

A BLOCK BASED PRECONDITIONER FOR FLUID-STRUCTURE INTERACTION PROBLEMS

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Abstract. A new block based preconditioner has been proposed to solve the algebraic equations resulting from the fully coupled (monolithic) discretization of fluid-structure interaction (FSI) problems. The present approach is motivated by the relatively simple LDU factorization of the projection method and the parallel algebraic multigrid solver BoomerAMG provided by the HYPRE library is used for the block corresponding to the scaled discrete Laplacian, which we access through the PETSc library. Then the factorization is further improved by employing the BoomerAMG for the blocks corresponding to each component of the displacement vector. The new block preconditioning method has been implemented within our monolithic fluid-structure interaction (FSI) algorithm and it has been applied to the deformation of thin shell structures in three-dimensions, such as red blood cells in small capillaries, where the shell elements have a very high aspect ratio leading to a very bad condition number.

1 INTRODUCTION

The fluid-structure interaction (FSI) problems emerge in many physical, biological, and engineering applications. In the literature, there are two main approaches to solve fluid-structure interaction problems: partitioned (segregated) or fully coupled (monolithic). In the partitioned approach, separate solvers are utilized for the fluid and structure sub-problems. The main advantage of the partitioned approach is the ability to reuse existing solvers, possibly more efficient, specifically developed for either the fluid or the structure subproblem. However, this approach tends to converge slowly and the iterations may diverge in the presence of strong fluid-structure coupling due to the high fluid/structure density ratio which causes the so-called artificial added mass effect. In the monolithic approach, the fluid and solid equations are discretized and solved simultaneously. Although the monolithic approach is highly stable, it requires a relatively robust preconditioner. In the literature, several block based parallel preconditioners are proposed. Heil [6] proposed a block factorization based on neglecting the fluid-solid or solid-fluid interaction blocks. Deparis et al. [3] used a similar preconditioner based on dropping the block associated with the transpose of the kinematic coupling condition. In these

approaches, the two-way coupling between the fluid and solid domains is ignored at the preconditioning level. This is improved in the block preconditioner proposed by Langer and Yang [7] based on the complete LDU factorization of the coupled system matrix.

2 MONOLITHIC SOLVER

The present monolithic fluid-structure interaction algorithm is initially implemented in [4]. The resulting coupled system of nonlinear algebraic equations can be written in the following block structure form including the velocity, displacement and pressure unknowns:

$$\begin{bmatrix} A_{uu} & A_{ud} & A_{up} \\ A_{du} & A_{dd} & A_{dp} \\ A_{pu} & 0 & 0 \end{bmatrix} \begin{bmatrix} \mathbf{u}^{n+1} \\ \Delta \mathbf{d}^{n+1} \\ p^{n+1} \end{bmatrix} = \begin{bmatrix} d_1 \\ d_2 \\ 0 \end{bmatrix} \quad (1)$$

The present block preconditioner is motivated by the relatively simple LDU factorization of the projection method [2] assuming that the time step is small and the viscous (not pressure) forces can be neglected. Then, the initial preconditioner matrix P_1 can be approximated as

$$P_1 = \begin{bmatrix} I & A_{ud} & A_{up} \\ 0 & I & A_{dp} \\ A_{pu} & 0 & 0 \end{bmatrix} = \begin{bmatrix} I & 0 & 0 \\ 0 & I & 0 \\ A_{pu} & -A_{pu}A_{ud} & I \end{bmatrix} \begin{bmatrix} I & 0 & 0 \\ 0 & I & 0 \\ 0 & 0 & S_{pp} \end{bmatrix} \begin{bmatrix} I & A_{ud} & A_{up} \\ 0 & I & A_{dp} \\ 0 & 0 & I \end{bmatrix} \quad (2)$$

where $S_{pp} = -A_{pu}A_{up} + A_{pu}A_{ud}A_{dp}$. The exact inverse of the first and third matrices can be easily computed since the matrices are triangular. Then P_1^{-1} can be computed as

$$P_1^{-1} = \begin{bmatrix} I & -A_{ud} & A_{ud}A_{dp} - A_{up} \\ 0 & I & -A_{dp} \\ 0 & 0 & I \end{bmatrix} \begin{bmatrix} I & 0 & 0 \\ 0 & I & 0 \\ 0 & 0 & S_{pp}^{-1} \end{bmatrix} \begin{bmatrix} I & 0 & 0 \\ 0 & I & 0 \\ -A_{pu} & A_{pu}A_{ud} & 1 \end{bmatrix} \quad (3)$$

For the second matrix, the matrix inverse S_{pp}^{-1} is approximated by employing two steps of the parallel algebraic multigrid solver BoomerAMG provided by the HYPRE library [5], which we access through the PETSc library [1]. In here, $A_{pu}A_{ud}A_{dp}$ term of the S_{pp} matrix should not be neglected, since the eigenvalue analysis of the $A_{pu}A_{up}$ matrix indicates that one of its eigenvalues is zero if the fluid domain is entirely enclosed by the solid domain. The present preconditioner can be further improved by employing the following block factorization.

$$P_2^{-1} = \begin{bmatrix} I & A_{ud} & A_{up} \\ 0 & I & S_{dp} \\ A_{pu} & 0 & 0 \end{bmatrix}^{-1} \begin{bmatrix} I & 0 & 0 \\ 0 & S_{dd} & 0 \\ 0 & 0 & I \end{bmatrix}^{-1} \begin{bmatrix} I & 0 & 0 \\ A_{du} & I & 0 \\ 0 & 0 & I \end{bmatrix}^{-1} = \begin{bmatrix} I & A_{ud} & A_{up} \\ A_{du} & A_{dd} & A_{dp} \\ A_{pu} & 0 & 0 \end{bmatrix}^{-1} \quad (4)$$

where $S_{dp} = A_{dd}^{-1}A_{dp}$ and $S_{dd} = A_{dd} - A_{du}A_{ud}$. In here, the S_{dp} term is approximated as $S_{dp} = \text{diag}(A_{dd})^{-1}A_{dp}$, where $\text{diag}(A_{dd})$ represents the diagonal entries of the A_{dd} matrix. The above first matrix is factorized using the same approach above. The PCFIELDSPLIT preconditioner within the PETSc library is used for the second matrix to implement

the block preconditioner for the S_{dd} matrix corresponding the each components of the displacement vector and the parallel algebraic multigrid solver BoomerAMG is also used for the each diagonal block.

