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An Improved Accuracy General Remapping Algorithm

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Extended Abstract

1. Introduction

Most numerical methods in fluid dynamics can be classified as being either Lagrangian or Eulerian. An important group of methods, however, is a combination of both. These methods generally derive from the ALE (Arbitrary-Lagrangian-Eulerian) method of Hirt et al. [1]. A computational cycle in these methods is divided into two main phases: a Lagrangian phase and a re-zone or remap phase (these two terms are used interchangeably). The remapping phase conservatively transfers quantities, calculated in the Lagrangian phase, from the Lagrangian mesh to some other specified mesh. For example, in a given time step the remap phase may be omitted, in which case the computation is purely Lagrangian, or the remapping may be back to the original mesh, in which case the computation is Eulerian. The remapping step, therefore, corresponds to the effect of the advection terms in Eulerian equations. It may also be viewed as a conservative interpolation procedure from one mesh to another, and so it is also useful in other more general applications, such as in adaptive mesh computations.

Formally, such a conservative remapping procedure may be specified by

$$Q_k = \iiint_{V_k} q(\underline{r})\, dV \quad , \tag{1}$$

where Q_k typically represents one of the conserved quantities (mass, components of momentum, total energy) associated with cell k of the new mesh, $q(\underline{r})$

represents the corresponding density distribution (mass density, momentum density, etc.) in the old mesh, which is assumed to be known or specified, and the integration takes place over the volume of the new cell V_k. These integrals must be evaluated for each cell of the mesh and for all variables to be remapped. In general, such a procedure is too formidable, and so instead it is in practice replaced by a "continuous" remapping in which the time step is limited in such a way that relative mesh displacement is small (a velocity Courant condition). This permits the approximation of the changes in Q_k in terms of fluxes across cell faces, a clear connection to the differencing of advection terms. This procedure, as compared to Eq. (1), has two main disadvantages: it can limit the time step, and it can be very diffusive because of the high frequency of remapping (every time step).

The alternative procedure of applying Eq. (1) is very complex for the case of two arbitrary meshes. The classic problem in Lagrangian hydrodynamics involves constant cell density and a two-dimensional mesh of arbitrary quadrilaterals. For this case Eq. (1) reduces to evaluating the volume of overlap between cells of the two meshes. Even for this relatively simple case the problem is logically very difficult because of the multiplicity of special cases to be considered. One published algorithm [2] uses a form of Monte-Carlo integration (a particle counting technique) to simplify the logical difficulties at the expense of substantial computational work and storage which are needed if large numbers of particles are used for accuracy.

A recent development [3] has permitted exact and efficient evaluation of Eq. (1) by converting the volume integral to a surface integral by a clever use of the divergence theorem. This reduction in dimensionality greatly reduces the complexity of the problem. The method has been worked out and demonstrated for the common case of constant cell density. This is the lowest

accuracy option for the density distribution in Eq. (1) since it leads to a large amount of numerical diffusion (corresponding to a donor cell or upwind differencing of the advection terms), which is however ameliorated by the fact that fewer remappings are necessary.

In this paper the new method is extended to the case of a more accurate density distribution: the density distribution within a cell is allowed to be linear, while preserving the average value of density over the cell. The orientation of this planar surface is given by the average local density gradient. Such a linear distribution, while more accurate in general, can cause undershoots or overshoots in regions of rapidly changing densities. This is avoided by placing monotonicity limits on the allowable gradients, similar to those used by Van Leer in one-dimension [4].

