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Conservative scheme for two-fluid compressible flows without pressure oscillations

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(joint work with Jung, Jonathan)

Compressible two-fluid flows are difficult to numerically simulate. Indeed, classic conservative finite volume schemes do not preserve the velocity and pressure equilibrium at the two-fluid interface. This leads to oscillations, lack of precision and even, in some liquid-gas simulations, to the crash of the computation. Several cures have been proposed to obtain better schemes (see [1] and included references). The resulting schemes are generally not conservative. Based on ideas of [2], we propose a new Lagrange-Projection scheme. The projection step is based on a random sampling strategy at the interface. The scheme has the following properties: it preserves constant velocity and pressure at the two-fluid interface, it preserves a perfectly sharp interface and it is fully conservative (in a statistical sense). The scheme can be extended to higher space dimensions through Strang dimensional splitting. Finally, it is very simple to implement and thus well adapted to massively parallel GPU computations.

We are interested in the numerical resolution of the following system of partial differential equations, modeling a liquid-gas compressible flow

$$(1) \quad \partial_t W + \partial_x F(W) = 0,$$

where

$$W = (\rho, \rho u, \rho v, \rho E, \rho \varphi)^T, F(W) = (\rho u, \rho u^2 + p, \rho u v, (\rho E + p)u, \rho u \varphi)^T.$$

The unknowns are the density ρ , the two components of the velocity u, v , the internal energy e and the mass fraction of gas φ . The unknowns depend on the space variables x and on the time variable t . The total energy E is the sum of the internal energy and the kinetic energy $E = e + (u^2 + v^2)/2$. The pressure p of the two-fluid medium is a function of the other thermodynamical parameters $p = p(\rho, e, \varphi)$. We consider a stiffened gas pressure law $p(\rho, e, \varphi) = (\gamma(\varphi) - 1)\rho e - \gamma(\varphi)\pi(\varphi)$, where γ and π are given functions of the mass fraction φ , and $\gamma(\varphi) > 1$.

At the initial time, the mass fraction $\varphi(x, y, 0) = 1$ if the point (x, y) is in the gas region and $\varphi(x, y, 0) = 0$ if the point (x, y) is in the liquid region. The mass fraction is transported with the flow, which implies that for any time $t > 0$, $\varphi(x, y, t)$ can take only the two values 0 or 1. However, classic numerical schemes generally produce an artificial diffusion of the mass fraction, and in the numerical approximation we may observe $1 > \varphi > 0$. In classic conservative schemes, the artificial mixing zone implies a loss of the velocity and pressure equilibrium at the interface.

We construct a better numerical scheme for solving (1). We consider a sequence of time t_n , $n \in \mathbb{N}$ such that the time step $\tau_n = t_{n+1} - t_n > 0$. We consider also a space step h . We define the cell centers by $x_i = ih$. The cell C_i is the interval $]x_{i-1/2}, x_{i+1/2}[$. We look for an approximation $W_i^n \simeq W(x_i, t_n)$. Each time step of

the scheme is made of two stages: an Arbitrary Lagrangian Eulerian (ALE) step and a Projection step.

ALE stage. In the first stage, we allow the cell boundaries $x_{i+1/2}$ to move at a velocity $\xi_{i+1/2}^n$. At the end of the first stage, the cell boundary is

$$x_{i+1/2}^{n+1,-} = x_{i+1/2} + \tau_n \xi_{i+1/2}^n.$$

Integrating the conservation law (1) on the moving cells, we obtain the following finite volume approximation

$$h_i^{n+1,-} W_i^{n+1,-} - h W_i^n + \tau_n (F_{i+1/2}^n - F_{i-1/2}^n) = 0.$$

The new size of cell i is given by

$$h_i^{n+1,-} = x_{i+1/2}^{n+1,-} - x_{i-1/2}^{n+1,-} = h + \tau_n (\xi_{i+1/2}^n - \xi_{i-1/2}^n).$$

