Reduced basis Nitsche-based domain decomposition: a biomedical application

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Abstract. *Nowadays, the personalized biomedical simulations demand real-time efficient and reliable method to alleviate the computational complexity of high-fidelity simulation. In such applications, the necessity of solving different substructure, e.g. tissues or organs, with different numbers of the degrees of freedom and of coupling the reduced order spaces for each substructure poses a challenge in the on-fly simulation. In this talk, this challenge is taken into account employing the Nitsche-based domain decomposition technique inside the reduced order model [D.Baroli]. This technique with respect to other domain decomposition approach allows obtaining a solution with the same accuracy of underlying finite element formulation and to flexibly treat interface with non-matching mesh. The robustness of the coupling is determined by the penalty coefficients that is chosen using ghost penalty technique [E.Burman 2015]. Furthermore, to reduce the computational complexity of the on-fly assembling it is employed the empirical interpolation approach proposed in [E. Schenone]. The numerical tests, performed using FEniCS[Logg et al. 2012], petsc4py and slepc4py [Dalcin et al. 2011], shows the good performance of the method and the reduction of computation cost.*

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