 and Eq.3).

Mesh convergence analyses were conducted by evaluating the velocity the magnitude at different locations along the domain. The convergence criterion was that upon duplicating the number of elements in a region, the velocity magnitude at each location remained within 2% of the previous value. The study was conducted under steady-state conditions using the PARDISO direct solver.

$$\rho(\vec{\boldsymbol{u}}.\nabla)\vec{\boldsymbol{u}} = -\nabla \mathrm{P} + \mu\nabla^2\vec{\boldsymbol{u}} + \vec{\boldsymbol{F}} \qquad \text{Eq.1}$$

$$\vec{\boldsymbol{F}}_D = \mathbf{3}\pi\mu d_p(\vec{\boldsymbol{u}} - \vec{\boldsymbol{v}}) \qquad \text{Eq.2}$$

$$\vec{\boldsymbol{F}}_L = \rho\frac{r_p^4}{D^2}\beta(\beta G_1(s) + \gamma G_2(s)) \qquad \text{Eq.3}$$

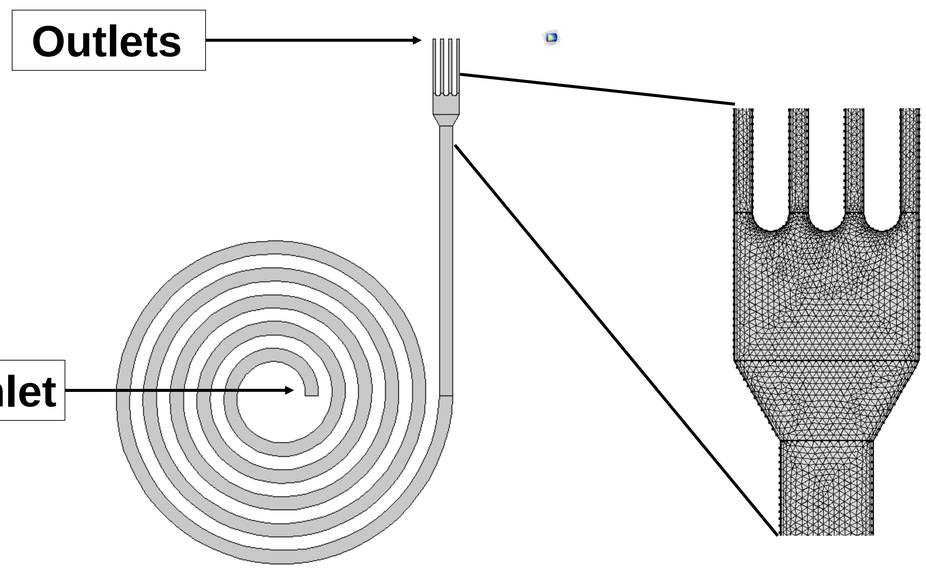


Figure 1. Computational domain and meshing

Results: Figure 2 shows the simulated velocity profile within the device, which was obtained under the best meshing conditions according to the convergence analysis (150,000 elements) (Figure 5). Figure 3 shows the particle trajectories under the same conditions. The number of particles coming out of the device per outlet are shown in Figure 4.