The numerical flux is of the form

$$F_{i+1/2}^n = F(W_{i+1/2}^n) - \xi_{i+1/2}^n W_{i+1/2}^n.$$

The intermediate state $W_{i+1/2}^n$ is obtained by the resolution of a Riemann problem. More precisely, we consider the entropy solution of

$$\begin{aligned} \partial_t V + \partial_x F(V) &= 0, \\ V(x, 0) &= \begin{cases} V_L & \text{if } x < 0, \\ V_R & \text{if } x > 0, \end{cases} \end{aligned}$$

which is denoted by $R(V_L, V_R, x/t) = V(x, t)$. The intermediate state is then $W_{i+1/2}^n = R(W_i^n, W_{i+1}^n, \xi_{i+1/2}^n)$. In practice, R can also be an approximate Riemann solver.

Finally, the interface velocity is defined by

$$(2) \quad \xi_{i+1/2}^n = \begin{cases} u_{i+1/2}^n & \text{if } (\varphi_i^n - 1/2)(\varphi_{i+1}^n - 1/2) < 0, \\ 0 & \text{else.} \end{cases}$$

The numerical flux is thus a classic Godunov flux in the pure fluid. It is a Lagrangian numerical flux at the two-fluid interface.

Projection step. The second stage of the time step is needed for returning to the initial mesh. We have to compute on the cells C_i of the initial mesh the averages of $W_i^{n+1,-}$, defined on the moved cells $C_i^{n+1,-} =]x_{i-1/2}^{n+1,-}, x_{i+1/2}^{n+1,-}[$. Instead of a standard integral averaging method, we rather consider a random sampling averaging process. We consider a pseudo random sequence $\omega_n \in [0, 1[$ and we perform the following sampling

$$(3) \quad W_i^{n+1} = \begin{cases} W_{i-1}^{n+1,-}, & \text{if } \omega_n < \frac{\xi_{i-1/2}^n \tau_n}{h}, \\ W_i^{n+1,-}, & \text{if } \frac{\xi_{i-1/2}^n \tau_n}{h} \leq \omega_n \leq 1 + \frac{\xi_{i+1/2}^n \tau_n}{h}, \\ W_{i+1}^{n+1,-}, & \text{if } \omega_n > 1 + \frac{\xi_{i+1/2}^n \tau_n}{h}. \end{cases}$$

A good choice for the pseudo-random sequence ω_n is the (k_1, k_2) van der Corput sequence. In practice, we consider the $(5, 3)$ van der Corput sequence.

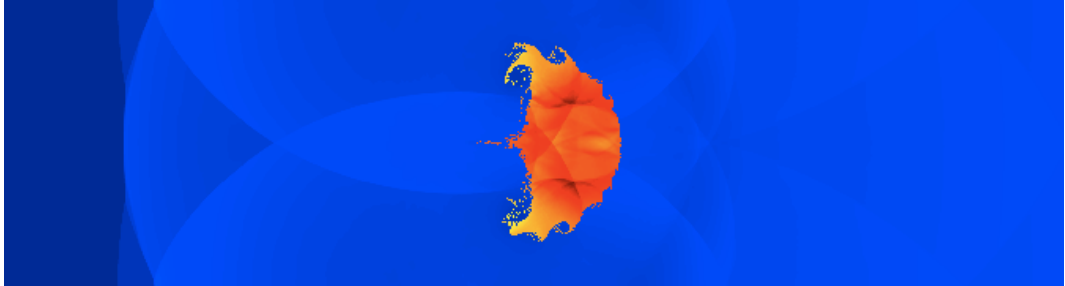


FIGURE 1. Shock-droplet simulation. Density plot.

We can extend the scheme to higher dimensions with dimensional splitting (more details in [3]). It is remarkable that the same random number can be used for one time step in the x and y directions. We present in Figure 1 the results of a two-dimensional shock-droplet GPU simulation. We observe that we are able to capture a sharp interface and small Kelvin-Helmholtz vortices. The numerical noise is moderate, despite the random nature of the scheme.

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