3 NUMERICAL RESULTS

The numerical algorithm [4] with the new preconditioner has been applied to the deformation of the red blood cells in a small capillary tube with a diameter of $10\mu m$. The red cell diameter is $7.8\mu m$ and its membrane thickness is set to $50nm$. The non-dimensional capillary number ($Ca = \mu_f U_{max} / \mu_s h$) is obtained to be 0.145. The physical parameters are provided in Table 1. The computed red cell deformations/positions are provided in Figure 1 and the results are compared with those of a sphere with the same diameter and membrane thickness. The red cell undergoes a cupcake shaped buckling instability in three-dimensions due to the compressive elastic tension forces along the red cell membrane surface and the resulting red cell geometry is no longer axisymmetric but three-dimensional. The comparison of the initial and final deformations are also provided in Figure 2.

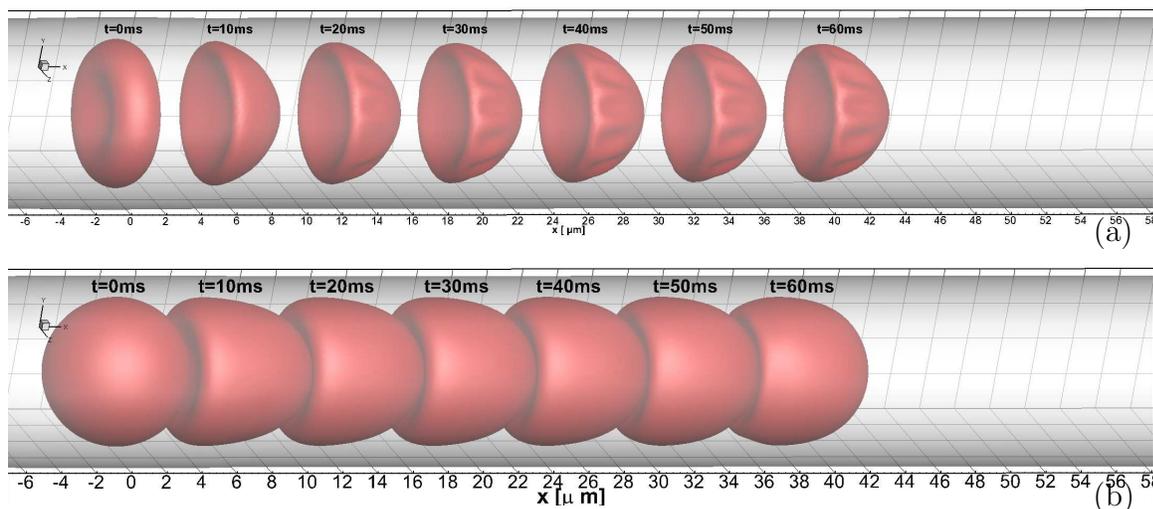


Figure 1: Red blood cell (a) and sphere (b) positions/deformations at several different time levels in a capillary tube with a diameter of $10\mu m$.

Table 1: Physical parameters for red blood cell and fluid plasma (pg : picogram).

Fluid	Density, ρ_f	$[pg/\mu m^3]$	1.025
	Dynamic viscosity, μ_f	$[pg/\mu m\mu s]$	1.1
	Maximum inflow velocity, U_{max}	$[\mu m/\mu s]$	0.001
Structure	Density, ρ_s	$[pg/\mu m^3]$	1.098
	Poison ratio, ν_s	–	0.45
	Young’s modulus, E	$[pg/\mu m\mu s^2]$	1.76

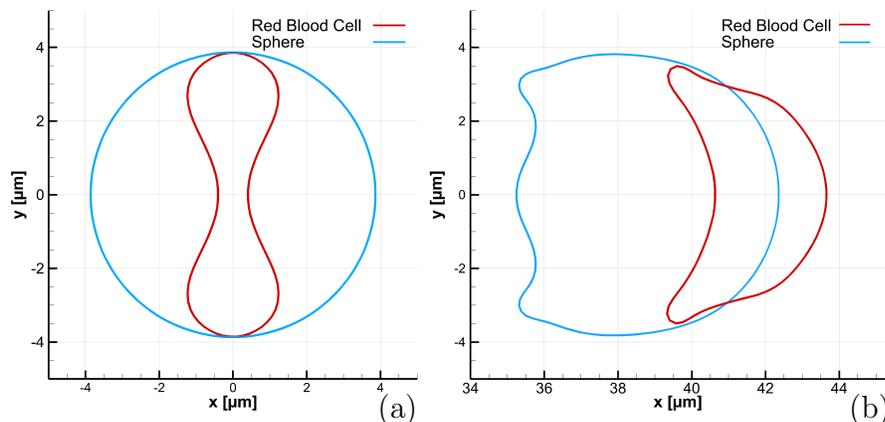


Figure 2: Initial (a) and final (b) shapes of red blood cell and sphere in a capillary tube with a diameter of $10\mu\text{m}$.

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