Project: An isogeometric finite cell method for FSI in biomechanics

Abstract

During the past two decades,computational biomechanics has become more and more popular and attracted the attention of the researchers in both medicine and engineering communities. Modelling and simulation of complex biological processes are essential for a better understanding and improved clinical treatments of human diseases.

Biological structures data are usually obtained through image-based techniques such as CT-scan or MRI, and recently with the advent of computers, complex biological structures can also be described by tools of Computational Geometry. Traditionally, Finite Element Methods (FEM) have been used to perform analysis. However, the preanalysis time in FEM can be very high for complex shape geometry, up to 80% of the total analysis time [1]. Hence, for complex bio-systems, there is a need of reducing the time of this preanalysis stage. Among advanced numerical methods, Isogeometric analysis (IGA), where splines are used as basis functions, and immersed methods emerge as the most potential candidates.

IGA, introduced by Hughes and co-workers in [2], is a framework in which the gap between Computer Aided Design (CAD) and FEA is reduced. This is achieved in IGA by employing the same basis functions to describe both the geometry of the domain of interest and the field variables. While the standard FEM uses basis functions based on Lagrange polynomials, the isogeometric approach utilizes more general basis functions such as B-splines and NURBS that are commonly used in CAD geometries. The exact geometry is therefore maintained at the coarsest level of discretization and remeshing is seamlessly performed on this coarse level without any further communication with CAD geometries. Furthermore, NURBS provide a flexible way to make refinement, derefinement, and degree elevation They allow to achieve easily the smoothness of arbitrary continuity in comparison with the C^0 continuity provided by the traditional FEM

Immersed boundary methods (some other names are embedded domain methods, fictitious domain methods), on the other hand, tackle the mesh burden issue from a different perspective. The main idea is extending the physical domain of interest with complex shape boundaries into a larger embedding domain of simple/regular geometry where a mesh is easily built. The Finite cell method (FCM) introduced recently by Rank and co-workers in [3] also belongs to this class. In FCM, a material parameter is used to identify the inside and outside of the physical domain, while an adaptive integration technique is employed to capture the geometry of the boundary.

By combining the two above ideas, we try to get the advantages of both worlds, deriving from the higher regularity of IGA basis functions, and from the geometrical flexibility of immersed boundary methods. Therefore, this approach has a great potential of applications for solving fluid-structure interaction (FSI) problems in biomechanics, which is the aim of the project. Some related researches on structural biomechanics can be found in [4, 5].

References

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[4] M. Ruess, D. Tal, N. Trabelsi, Z. Yosibash, and E. Rank. The finite cell method for bone simulations: Verification and validation. *Biomechanics and Modeling in Mechanobiology*, 2011.

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Figures from on-going work

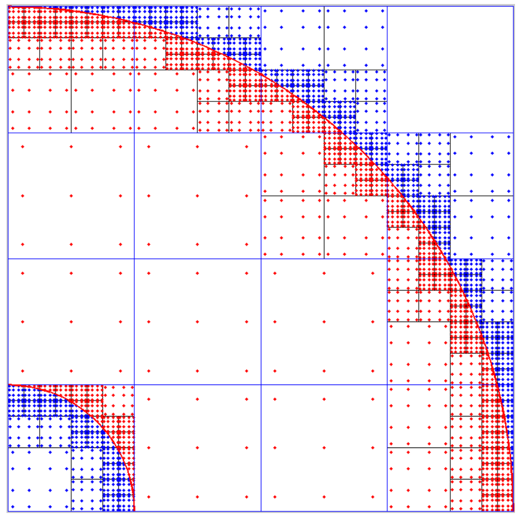

Figure 1: Finite cell method discretization 4x4 cells along with Gauss points distribution; Red points: inside physical domain, Blue points: outside physical domain; here refinement depth = 4

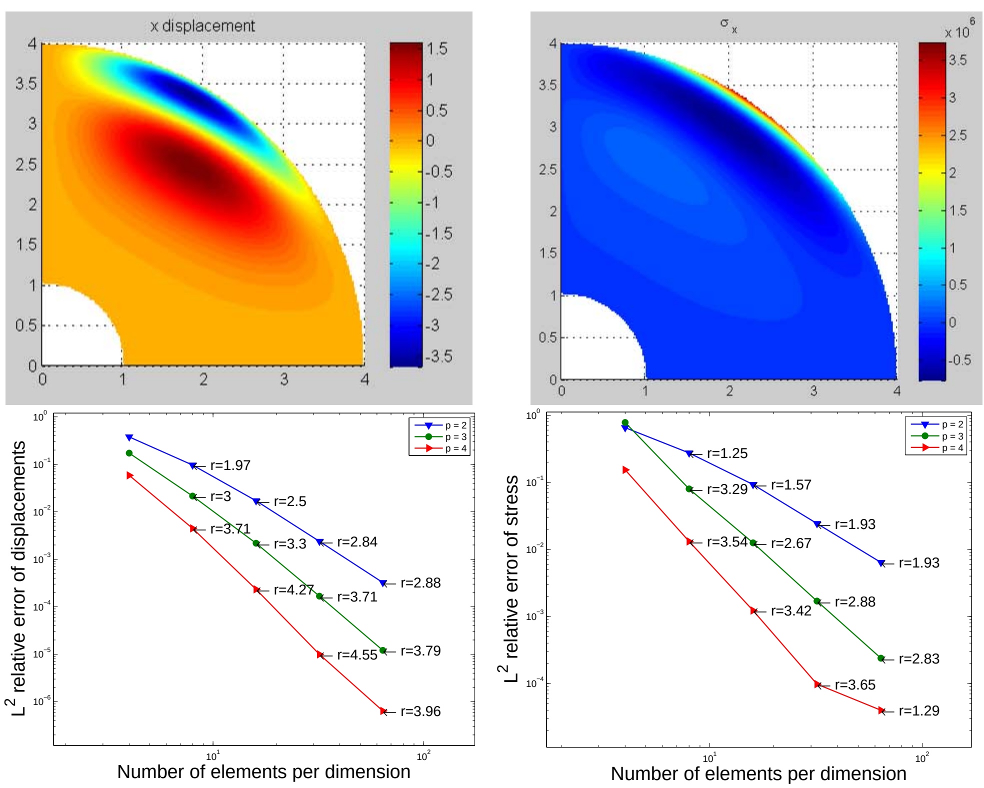

Figure 2: Finite cell method using B-spline TaylorHood elements for nearly incompressible elasticity: (Top) solution with 8x8 cells and $order_u = 3, order_p = 2$ displacement x and stress σ_x; (bottom) optimal convergences of the method