Presented is a memory-efficient and highly parallelizable method for reconstructing volumes, based on a homography fit synthetic aperture refocusing method. This technique facilitates rapid processing of very large amounts of data, such as that recorded using high-speed cameras, for the purpose of conducting 3D particle imaging velocimetry and particle tracking velocimetry.

1 Introduction

1.1 Motivation

Given the unsteady, three-dimensional nature of fluid flows encountered in both research and industry, there is significant demand for advanced experimental techniques that fully resolve velocity fields in time and space. PIV has been widely and successfully used to resolve 2D velocity fields. However, 2D velocity fields come with certain limitations. For example, since 2D velocity fields do not provide out-of-plane velocity gradient information, a pressure field calculated from a 2D velocity field contains errors. 2D fields are often insufficient for studying complex, non-symmetric flows such as highly 3D, turbulent flows.

Tomographic PIV (TomoPIV), pioneered by Elsinga et al. (2006), is a widely adopted 3D PIV technique that has been used in a wide range of fluid experiments. The TomoPIV technique relies on images from about four or five cameras looking at a scene from different viewpoints to facilitate tomographic reconstruction of the investigation volume using a multiplicative algebraic reconstruction technique (MART). Synthetic aperture (SA) PIV (SAPIV) was introduced by Belden et al. (2010) blending light field imaging concepts into a 3D quantitative velocimetry method. SAPIV uses an array of up to ten cameras and can spatially resolve densely seeded velocity fields. Because SA imaging facilitates focusing at any arbitrary depth in a volume of interest, accurate intensity volumes could be reconstructed for use in 3D cross-correlation-based PIV. However, the original implementation of SA reconstruction took considerable computational time.

In an entire 3D PIV process, reconstruction often accounts for a significant portion of the total computation time (see Fig. 1). Since TomoPIV was introduced in 2006 Elsinga et al. (2006), several improvements to tomographic reconstruction time have been made by Worth and Nickels (2008) (MFG-MART), Atkinson and Soria (2009) (MLOS-SMART), Discetti and Astarita (2012) (MLOS-MR-SMART) and Lynch and Scarano (2015) (SMTE-MART) in 2008, 2009, 2012 and 2015, respectively. However, reconstruction time still remains a significant hurdle to processing large data sets, often acquired using high-speed cameras. In addition, computation time for SA reconstruction is in the same order of magnitude as that for tomographic reconstruction. This drawback and the need for processing large data sets motivates the development of the HF method.

This paper introduces a memory-efficient, faster reconstruction technique, based on a new homography fit (HF) algorithm, for synthetic aperture (SA) refocusing. This new algorithm is highly parallelizable and can be implemented
readily on an off-the-shelf graphics processing unit (GPU) for further improvement in computational speed.

1.2 Synthetic aperture imaging and 3D PIV

Synthetic aperture (SA) imaging projects images of a scene captured from multiple cameras (different view points) onto a virtual focal plane. SA imaging, in a way, simulates images captured via a lens of an arbitrary sized aperture. In principle, as the aperture size of a lens increases, its depth of field becomes smaller. SA imaging allows one to simulate a lens with an arbitrarily large aperture, which would not be feasible to manufacture, using an array of multiple cameras looking at the same scene from slightly different viewpoints. By increasing the distance between cameras, the depth of field of such an array can be reduced sufficiently such that it can be used to image particles in a flow field essentially lying only on the focal plane of the calculated images. Particles away from the focal plane are significantly blurred and can be removed owing to the characteristic discrete blur, as discussed by Bajpayee and Techet (2013). This allows one to reconstruct the entire volume of interest, in a particle laden tank to conduct 3D PIV, as demonstrated by Belden et al. (2010) or PTV as demonstrated by Bajpayee and Techet (2013).

2 Synthetic aperture refocusing

Once a multi-camera system looking at the same scene has been calibrated, images from each camera can be used to calculate images that are sharply focused at arbitrary depths in the scene spanning the entire volume of interest. This is achieved by back projecting images from each camera to a given depth followed by merging these images. This process is called SA refocusing. The SA refocusing process is covered in more detail by Isaksen et al. (2000) and Vaish et al. (2005) and later formalized for PIV reconstruction purposes as the map–shift-average algorithm by Belden et al. (2010). SA refocusing, when there are no refractive interfaces between the objects of interest and the cameras, is computationally inexpensive. However, refractive interfaces, such as a tank wall and water interface, are present in most PIV/PTV experiments, and thus refractive SA refocusing must be used.

2.1 Refractive SA refocusing

Refractive SA refocusing takes into account the bending of light rays at each refractive interface when back projecting images. This would correspond to a modified map–shift-average algorithm in which the map and shift operations are nonlinear. Multi-camera systems in scenes that contain refractive interfaces can be calibrated to a sub-pixel accuracy using a refractive bundle adjustment process outlined by Belden (2013) which is also able to take lens distortion into account.

