Contents lists available at ScienceDirect

Journal of Computational Physics

www.elsevier.com/locate/jcp

An interface reconstruction method based on analytical formulae for 2D planar and axisymmetric arbitrary convex cells

S. Diot^{a,*}, M.M. François^a, E.D. Dendy^b

^a Fluid Dynamics and Solid Mechanics (T-3), Los Alamos National Laboratory, Los Alamos, NM 87545, USA
^b Computational Physics and Methods (CCS-2), Los Alamos National Laboratory, Los Alamos, NM 87545, USA

ARTICLE INFO

Article history: Received 26 November 2013 Received in revised form 25 June 2014 Accepted 30 June 2014 Available online 8 July 2014

Keywords: Interface reconstruction Non-iterative PLIC Volume-of-fluid (VOF) Polygonal cells

ABSTRACT

In this paper, we propose a non-iterative interface reconstruction method for 2D planar and axisymmetric geometries that is valid for arbitrary convex cells and intended to be used in multi-material simulation codes with sharp interface treatment for instance. Assuming that the normal vector to the interface is known, we focus on the computation of the line constant so that the polygon resulting from the cell-interface intersection has the requested volume. To this end, we first decompose the cell in trapezoidal elements and then propose a new approach to derive an exact formula for the trapezoids volumes. This formula, derived for both the planar and axisymmetric cases, is used to first bracket and then find the line constant that exactly matches the prescribed volume. The computational efficiency of the proposed method is demonstrated over a large number of reproducible conditions and against two existing methods.

© 2014 Elsevier Inc. All rights reserved.

0. Introduction

Volume-tracking methods for multi-material flow simulations have been introduced in the early seventies with three different approaches in [8,11,10]. Their common points are 1) the different materials are represented by their volume fractions, 2) these volume fractions are advected with the flow velocity to follow the materials evolution, 3) a cell-wise interface is reconstructed at each time step from the volume fractions to prevent its numerical diffusion. Many extensions and improvements have been proposed to these methods in the last decades, and nowadays the most widespread volume-tracking method uses a PLIC interface reconstruction technique (Piecewise Linear Interface Calculation) [17,13]. In this method, the material volume fractions equation is geometrically solved by making use of the cell-wise reconstructed linear interface in order to keep the interface sharp during simulation.

In this work, we are interested in the reconstruction process of a cell-wise linear interface that is represented by the line equation

 $n_x x + n_y y - c = 0$

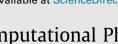
where $\vec{n} = (n_x, n_y)$ is the unit normal vector to the interface and *c* its line constant. The reconstruction step classically consists of two steps, firstly the computation of \vec{n} and secondly the computation of the line constant *c* such that the

http://dx.doi.org/10.1016/j.jcp.2014.06.060 0021-9991/© 2014 Elsevier Inc. All rights reserved.









^{*} Corresponding author. *E-mail address:* diot@lanl.gov (S. Diot).

interface splits the cell in two sub-cells whose volumes correspond to the material volume fractions. In this work, we only focus on the latter step that we call *volume-matching* step by assuming that the normal vector is known. We remind that \vec{n} is usually computed as the volume fraction gradient by any existing gradient computation technique as instance a least-squares method (*e.g.* (E)LVIRA in [12] or *k*-exact in [2]) or a height function method [6]. A good review of these techniques can be found in [14].

The purpose of this paper is to propose an original non-iterative technique to the volume-matching problem for any convex polygonal cell. Let us first point out that several methods already exist for particular cell shapes, see [16] for triangles/tetrahedra and [15,7] for squares/hexahedra, and are widely used in simulation codes. However, up to our knowledge, only the two methods presented in [4,9] are available for arbitrary cells in planar geometry while in the axisymmetric geometry only a very recent extension of [4] can be found in [1]. This recentness is most likely the reason why for complex polygonal meshes (*e.g.* Voronoi meshes), the volume-matching technique proposed by Rider and Kothe in [13] is still mainly used in industrial or academic codes. Therefore we will use it as a reference to evaluate the cost of our method in the numerical results section. This volume-matching technique [13] is made of two sub-steps, the first one consists in computing the line constants and the resulting material volumes when lines parallel to the interface pass through all nodes of the cell in order to bracket the interface line constant. Then, once the two closest bounds are found, a Brent's iterative method [3] is used to find the interface line constant that matches the requested volume fraction. This iterative procedure may be very costly since the intersection between the cell and the interface, and the resulting volumes must be computed at each iteration. In the sequel, we use *Brent's method* to refer to the method used by Rider and Kothe in [13].

