

# **An efficient multigrid solver based on aggregation**

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## **ABSTRACT**

Modeling in biomedical applications often leads to complex coupled systems of PDEs that can only be solved numerically. After discretization, one is left with a huge set of linear or nonlinear equations, whose solution requires proper techniques. And the latter often need as building block an inner procedure able to quickly solve discrete Poisson-like or convection-diffusion equations, sometimes with complex geometries and highly varying coefficients.

In this talk, we present a solver having these capabilities. It is of algebraic multigrid type, but uses a somehow nonstandard coarsening based on the aggregation of the unknowns. Among its attractive features, it offers stable performances without parameter tuning or variant switch; that is, using the code in a purely black box fashion. It also scales well in parallel. This is illustrated with numerical results obtained on a set of examples that includes symmetric and highly nonsymmetric 2D and 3D problems, with both structured and unstructured grids, some of them with local refinement and/or higher order finite element discretization, and possible strong jumps or anisotropies in the coefficients. Results in parallel with many cores are also presented. Eventually, a numerical comparison with other solvers, suggests that the aggregation-based method can be significantly faster, especially on "difficult" 3D examples.