Master Thesis Experiment Report VIII: Clot dissolution

Jérémie Guy

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Abstract

Dissolving the clot

1 Context

Now that we have a fully stable and functioning branching system with a clot, we will attempt to dissolve it progressively.

2 Experiment 1

2.1 Description

The clot is defined by a force field K(x, y, t) which forces the PDFs in the opposite direction. The dissolution in the case of Thrombolysis comes form a coagulant such as tPA, which binds to fibrin and facilitates the conversion of plasminogen to plasmin, a molecule that cleaves the fibrin strands. The amount of tPA present in the system can be considered proportional to the flow of the fluid:

$$flow(x, y, t) = \|\mathbf{u}(\mathbf{x}, \mathbf{y}, \mathbf{t})\|_{2} * \rho(x, y, t)$$
(1)

where u(x, y, t) is the velocity at coordinate (x, y) and time t, and ρ the density. As in a 2DQ9 lattice the velocity is bi-directionnal, we use here norm2 to compute the total amount of velocity in any given cell. Using said proportionality, we implemented a first equation to determine the amount of dissolution for each clot site:

$$\tau(x, y, t) = d * flow(u, x, t) * K(x, y, t) * dt$$
(2)

where d is the dissolution rate. The new clot resistance value K is then computed following the equation :

$$K(x, y, t) = K(x, y, t - 1) - \tau(x, y, t)$$
(3)

In addition, we now added a systematic control: if the result K after equation 3 is smaller than 0, we cap it to 0 as no clot means K = 0.

To test the dissolution method, we started from a stable system state which was obtained using viscosity $\nu=0.01$, initial density $\rho=2.5$, pulse field acceleration F=[0,-0.001] and initial clot resistance K=[0.001,0.001] after running for 60'000 iterations. To make the dissolution faster for testing purposes, we set d=2.

2.2 Results

To monitor the dissolution, we displayed the K values within the clot and followed the results every 10 iterations. Figure 1 shows the results. We can see that the clot dissolves starting from the center: as the fluid follows a Poiseuille parabola, the particle density is higher in the center than in the border of the tube. As such, the clot dissolves from the center to it outside layer.

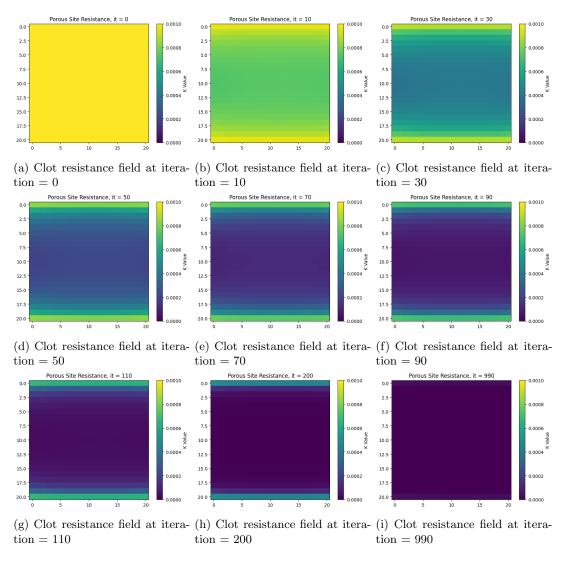


Figure 1: Clot dissolution

3 Experiment 2

3.1 Description

Instead of the simple dissolution implemented as a test in the previous experiment, we will proceed with an Advection-Diffusion to simulate the amount of tPA diffusing through the system. Advection-diffusion describes the diffusion of a quantity ρ subject to an external drift \mathbf{u} . The formal differential equation goes :

$$\partial_t \rho + \nabla(\mathbf{u}\rho) = D\nabla^2 \rho \tag{4}$$

where D is the diffusion coefficient and \mathbf{u} the velocity of the fluid.

3.1.1 Lattice constants

To implement such method in the Lattice-Boltzmann context, we will implement the tPA advection-diffusion process as a second lattice evolving in the same way as the fluid. The first thing to define is the velocity direction vector for tPA. The system will be a D2Q4. We first defined the four velocity vectors as shown in Figure 2 and the directional weights illustrated in Figure 3. We omitted here the stationary direction to make the system simpler and converge faster.

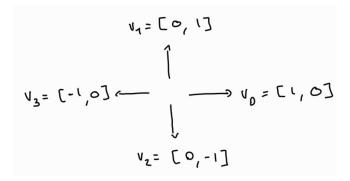


Figure 2: tPA lattice velocity vectors

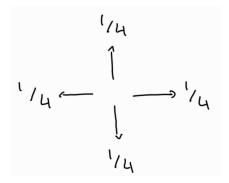


Figure 3: tPA lattice directionnal weights

Following the same logic, we determined the directions for the tPA PDFs going in a lattice cell called tPAin and the ones going out of a cell called tPAout. Both are illustrated in Figures 4a and 4b.

3.1.2 Macroscopic variables

The next step is to determine the macroscopic variables: the density ρ and the velocity \mathbf{u} . The density of tPA will be called ρtPA and as the tPA will here follow the fluid we are building upon, it will not have its own velocity. Instead the velocity of tPA will be same as the fluid velocity \mathbf{u} . The density will then be obtained as standard:

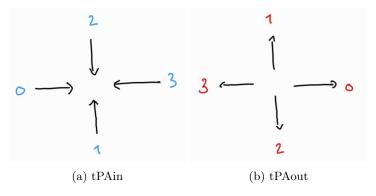


Figure 4: tPAin and tPAout directions and indexes

$$\rho t PA(\mathbf{x}, t) = \sum_{i} t PAin_{i}(\mathbf{x}, t)$$
(5)

where i = 0..3. The tPA equilibrium distribution will be obtained using the following equation [1]:

$$tPAin_i^{\text{eq}} = t_i \rho \left(1 + \frac{1}{c_s^2} \mathbf{v}_i \cdot \mathbf{u} \right) \tag{6}$$

3.1.3 Streaming and Collision

The streaming and collision step will be exactly the same as for the main fluid, only being limited to 4 directions instead of 9. The lattice topology being the same as the main fluid, the tPA will also have separate BGK and bounceback collisions.

3.1.4 Initialization and injection

mk We initialized the tPA's density to be completely null except for a single line in the middle of the left tube section (SEE PREVIOUS SYSTEM). At each iteration, we will simulate the continuous injection by imposing a constant density $\rho tPA_initial = 1$ on said line.

4 Conclusion

5 References

[1] Bastien Chopard, Jean-Luc Falcone, and Jonas Latt. "The lattice Boltzmann advection-diffusion model revisited". In: *The European Physical Journal Special Topics* 171.1 (2009), pp. 245–249. DOI: 10.1140/epjst/e2009-01001-6.