Let us now point out the differences between the approach we propose and the non-iterative ones of [4,1] and [9]. In [9], an analytical formula is deduced from the polygonal volume formula that uses the cell nodes coordinates. We did not choose this approach as we believe the reconstruction could be done more efficiently. Instead we use the same trapezoidal decomposition of the cell as the one adopted in [4,1] that allows an incremental bracketing of the solution (see Section 1). However our philosophy is to derive an analytical formula that can be used for both bracketing and finding the interface line constant. This is a major difference compared to [4,1], where they use a classical formula for the trapezoidal volumes during the bracketing step and then use an interpolation technique to find the interface line constant. More specific differences will be highlighted in the text when relevant. We claim that our approach leads to a clearer and more robust technique in addition to be less computationally expensive and more accurate volume-matching as demonstrated in the last section of this paper.

Finally let us add that the interface reconstruction technique we propose in this note is devised for two materials and that it could be adapted for more than two materials per cell by assuming a certain configuration (*e.g.* onion-skin or nested dissection [5]) as done with other classical two-material techniques.

The paper is split in three parts. The first part describes how the cell is decomposed. The next one presents the derivation of the analytical formulae for the planar and axisymmetric geometries and to their uses while the last one gathers the numerical results that demonstrate the improved efficiency of our method.

1. Cell decomposition and line constant bracketing

Let us consider an arbitrary convex polygonal cell with *N* nodes of coordinates $X_l = (x_l, y_l)$, l = 1, ..., N with *l* the nodes indexes. We denote by V_{cell} its volume, and by $\alpha \in [0, 1]$ and $\overline{V} = \alpha V_{cell}$ the material volume fraction and associated material volume respectively. We recall that the unit normal vector to the interface $\vec{n} = (n_x, n_y)$ is known and assume that it points from the material under consideration to the other one. We also remind that the volume-matching problem consists in finding the line constant *c* of the interface that splits the cell according to the given volume \overline{V} .

In the sequel, for any given line constant *c*, we call *c*-line the line parallel to the interface defined by the equation $n_x x + n_y y - c = 0$. Moreover we call *c*-volume and denote by V_c the volume of the material polygon resulting from intersection of the *c*-line with the cell. At last, we assume that for all *N* faces f_l of the cell, the outward unit normal vector $\vec{n}_{f_l} = (n_{f_l,x}, n_{f_l,y})$ is known and so is the tangential one $\vec{t}_{f_l} = (-n_{f_l,y}, n_{f_l,x})$.

The starting point of our procedure is to decompose the cell. To this end, we follow the same idea as in [4] and start by computing and sorting in increasing order the line constants $\tilde{c}_l = n_x x_l + n_y y_l$ of the lines parallel to the interface and passing through all nodes X_l . The sorted line constants are denoted c_k in the following and are such that $c_1 < c_2 < ... < c_N$. These $N c_k$ -lines define a natural partition of the cell made of (possibly degenerated) trapezoids, that we further denote T_k , formed by the portions of the cell lying between the c_k - and c_{k+1} -lines. It is important to remark that the volumes V_{c_k} are monotonically increasing with the constant lines c_k , thus ensuring a unique solution to the volume-matching problem. We provide an illustration of the result of this procedure in Fig. 1 in which we have rotated the polygonal cell in order to plot the c_k -lines horizontally.

As in existing methods [13,4], the next step is to bracket the solution line constant which consists of finding the closest lower and upper bounding values c_{lo} and c_{up} in $\{c_1, ..., c_N\}$ such that $V_{c_{lo}} \leq \overline{V} \leq V_{c_{up}}$. To this end, we compute the increasing c_k -volumes until \overline{V} is bounded. This step is made easier by using the formula derived in next section to compute the volumes $(V_{c_{k+1}} - V_{c_k})$ of the trapezoids T_k and summing them to get the current $V_{c_{k+1}}$. Let us remark that as suggested in [4,9], if α is close to 1, it may be more efficient to apply this procedure to $(1 - \alpha)$ using the opposite of the normal vector.

Download English Version:

https://daneshyari.com/en/article/6932302

Download Persian Version:

https://daneshyari.com/article/6932302

Daneshyari.com