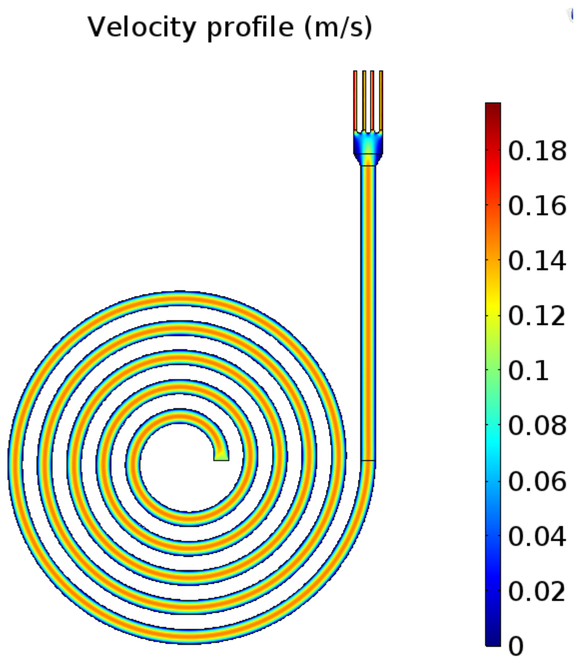


Figure 2. Velocity profile

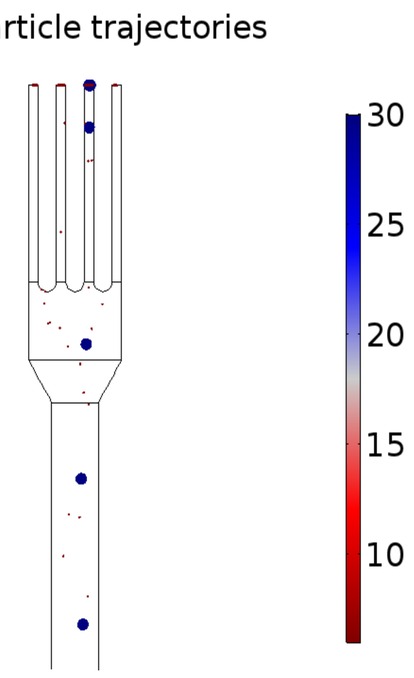


Figure 3. Particle trajectories

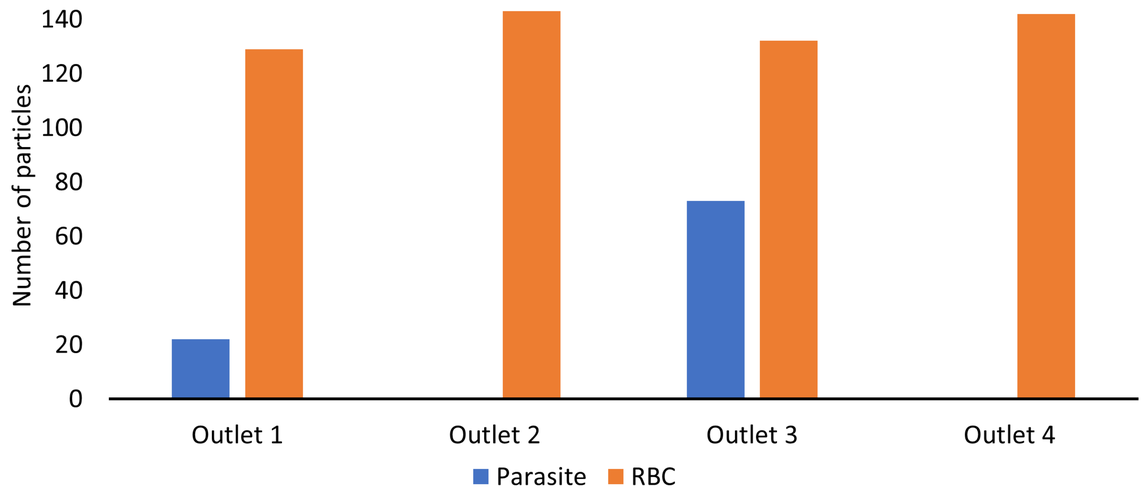


Figure 4. Particle distribution per outlet

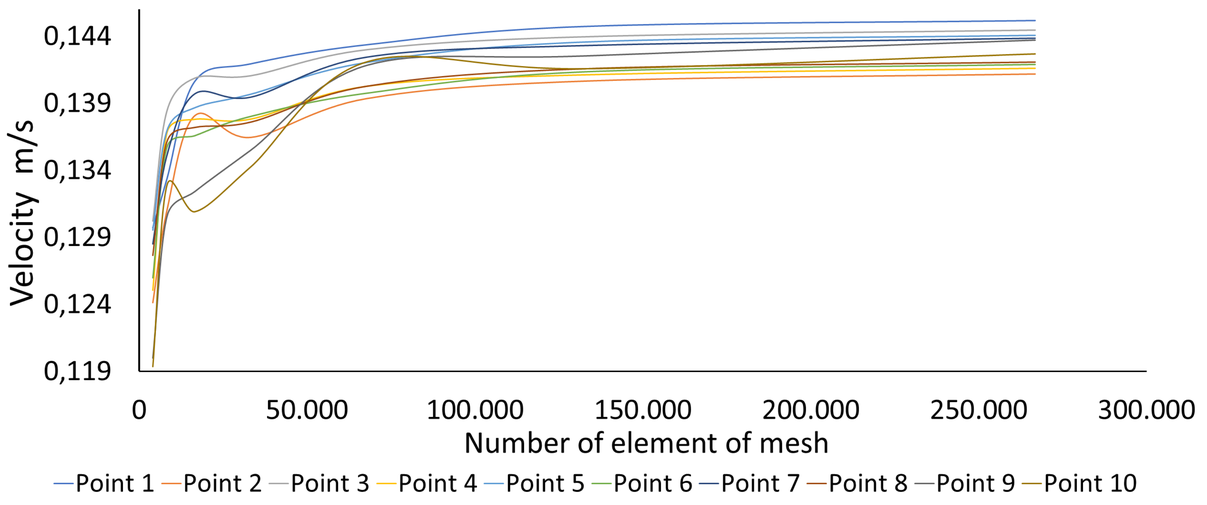
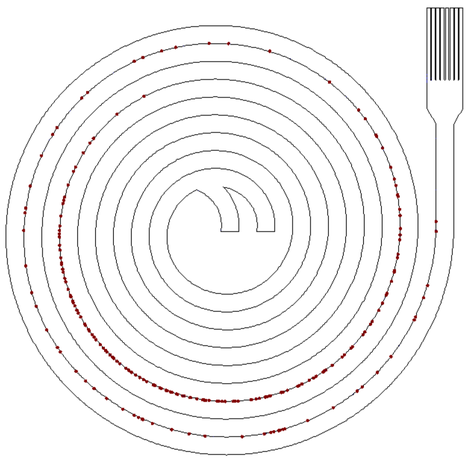


Figure 5. Mesh convergence analysis

Conclusions: There appears to be a preferential separation of the parasite within the device as evidenced by their higher number in outlets 1 and 3. Complete RBC separation however, remains a challenge. This could be potentially accomplished by changing the length of the channel and the number of inlets and outlets.

Future work: Increase the number of outlets, incorporate one more inlet to inject a solvent, and decrease the distance between the spiral end and the outlets to avoid undesirable mixing.



References:

1. "Chagas disease (American trypanosomiasis)", World Health Organization, 2017. [Online]. Available: http://www.who.int/chagas/en/. [Accessed: 23- Jun- 2017].

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