



# High-order remapping with piece-wise parabolic reconstruction



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## ABSTRACT

High-order remapping methods, using piece-wise parabolic reconstruction with different limiting techniques trying to keep monotonicity (defined in terms of bounds on remapped solution) in the neighborhood of discontinuities, are investigated and compared on cyclic remapping tests. Piece-wise parabolic remapping methods based on PPM and FCT approaches keep the solution bounds in all the cases. These methods provide more accurate results than the standard remapping method using piece-wise linear reconstruction, usually with Barth–Jespersen limiter.

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## 1. Introduction

The Arbitrary Lagrangian Eulerian (ALE) method is an extension of Lagrangian hydrodynamical methods which allows to overcome the difficulties connected with moving Lagrangian mesh, which for some flow patterns, as e.g. shear or vortex flows, becomes distorted so much that the Lagrangian computation cannot continue. In such a case (or regularly after some number of Lagrangian time steps) the ALE method rezones the distorted mesh to a new smoother one and interpolates the conservative quantities (mass, momentum and energy) from the old mesh to the new one. The interpolation has to be conservative and is called remapping. The remapping methods [1–3] typically use piece-wise linear (or constant) reconstruction of the conserved quantities on the old mesh. During the remapping, the reconstruction is integrated over the new cells to get remapped quantities on the new mesh. The piece-wise constant reconstruction leads to the first-order remapping, while piece-wise linear reconstruction is second-order accurate in regions of smooth flow. Here we investigate the usage of piece-wise quadratic reconstruction for the remapping which should be third-order accurate.

It is well-known that using standard piece-wise linear reconstruction works fine in the regions of smooth flow, however produces overshoots and undershoots (or even oscillations) when employed for remapping in the vicinity of discontinuities. These monotonicity violations are usually treated by applying limiters which effectively reduce the slopes of linear reconstructions around discontinuities

resulting in monotone remapping. In the remapping context the monotonicity requirement requests the remapped data to be monotone when the initial data are monotone. Monotonicity of remapping is usually formulated in terms of bounds preservation and is reasonably well understood for piece-wise linear reconstructions. Here we look into the issue of how to limit piece-wise parabolic reconstructions, so that remapping results will stay monotone, in bounds, where we use the standard definition of bounds. We try in the remapping context several types of limiting of piece-wise parabolic reconstruction [4–6]. Instead of limiters one can use flux corrected remapping [7,8] combining low-order and high-order numerical remapping fluxes in a way satisfying the bounds. An option to correct remapping results being out of bounds is to use repair techniques [3,2] which redistributes conservatively the quantities being out of bounds into the neighboring cells. Remapping with piece-wise quartic reconstruction, being the extension of the PPM method [6], has been investigated in [9] for ocean modeling.

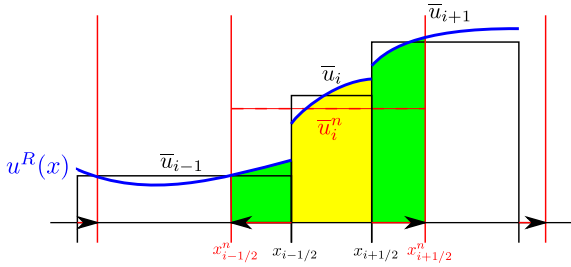
The rest of the paper is organized as follows. Section 2 contains general introduction into the remapping in the flux form and definition of the remapping monotonicity. Different methods for piece-wise parabolic reconstruction as well as introduction to flux corrected approach for the remapping are described in Section 3. In the next section, the order of convergence and bound-preservation of the methods are verified numerically on a set of cyclic remapping tests for few types of smooth and discontinuous functions.

## 2. Remapping

In the selected approach the remapping can be divided into two stages. At the first stage the remapped quantity is reconstructed on

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**Fig. 1.** Remapping in a single cell. The old computational mesh with nodes  $x_{i±1/2}$  and means  $\bar{u}_i$  are in black, the new ones are in red. The reconstructed piece-wise parabolic function  $u(x)$  is in blue. The green areas correspond to the numerical fluxes  $F_{i±1/2}$ . (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

the old mesh. At the second stage the reconstructed function is being integrated over all cells of the new mesh (see Fig. 1). We denote the nodes of the old mesh by  $x_{i-1/2}$  and the nodes of the new mesh by  $x_{i-1/2}^n$ . The mean value  $\bar{u}_i$  of the conserved quantity  $u(x)$  in the old cell  $(x_{i-1/2}, x_{i+1/2})$  is defined as

$$\bar{u}_i = \frac{1}{\Delta x_i} \int_{x_{i-1/2}}^{x_{i+1/2}} u(x) dx, \quad (1)$$

