Sujet de Master : Validation numérique en 1D, 2D et 3D de la méthode de la frontière élargie dans le cadre des éléments finis d'ordre élevé et d'une description d'ordre élevé de la géométrie

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On se place dans le cadre de problèmes elliptiques posés dans des domaines perforés. Il s'agit typiquement de problèmes découlant de la modélisation d'écoulements de mélanges fluide/particules. Ainsi, le domaine occupé par le fluide dans un tel mélange peut être perçu comme un domaine perforé.

De part leur forme complexe, les domaines perforés ne s'apprêtent pas à l'utilisation de solveurs rapides et/ou de préconditionnneurs efficaces. Il est donc utile de reformuler le problème initial afin de ramener la résolution en un problème dans un domaine de forme simple. C'est l'idée de base des méthodes de type domaines fictifs. Néanmoins, du fait de la non-conformité du maillage, l'ordre optimal au sens éléments finis n'est pas préservé, notamment quand il s'agit d'éléments finis d'ordre élevé.

Avec la méthode de la frontière élargie nous avons pallié [1] à ce problème en ajoutant un problème auxiliaire au voisinage de chaque inclusion permettant de récupérer l'ordre optimal.

Les deux principaux objectifs de ce stage sont :

- la validation numérique en 1D/2D/3D de la méthode de la frontière élargie en utilisant la librairie Life [3] non seulement pour des approximations d'ordre élevé en espace mais également en décrivant la géometrie par une approximation d'ordre élevé.
- son intégration à Life et en particulier dans le langage spécifique aux équations aux dérivées partielles proposé par Life [2]

Ce projet nécessitera une bonne connaissance de la méthode des éléments finis et une recherche bibliographique sur la méthode frontière élargie. Il se prolonge naturellement sur une thèse autour de cette méthode, voir le sujet les pages suivantes.

Il fera l'objet, pendant le stage de M2 comme pendant la thése d'une collaboration avec Bertrand Maury professeur à l'université Paris Sud et Silvia Bertoluzza directrice de recherche au CNR dans l'équipe d'analyse numérique de Pavie (Italie).

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Towards Blood Flow Simulation : fully parallel numerical simulation of complex fluids with arbitrary order finite elements in moving domains.

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Context

Unlike ordinary liquids and elastic solids, complex fluids exhibit several puzzling behaviours that critically depend on the underlying structures that compose the fluids. Indeed, many complex fluids are made of microscopic entities (such as rigid or soft particles, biological cells, macromolecules etc...) which are suspended in a liquid, and whose individual and collective behaviours strongly impact on the overall rheological properties of the fluid at the global scale. It is this feedback from the microscale to the macroscale that confers to complex fluids nontrivial behaviours that continue to pose a formidable challenge to theoretical modelling. Typical examples of complex fluids are suspensions (rigid particles suspended in a Newtonian fluid), emulsions (droplets suspended in a Newtonian fluid), blood (red blood cells suspended in the plasma), and so on. Complex fluids are the rule in the industrial and biological worlds, conferring thus to this topic an important interest in various domains ranging from the fundamental to the technological level. A significant challenge in complex fluids lies in the understanding of *(i)* the fluid/structure interaction at the individual level and *(ii)* the spatio-temporal organisation of the entities (i.e. their collective behaviours, like jamming, formation of bands...) composing the complex fluid.

Objective

The aim of this project is to *simulate suspensions of a large number of vesicles — acting as models for blood cells — in moving domains*. It has shown that there are several similarities between vesicules and red blood cells (RBC). Particulary from the mechanical point of view. For example, like RBC, vesicles under shear flow exhibit various dynamics : tank treading, tumbling, and vacillating breathing.

The scope is to study pulsed blood flow in medium to small arteries. In this context great displacements of the membrane (over 10% of the radius) of arteries coexist together with confinement of blood flow. This work will build on four ingredients : *(i)* high order discretization methods in space, time and geometry applied to flows in moving domains, see [7, 4], *(ii)* a fictitious domain method, the so called FBM method [6, 3, 5], *(iii)* efficient domain decomposition methods [1] and parallel solver strategies (*e.g.* MUMPS [2]) and *(iv)* efficient use of high performance computing architectures — *e.g.* distributed, parallel and GPU computing.

A word on the FBM

Initially, the Fat Boundary Method is dedicated to the direct simulation of flows containing rigid particles. This method uses a fixed cartesian mesh : the initial problem stated in a perforated

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domain (the fluid domain without the particles) is decomposed into two new problems. The first one is set on the global domain (fluid+particles) and is thus easy to solve on a cartesian mesh with fast solvers. The second is set in a thin layer surrounding each particle, and aims to correcting the error introduced by the global resolution on a neighborhood of the particles. As these particles layers are thin, they could be meshed with a high resolution without a significant increase of computational cost. Moreover the method is well designed for moving particles, since one could move each particle layer mesh independently of the global fixed mesh. This avoid complex (and cpu consuming) adaptative mesh strategies to follow the displacement of particles. At the moment, the FBM has been developed for moving rigid particles without handling contacts. In this project we intend to generalize this method to handle deformable entities. The strategy consists in using a capture interface method such as level sets.

The method offers several opportunities — thanks to the local numerical resolution in the vicinity of vesicles — to develop efficient computing strategies — to handle a large number of vesicles and thus to do numerical studies of the suspensions rheology — such as *(i)* build on *standard* fluid structure interation methods coupled with efficient parallel solvers or *(ii)* solve the many local *small* vesicule problems on very efficient hardware such as GPUs.

Validation

The advantage to use vesicles is their simplicity comparing to red blood cells and especially the possibility to compare numerical results with experimental data. Indeed, there are several experimental works on vesicles in Grenoble and also the begining of a new collaboration between « Laboratoire de Spectrométrie Physique » and Hospital « la Tronche » to study red blood cells.

Collaboration

In the framework of CHPID, a collaboration with Jean-Yves L'Excellent from the GRAAL team at the LIP laboratory is expected around MUMPS [2] as a parallel direct solver. From a theoritical point of view, we shall collaborate with Bertrand Maury, professor at université Paris Sud, and Silvia Bertoluzza, research director at the CNR in the numerical analysis team in Pavia (Italy).

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