2. Outline of the Basic Method

We wish to find a vector function $\underline{F}$ such that we can write

$$\iiint_{V^*} \underline{\nabla} \cdot \underline{F} \, dV = \iiint_{V^*} q(\underline{r}) \, dV \tag{2}$$

for any volume V*. Given such a function we can apply the divergence theorem

$$\iiint_{V_k} \underline{\nabla} \cdot \underline{F} \, dV = \iint_{S_k} \underline{n} \cdot \underline{F} \, dS \tag{3}$$

to evaluate the integral efficiently. Here S_k is the surface of volume V_k, and $\underline{n}$ is the outward unit vector normal to the surface. The necessary and sufficient conditions for Eq. (2) to be valid for arbitrary volumes of integration are

$$\underline{\nabla} \cdot \underline{F} = q(\underline{r}) \quad , \tag{4}$$

and

$$\underline{n} \cdot \underline{F}_1 = \underline{n} \cdot \underline{F}_2 \quad . \tag{5}$$

That is, the normal component of $\underline{F}$ across any surface must be continuous (any discontinuity can only occur in the tangential component). Thus, the procedure is to find a function $\underline{F}$ which satisfies Eqs. (4) and (5), and then use it in Eq. (1) to obtain

$$Q_k = \iint_{S_k} \underline{n} \cdot \underline{F} \, dS \quad . \tag{6}$$

However, Eqs. (4) and (5) do not determine $\underline{F}$ uniquely. A practical method is obtained by making the choice $\underline{F} = (P, 0, 0)$, i.e., $\underline{F}$ has only one component. As a result, condition (5) requires that we use a transformed coordinate system in which cell faces are perpendicular to coordinate directions.

To simplify, we now confine ourselves to two dimensions. We introduce a coordinate transformation from (x,y) to (i,j), characterized by the Jacobian J(i,j). The simplest such transformation is a bilinear transformation which takes an arbitrary quadrilateral into the unit square. The method is now summarized by the following, corresponding to Eqs. (4) and (6),

$$\frac{\partial P}{\partial I} = q(i,j)J(i,j) \quad , \tag{7}$$

$$Q_k = \oint_{C_k} P \, dj \quad , \tag{8}$$

where the integration takes place around the cell contour C_k in the positive, or counterclockwise direction. The procedure is to use Eq. (7) to evaluate P(i,j) in each cell of the old mesh (P is typically a simple polynomial), and then to integrate P according to Eq. (8) over the faces of the cells of the

new mesh. This is done efficiently by computing the integral numerically as one sweeps along the entire length of the mesh lines of i and j constant.

The more accurate, linear density distribution in each cell is given by

$$q(\underline{r}) = \bar{q} + \alpha\, \underline{\nabla} q \cdot (\underline{r} - \bar{\underline{r}}) \quad , \tag{9}$$

where $\bar{q}$ is the average density in a cell, $\bar{\underline{r}}$ is the cell centroid, $\underline{\nabla} q$ is a local gradient determined from average densities in neighboring cells, and α is a limiting coefficient ($0 \leq \alpha \leq 1$) determined by enforcing local monotonicity such that the density within each cell does not lie outside the range of the average densities in the neighboring cells. We specify α to be

$$\alpha = \min \{1, [\bar{q}_{max} - \min(\bar{q}_{max}, \bar{q})]/(q_{max} - \bar{q}),$$

$$[\bar{q}_{min} - \max(\bar{q}_{min}, \bar{q})]/(q_{min} - \bar{q})]\} \quad , \tag{10}$$

where $\bar{q}_{max}, \bar{q}_{min}$ are the maximum and minimum values of $\bar{q}$ in neighboring cells, and q_{max}, q_{min} are the maximum and minimum values of q in the given cell.

3. Computational Examples

To illustrate the technique we will consider the case of simple advection of a scalar. The initial density distribution is shown in Fig. 1. This is advected with a circular motion such that each point traces a circle with a radius of 5 units. The following figures show the results following the completion of a full revolution. Figure 2 shows the severe diffusion which takes place for the case of constant cell density at a Courant number of 0.2. Figure 3 shows the much better results with the present, more accurate technique, also at a Courant number of 0.2. Finally, Fig. 4 illustrates the further improvement possible with the present technique by reducing the number of remappings, here using a remapping Courant number of 1.

References

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4. B. van Leer, J. Comput. Phys. 32, 101 (1979).

Figure Captions

Fig. 1. Initial density distribution for the advection problem.

Fig. 2. Remapping using constant density in a cell, Courant No. = 0.2.

Fig. 3. Remapping using linear density distribution in a cell, with monotonicity constraints. Courant No. = 0.2.

