PARALLELIZATION OF A NEW CFD BOUNDARY CONDITION FOR EVOLVING ARTERIOVENOUS MALFORMATIONS

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Summary. *In this study, we investigate the parallel scalability of a blood flow simulation which has a novel approach to couple the arteries and veins through a capillary model. The arteries and veins are modeled in three dimensions while the corresponding capillaries are included into the simulation using zero-dimensional resistance boundary condition. We perform speed-up and data saturation tests to measure the parallel efficiency of our novel coupling algorithm.*

1 INTRODUCTION

3D computational fluid dynamics (CFD) has been widely used to simulate blood flow in patient-specific cardiovascular systems[1,2,3]. Arterial or venous systems have been mostly modeled and investigated separately. However, the coupling of arteriovenous system is inevitable for several diseases such as cerebral arteriovenous malformation and pulmonary artery hypertension. Ignoring the coupling and thus the capillaries, would lead to a substantial inaccuracy in the simulation results. In a previous study, we have developed a new boundary condition to mimic arteriovenous flow by representing capillaries as an additional energy loss between artery and vein systems[4]. This brings out the question of parallel efficiency of the model, since the simulation of realistic cardiovascular systems requires huge amount of computational source. Here, we investigate the answer of this question in the present study.

2 METHODOLOGY

This section covers the details of CFD simulation of blood flow and its parallelization methodology. To take advantage of customization of open source code and avoid the license limitations of commercial software, we use OpenFOAM (openfoam.org) for CFD simulations. Computer generated, idealized geometry including one level of bifurcation was used to represent arteriovenous structure. Resistance boundary conditions were implemented at the arterial outlets (Figure 1a) to represent the pressure drop caused by capillaries before the vein inlets (Figure 1b) using Eq. (1),

$$p = Q * R + p_{vein/atrium} - 0.5 * \rho * (\frac{Q}{A})^2 \qquad (1)$$

where p is the pressure, Q the flow rate, R the resistance of the corresponding outlet, $p_{vein/atrium}$ the end pressure (inlet of the vein or atrium) for the artery or vein, respectively, A the area, and ρ the blood density. Blood is modeled as non-Newtonian fluid using the generalized power-law model. Volumes were meshed with four different meshes size resulting in 40K, 220K, 700K and 1.1M cells. Each mesh is decomposed into 2, 4, 8, 16, 32, 64, 128 and 256 processors using Scotch algorithm (Figure 1c).

3 RESULTS

Figure 1 shows the pressure distribution and velocity streamlines of the arteriovenous system for verification of the CFD results. Results of the parallel tests are presented in Figure 2. Computation time versus number of cores is given for all mesh sizes in Figure 2a. Figure 2b shows the scaled speedup curve with respect to the results of simulations with 4 cores.

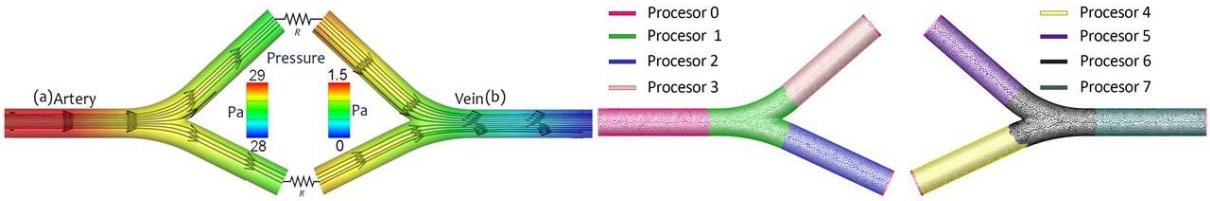

Figure 1: Pressure field and velocity streamlines of the vessel system coupling arteries (a) and veins (b). A sample partition decomposition (c).

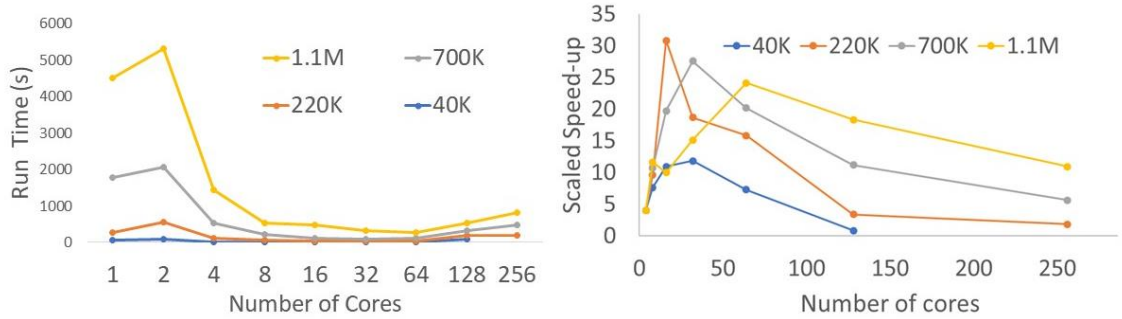

Figure 2: Computation time and speedup graphics for all tests

4 DISCUSSION AND CONCLUSION

The parallel run tests of our novel coupling model shows that our methodology can be run simultaneously in a distributed multicore environment. As the number of cores increases, the run time of the model decreases starting from 2 cores for all mesh sizes. The run is related to the size of the problem (number of meshes) via a 2^{nd} order relation; i.e. doubling the mesh size increases the run time 4 times. Efficiency of the parallelization can be checked using the speedup figure. First of all, the speedup of the simulation tends to increase as the problem size increases which is acceptable in terms of general matrix solution technique. The speedup also increases up to 50 cores and then decreases due to saturation of communication computation ratio.

Overall, the results show that our model can be parallelized with a reasonably good speed-up value. But it needs further improvement by designing new partitioning algorithm and thus reducing communication. This could be achieved by excluding the coupling region as much as possibly from the partitioning cross sections.

REFERENCES

[1] S. Piskin et al., Cardiovascular Eng. And Tech., 2017 Jun;8(2):107-119.
[2] S. Piskin et al., Journal of Biomechanics, Vol 50, 166-171.
[3] G.N. Oguz et al., *J.* Med. Devices 11(2), 021012 (May 03, 2017)
[4] G.N. Oguz et al., *submitted to WCB 2018 Dublin*