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A multi-domain approach for smoothed particle hydrodynamics simulations of highly complex flows

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Highlights

- A novel multi-domain approach is proposed in smoothed particle hydrodynamics method.
- The computational domain is partitioned into non-overlapping blocks.
- Particles leave and enter subdomains through a procedure ensuring mass conservation.
- A fast and efficient matching procedure at the block interfaces is employed.
- 2D and 3D test cases confirm the seamless flow transition through the interfaces.

Abstract

An efficient and accurate method is proposed to solve the incompressible flow momentum and continuity equations in computational domains partitioned into subdomains in the framework of the smoothed particle hydrodynamics method. The procedure does not require any overlap of the subdomains, which would result in the increase of the computational effort. Perfectly matching solutions are obtained at the surfaces separating neighboring blocks. The block interfaces can be both planar and curved surfaces allowing to easily decompose even geometrically complex domains.

The *smoothing length* of the *kernel* function is maintained constant in each subdomain, while changing between blocks where a different resolution is required. Particles leaving each block through the interfaces are deactivated and correspondingly new particles are generated at the neighboring block using a dynamically adaptive procedure to control their frequency of release. No splitting and coalescing method is thus employed to take into account the different size and mass of the particles going through the interfaces. Mass conservation is guaranteed during the procedure, which is a challenging task in a Lagrangian method based on the domain decomposition.

The test cases in both 2D and 3D approximation show the accuracy of the method and its ability to strongly reduce the computational efforts through a multi-resolution approach.

Keywords: Smoothed particle hydrodynamics; ISPH; Multi-block; Domain decomposition; Boundary conditions; Mirror particles

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1. Introduction

Smoothed particle hydrodynamics (SPH) is a Lagrangian particle method in which the equations are solved using discrete convolution integrals with filter functions of assigned shape, indicated as *kernel* functions. Each particle is assigned a *support domain*, including all the surrounding particles having distance lower than the product between the characteristic width h of the *kernel function* (known as *smoothing length*) and a constant k depending on the shape of the *kernel* function. The accuracy of the computation is directly related to the *smoothing length*, which plays a role corresponding to the cell dimension in grid-based methods. In order to obtain high quality solutions, a reasonably high number of particles must be contained in each *support domain*, maintaining a relatively regular space distribution during the time evolution of the simulation.

The number of particles N depends on their isotropic initial distance Δx, which is commonly assigned as proportional to the *smoothing length* h. Thus, in 3D computations, it is $N \propto h^3$. Each particle moreover is assigned a given mass $m = \rho \Delta x^3$, where ρ is the particle density.

In mesh methods, in order to reduce the computational efforts, grids are usually non uniform, being stretched and/or clustered close to external or internal boundaries and in regions of the computational domains with high gradients of the hydrodynamic variables. On the contrary, in the classic SPH approach the *smoothing length* is uniform in space due to the difficulty of changing the width of the *kernel function* while the particles move from one region to another. The computational efforts are thus very high, since the value of the *smoothing length* must be chosen according to the one imposed by the regions requiring the finest discretization. The same computational overload would be undergone by grid-based methods employing in the whole domain cubic cells with constant size.

In order to overcome this drawback, several refinement strategies have been proposed in the SPH approach, using a variable *smoothing length* ($h = h(\mathbf{x_p})$, where $\mathbf{x_p}$ is the particle position) to increase the computational efficiency [1,2]. Due to the Lagrangian nature of the method, these approaches require introducing splitting and coalescing techniques for the particles, since their dimension and support domain are required to adapt to the space dependent h [3–9].

Here a different approach is proposed, based on multi-domain decomposition, which allows to use different values of the *smoothing length* in the blocks, while maintaining inside each of them the simplicity of the classic SPH method with constant h. In the proposed procedure, differently from [10], no overlapping of the subdomains is employed, thus avoiding any artificial increase of the computational domain. During the simulations the particles leaving each subdomain through the internal interfaces (outflow) are removed from the computation, while a specific procedure allows to generate new particles in correspondence of inflow interfaces. The procedure, which is similar to the one employed by Napoli et al. [11] in the coupling of the SPH and finite volume methods, guarantees perfect mass conservation in each block and in the whole domain and allows each interface to switch from inflow to outflow (and *vice verse*) during the simulation. Inflow and outflow conditions are allowed to coexist in the same interface, as discussed by Monteleone et al. [12].

The proposed multi-domain technique is employed here in the framework of the Incompressible SPH approach [13–15], based on the fractional-step resolution of the Navier–Stokes equations. The discretized Pressure Poisson equations, required to impose the null-divergence condition, are solved using for the whole domain a unique equation system, obtained putting together the single sub-systems of each subdomain. The solution of the system is obtained through a pre-conditioned BicGStab algorithm [16]. The simultaneous solution of the sub-systems allows to obtain a perfectly matched solution among the single subdomains, where different particle sizes are employed.

Three different test cases are used to show the efficiency and accuracy of the proposed method: the 3D unsteady channel flow in a cylindrical pipe, the 2D vortex shedding in the wake of a circular cylinder and the hemodynamic systolic cycle in a cerebral vessel with an aneurysmatic sac. Although all the test cases are relative to confined flows, in principle no limitation exists to the application of the proposed method to free-surface flows.

The paper is organized as follows: in the second section a general description of the ISPH method is given, in the third the proposed multi-domain technique is described in detail and in the fourth the validation through the employed test cases is discussed. Some conclusions are finally drawn in the last section.

2. ISPH basic formulation

The generic function f at the position $\mathbf{x}$ can be expressed in the *smoothed* form $\langle f(\mathbf{x}) \rangle$ through the integral convolution:

$$\langle f(\mathbf{x}) \rangle = \int_D f(\mathbf{x})\, W(\mathbf{x} - \mathbf{x}', h)\, d\mathbf{x}' \tag{1}$$

where W is a *kernel function* of *smoothing length* h and D is the computational domain.