Fig. 4. Remapping using linear density distribution in a cell, with monotonicity constraints. Courant No. = 1.0.

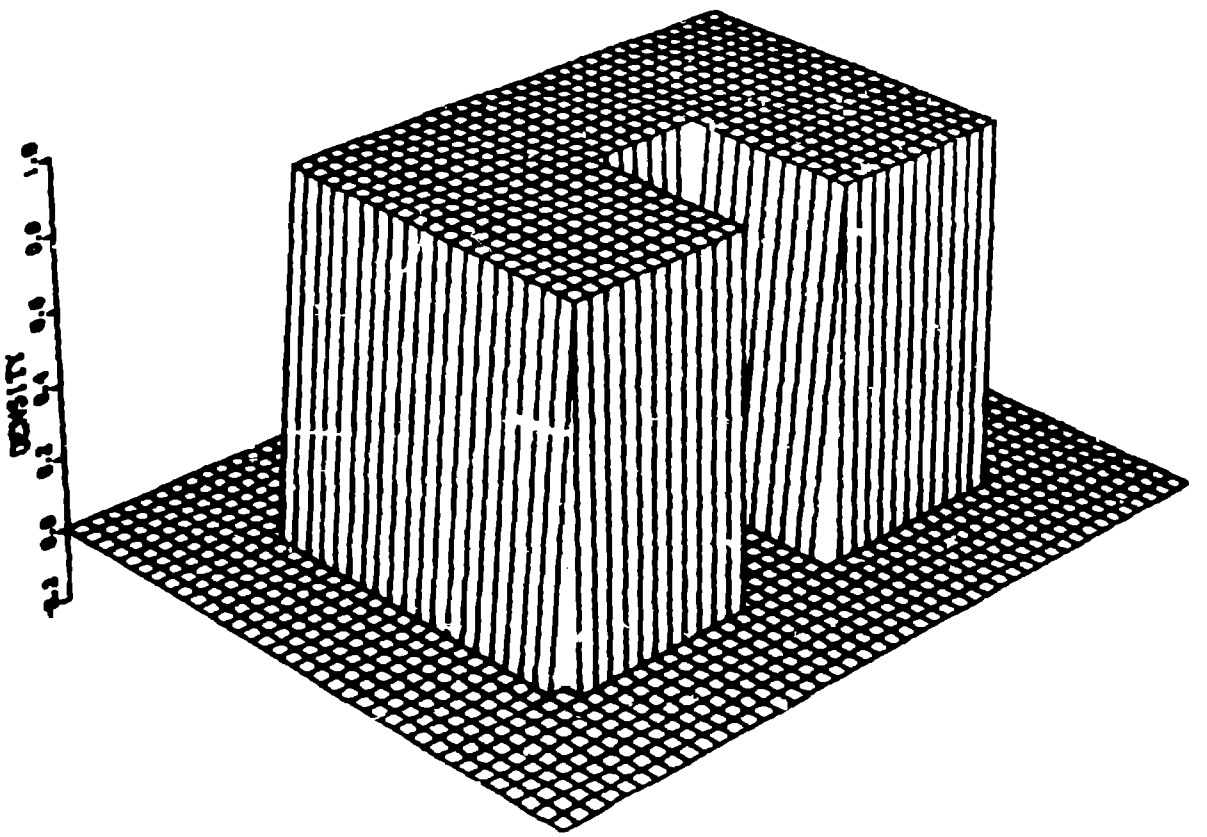

Fig. 1

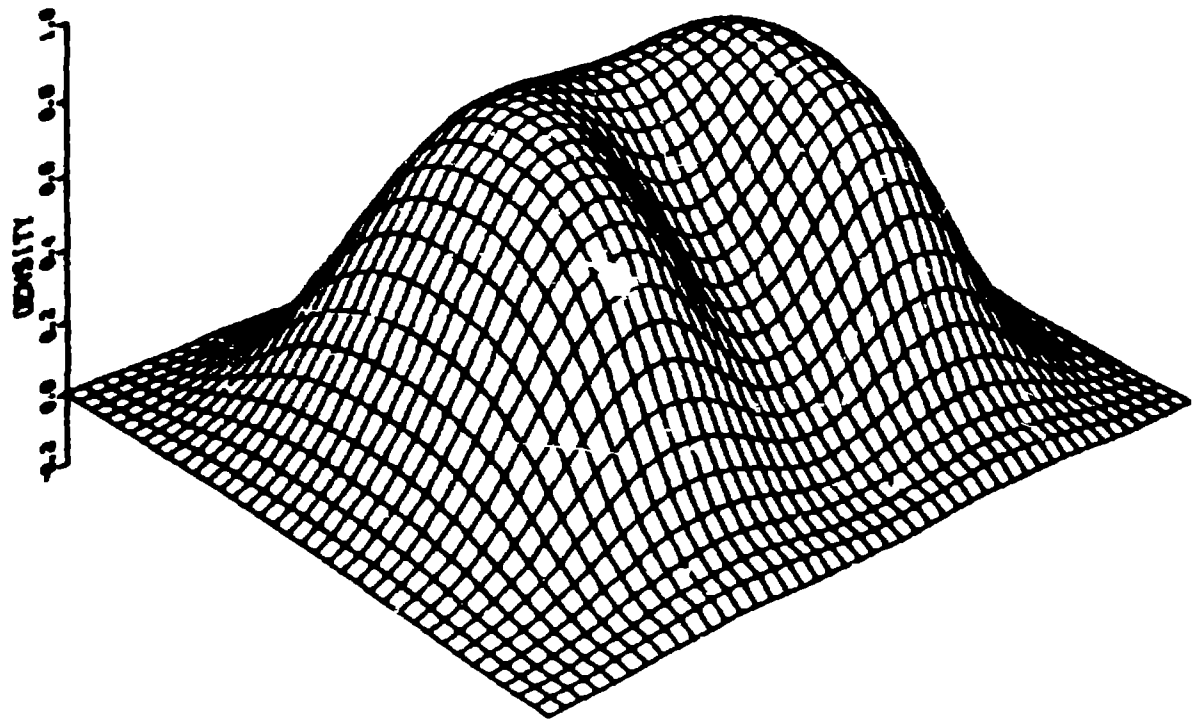

