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Partitioning of arterial tree for parallel decomposition of hemodynamic calculations

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Abstract
Modeling of fluid mechanics for the vascular system is of great value as a source of knowledge about development, progression, and treatment of cardiovascular disease. Full three-dimensional simulation of blood flow in the whole human body is a hard computational problem. We discuss parallel decomposition of blood flow simulation as a graph partitioning problem. The detailed model of full human arterial tree and some simpler geometries are discussed. The effectiveness of coarse-graining as well as pure spectral approaches is studied. Published data can be useful for development of parallel hemodynamic applications as well as for estimation of their effectiveness and scalability.

Keywords: hemodynamics, vascular net, scalability, graph partitioning, coarse-graining, spectral methods, hill-climbing

1 Introduction

Computational modelling is being increasingly used for biomedicine applications (Winslow, Miller, 2012). One important set of applications is modelling the heart and the vascular system (Wootton, 1999; Taylor, 2004). Many highly advanced examples, which are at the same time close to clinical practice, related to the development, progression, and treatment of cardiovascular disease can be found among them (Tarbell, 2003; Vieira, 2015). The key role of fluid mechanics for vascular system models renders computational hemodynamics a vast and growing field (Sforza, 2009; Taylor, 2013). Many biologically significant features of blood flow cannot be reproduced by approximated hemodynamic models (Reymond, 2013) and full 3D blood flow simulations are required. Possible restrictions on the time of solving in some medical applications make modelling of the heart and vascular system an advanced computational problem. Building multiscale models (Lee, 2012) can be a possible way of improving computational efficiency, however, on the other hand, since the particular

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task of simulating blood flow can be considered as a problem of PFLOPS scale (Grinberg, 2012), effective use of parallel computational resources becomes a critical part of the problem.

Blood flow modelling is different from many conventional hydrodynamics simulations in the sense that the flow domain is often very complex, that is, highly tortuous with many branches and several inlets and outlets. A space decomposition of hydrodynamics problem on such complex domain can results in a very suboptimal configuration with high communication costs and load imbalances. This happens even for relatively simple flow domains like aneurisms (Chopard et al., 2010), and for a full-body model the result should be even worse. For aneurisms though, covering the flow domain with cubic block structure can result in a rather good partition. However, heterogeneity of whole-body networks makes this approach futile.

In this study we discuss the formulation of the problem of parallel decomposition of blood flow simulation domain as graph partitioning problem. We reduce the 3D mesh of vascular system to 1D network, which is then interpreted as a graph, partitioned in a way that minimizes communication and assigned to the processors to compute blood dynamics.

2 Related work

The problem of graph partitioning is a well known. Theoretically it is itself an NP-complete problem (Garey et al, 1976). However, a lot of heuristic algorithms which show reasonably good results on many graphs from different real-life domains were suggested and applied (Safro et al, 2012; LaSalle et al, 2015; Karypis et al, 1988). Some major types of partitioning methods can be distinguished (Buluç, 2013).

The main approaches are coarse-graining the graph to solve the partitioning problem for a smaller number of nodes and then refine it (Safro et al, 2012; Karypis et al, 1988); geometrical methods, which split the graph according to spatial coordinates of the nodes (if such coordinates exist) (Gilbert et al, 2007); spectral methods, which are often used as an intermediate step of coarse-grained schemes; and genetic algorithms (Steenbeek et al, 1998). Some attempts are made to utilize max-flow min-cut theorem to find minimal cut via flow. This approach ignores balance completely, but it can produce good results for regular random graphs (Bui et al, 1987). Also, for some classes, for example planar graphs, exact solutions can be found in polynomial time (Seidel, 2005).

All methods are well represented in studies and the features of applying them to various types of graph are known in general. Despite that, we believe that the issue of partitioning the arterial network has to be considered separately. First of all, the graph based on 1D arterial network has some noticeable features, which cannot be recognized using the common characteristics of graphs such as average degree of vertex, centrality, diameter and etc. While the effectiveness of partition algorithms for various types of graphs is usually classified by these characteristics (LaSalle et al, 2015), extrapolation of these results to the arterial graph is hardly possible. Additionally the common major objectives of developing partitioning algorithms are different from ours. Whereas the performance and parallelization of algorithms is often critical (Benlic, 2011; LaSalle, Karypis, 2015), our graphs are small enough (thousands of vertices) to neglect this issue. Quality of partitioning and its imbalance, on the other hand, are absolutely critical for the obtainable parallel effectiveness of the hypothetical calculation performance.

We apply graph partitioning techniques to anatomical arterial structures to obtain balanced partitions with minimal interconnections. In biomedical disciplines, the graph partitioning problem usually comes up in the context of image recognition and area detection (see for example (Song et al., 2015; Almasi et al., 2014)). When vascular trees have to be partitioned for various purposes, it is usually done by hand or semi-automatically, based on anatomical classification (Malossi et al, 2012; Passerini et al, 2009; Reymond et al, 2009). We aren't aware of any systematic studies of automatic partitioning of large vascular trees.

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