where  $\Delta x_i = x_{i+1/2} - x_{i-1/2}$  denotes the old cell volume. After the Lagrangian step one does not know the function  $u(x)$ . Only the old means  $\bar{u}_i$  and old mesh  $x_{i-1/2}$  are known. The new mesh  $x_{i-1/2}^n$  is constructed during the rezone stage (here we assume that the rezoned nodes  $x_{i-1/2}^n$  do not move outside the neighboring old cells, i.e.  $x_{i-3/2} \leq x_{i-1/2}^n \leq x_{i+1/2}, \forall i$ ) and the remapping task is to compute the new means  $\bar{u}_i^n$

$$\bar{u}_i^n \approx \frac{1}{\Delta x_i^n} \int_{x_{i-1/2}^n}^{x_{i+1/2}^n} u(x) dx, \quad (2)$$

on the new mesh, where  $\Delta x_i^n = x_{i+1/2}^n - x_{i-1/2}^n$  is the volume of the new cell. The quantity  $u$  is conservative, so we naturally require the remapping to be conservative, i.e.

$$\sum_i \bar{u}_i \Delta x_i = \sum_i \bar{u}_i^n \Delta x_i^n. \quad (3)$$

Standard way to proceed is to derive a piece-wise polynomial reconstruction function  $u^R(x)$  from the old means  $\bar{u}_i$  and the old mesh  $x_{i-1/2}$  (the formula (1) has to be valid for  $u^R(x)$  and all cells  $i$ ). The reconstruction function  $u^R(x)$  is then used in (2) to compute the new means  $\bar{u}_i^n$ . Now if we define the numerical remapping fluxes (corresponding to the green areas in Fig. 1) as

$$F_{i-1/2} = \begin{cases} \int_{x_{i-1/2}}^{x_{i-1/2}^n} u_i^R(x) dx & \text{for } x_{i-1/2}^n > x_{i-1/2} \\ - \int_{x_{i-1/2}^n}^{x_{i-1/2}} u_{i-1}^R(x) dx & \text{for } x_{i-1/2}^n < x_{i-1/2} \end{cases}, \quad (4)$$

where  $u_i^R(x)$  stands for the polynomial reconstruction function in the cell  $i$ , then the remapping is given by (see Fig. 1)

$$\bar{u}_i^n \Delta x_i^n = \bar{u}_i \Delta x_i + F_{i+1/2} - F_{i-1/2}, \quad (5)$$

and it is conservative. To specify the monotonicity requirement we first define the bounds for the remapped values

$$u_i^{\min} = \min \{ \bar{u}_{i-1}, \bar{u}_i, \bar{u}_{i+1} \}, \quad u_i^{\max} = \max \{ \bar{u}_{i-1}, \bar{u}_i, \bar{u}_{i+1} \}. \quad (6)$$

We say that remapping is in bounds if for all cells  $i$

$$\forall i \quad u_i^{\min} \leq \bar{u}_i^n \leq u_i^{\max}. \quad (7)$$

### 3. Piece-wise parabolic reconstruction

Inside each cell we choose a parabolic reconstruction

$$u_i^R(x) = u_i + u_i^x(x - x_i) + \frac{1}{2} u_i^{xx}(x - x_i)^2,$$

where  $x_i$  is the center of cell  $x_i = (x_{i+1/2} + x_{i-1/2})/2$ . The unknown coefficients of this reconstruction  $u_i, u_i^x, u_i^{xx}$  have to be computed from the old means  $\bar{u}_{i-1}, \bar{u}_i, \bar{u}_{i+1}$  on the old mesh. The conservation in the cell  $i$  implies  $u_i = \bar{u}_i - \frac{1}{24} u_i^{xx} \Delta x_i^2$ . The remaining unknown coefficients are computed by the least squares minimization of reconstruction error  $\Phi(u_i^x, u_i^{xx})$  in the neighboring cells  $i-1$  and  $i+1$ , namely

$$\Phi(u_i^x, u_i^{xx}) = \sum_{j \in \{i-1, i+1\}} \left( \bar{u}_j - \frac{1}{\Delta x_j} \int_{x_{j-1/2}}^{x_{j+1/2}} u_i^R(x) dx \right)^2.$$