Fig. 2

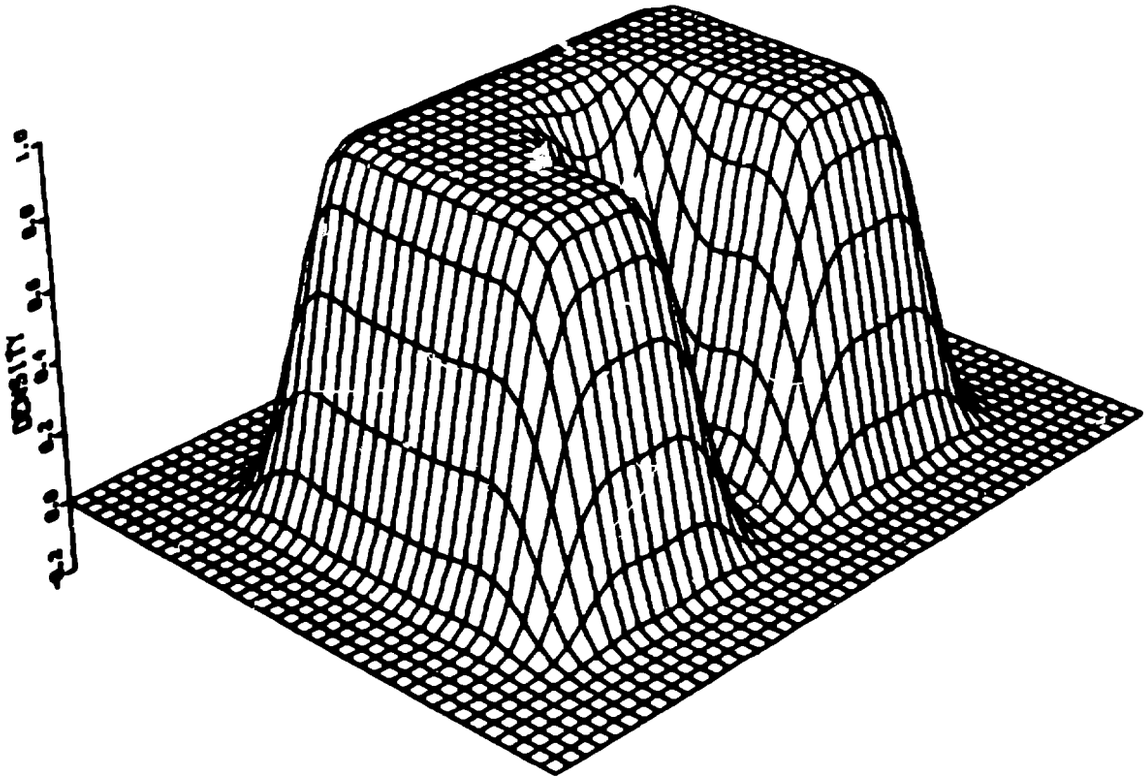

Fig. 3

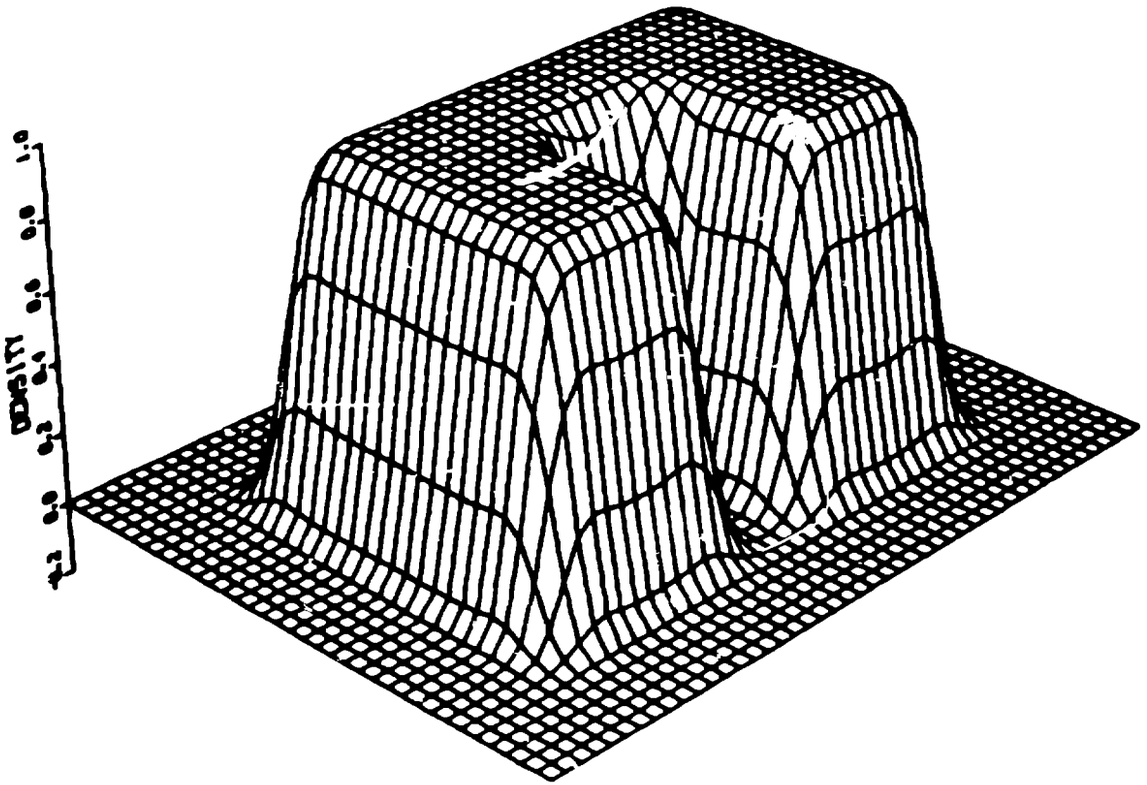

Fig. 4