This minimization, i.e. solution of the system  $\frac{\partial \Phi(u_i^x, u_i^{xx})}{\partial u_i^x} = 0, \frac{\partial \Phi(u_i^x, u_i^{xx})}{\partial u_i^{xx}} = 0$  is equivalent to both zero contributions in the error sum  $\Phi(u_i^x, u_i^{xx})$  in the presented case (parabolic reconstruction in 1D). Resulting coefficients for the unlimited reconstruction are

$$u_i^x = 2 \frac{(\bar{u}_{i+1} - \bar{u}_i) \Delta x_{i-1} \Delta x_{i+1} + (\bar{u}_i - \bar{u}_{i-1}) \Delta x_{i+1} \Delta x_{i-1}}{\Delta x_{i-1} \Delta x_{i+1} (\Delta x_{i-1} + \Delta x_{i+1})}, \quad (8)$$

$$u_i^{xx} = 12 \frac{(\bar{u}_{i+1} - \bar{u}_i) \Delta x_{i-1} - (\bar{u}_i - \bar{u}_{i-1}) \Delta x_{i+1}}{\Delta x_{i-1} \Delta x_{i+1} (\Delta x_{i-1} + \Delta x_{i+1})}. \quad (9)$$

where  $\Delta x_{i±1} = \Delta x_{i+1} + \Delta x_i, \Delta x_{i±1} = 2\Delta x_{i+1} + \Delta x_i$ . The reconstruction, as well as the complete remapping, is exact for quadratic function.

Limiting of these unlimited coefficients with respect to standard limiting of a piece-wise linear reconstruction is described in the following section.

#### 3.1. Reconstruction coefficients limiting

Minmod (MM) limiter's extension to piece-wise parabolic reconstruction [10] is done as a sequential application of minmod function to the second derivative approximation and then to the first one, i.e.

$$m u_i^{xx} = \text{minmod} \left( u_i^{xx}, \beta \frac{u_{i+1}^x - u_i^x}{\Delta x_{i+1/2}}, \beta \frac{u_i^x - u_{i-1}^x}{\Delta x_{i-1/2}} \right), \text{ where } \beta \in (1, 2).$$

In our tests we use  $\beta = 1.5$ . If the limiting of second derivative is not necessary (i.e.  $m u_i^{xx} = u_i^{xx}$ ), then we set also  $m u_i^x = u_i^x$ , otherwise

$$m u_i^x = \text{minmod} \left( u_i^x, \beta \frac{\bar{u}_{i+1} - \bar{u}_i}{\Delta x_{i+1/2}}, \beta \frac{\bar{u}_i - \bar{u}_{i-1}}{\Delta x_{i-1/2}} \right). \quad (10)$$

Note that standard piece-wise linear MM limited reconstruction uses this slope (10) everywhere. The final formula for MM limited parabolic reconstruction is

$$u_i^{\text{MM}}(x) = \bar{u}_i + m u_i^x(x - x_i) + \frac{1}{2} m u_i^{xx} \left[ (x - x_i)^2 - \frac{1}{12} \Delta x_i^2 \right]. \quad (11)$$

Kuzmin–Barth–Jespersen [4] (KBJ) limiter is based on the Barth–Jespersen (BJ) limiter [11]  $BJ(\bar{u}_{i-1}, \bar{u}_i, \bar{u}_{i+1}, u_i^x, \Delta x_i)$  returning limiting factor  $\alpha_i = \min(\alpha_i^{i-1/2}, \alpha_i^{i+1/2})$  in the cell  $i$ . The limiting factors  $\alpha_i^{i±1/2}$  at two nodes  $i ± 1/2$  of the cell  $i$  are given by

$$\alpha_i^{i±1/2} = \begin{cases} \min \left( 1, \frac{u_{i±1/2}^{\max} - \bar{u}_i}{u_{i±1/2}^{\min} - \bar{u}_i} \right) & \text{for } u_{i±1/2}^{\min} - \bar{u}_i > 0 \\ 1 & \text{for } u_{i±1/2}^{\min} - \bar{u}_i = 0, \\ \min \left( 1, \frac{u_{i±1/2}^{\min} - \bar{u}_i}{u_{i±1/2}^{\max} - \bar{u}_i} \right) & \text{for } u_{i±1/2}^{\max} - \bar{u}_i < 0 \end{cases} \quad (12)$$

where the bounds at the nodes are  $u_{i-1/2}^{\min} = \min(\bar{u}_{i-1}, \bar{u}_i)$ ,  $u_{i-1/2}^{\max} = \max(\bar{u}_{i-1}, \bar{u}_i)$  and the unlimited reconstruction from the cell  $i$  at the nodes  $u_{i±1/2}^u = u_i^u(x_{i±1/2}) = \bar{u}_i - u_i^x \Delta x_i/2, u_{i±1/2}^u = u_i^u(x_{i±1/2}) = \bar{u}_i + u_i^x \Delta x_i/2$ . Now the parabolic KBJ limiter is defined as

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