To refocus in a case with refractive interfaces, let $P_j^z$ be a set of points representing the location of each pixel of the final back projected image $I_j$ and let $I_j$ be the image recorded by the $j$th camera for the time step being considered. Note that since we know the $z$ coordinate of the back projected image we wish to calculate, we know $z$ the points in set $P_j^z$. To implement the desired back projection, the points in $P_j^z$ are projected into the $j$th camera through the water and glass to a set of points $R_j$ using the same method that is used to project a 3D point into a camera during the calibration process (Belden 2013). Points in $R_j$ are then used to calculate $I_j$ using an inverse mapping function via which the portion of image $I_j$ contained in the convex hull of $R_j$ is warped to a regular rectangle of the same size as

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1 The $z$ depth we wish to calculate the refocused image at is the $z$ depth in the calibrated world coordinate system. Note that conversion of $P_j^z$ from world units to pixel units (such that the extent of $P_j^z$ in pixel units is the size, in pixels, of the refocused image being calculated) and vice versa will be required as needed.
the image to obtain $I_j$. A schematic of this process is shown in Fig. 2. This is repeated for all cameras and then the back projected images can either be combined by averaging as:

$$I_z = \frac{1}{N} \sum_j I_j,$$

or by multiplying as:

$$I_z = \prod_j (I_j)^\alpha,$$

to calculate the refocused image $I_z$ at depth $z$. In Eqs. 1 and 2, $N$ is the number of cameras in the array and $\alpha$ is an exponent each image is raised to prior to multiplying.

2.2 Fast refractive refocusing: homography fit method

The reconstruction step in all PIV experiments is preceded by a calibration step. This takes the form of polynomial calibration and volume self-calibration for tomographic PIV and refractive bundle adjustment for SAPIV. Furthermore, calibration has to be conducted only once for an experiment and takes a few minutes. The reconstruction and cross-correlation steps are the most computationally intensive and the technique discussed herein addresses improving performance of step 3, as shown in Fig. 1.

SA reconstruction is computationally intensive because back projection through refractive interfaces involves an iterative step for each pixel to ensure that Snell’s law is satisfied for each ray. During the calibration process, the glass wall of the tank is assumed to have flat interfaces. Therefore, all light rays are refracted at planar interfaces. For a simple scene without refractive interfaces, the back projection process can be reduced to a homography transform, since points in one image are mapped to another such that straight lines remain straight (property of projective transforms in the absence of distortion). It can be shown that collinear 3D points when refracted through planar interfaces and then projected into a camera remain collinear in the image. As a result, the projection of 3D points into a camera through planar refractive interfaces can also be approximated with a simple projective transform. The back projection step can thus be achieved by reducing the required inverse mapping to a simple homography transform, as in the case of pinhole back projection. A homography matrix $H$ for this approximation can be computed using a minimum of four non-collinear points in $R_j$.

Let $P_j^z$ be a subset of $P_j$ containing only the corner points of $P_j^z$ (shown in Fig. 2 as red dots). Similarly, let $R_j^z$ be a set containing the corner points of $R_j$. The points $R_j^z$ can be calculated by projecting the points $P_j^z$ in a similar fashion to the original method. Following this, a matrix $H$ can then be calculated such that:

$$P_j^z = HR_j^z$$

and $H$ can then be used to apply a homography transform to image $I_j$ to calculate $I_j$.

This homography fit (HF) method drastically reduces the computational cost as now only four points have to be projected through refractive interfaces instead of as many points as the number of pixels ($512 \times 512$ in this study) in the images being used. It must be noted that as long as the experimental setup contains only planar refractive interfaces, the HF method is an exact simplification of the original SA reconstruction method. Therefore, it does not affect the reconstruction quality $Q$ which will follow the same trends as reported by Belden et al. (2010) for all reconstructions in this study. Most PIV experiments contain either flat refractive interfaces or negligible refractive effects through index matching, flat view boxes, etc. For experiments containing non-planar refractive interfaces, the HF method will not be valid.

2.3 Benchmarking of the HF method

The code used for SA reconstruction in this study is implemented in C++ and also written to be parallelized on CUDA capable GPUs. Table 1 lists code benchmarking results, on two different machines with and without using a GPU, for reconstructing (and thresholding) a

|                | Original method | HF method | Speedup (over original method) |
|----------------|-----------------|-----------|------------------------------|
| Desktop: CPU only | 14.19 mins     | 4.09 s    | 208×                         |
| Server: CPU only  | 13.50 mins     | 7.41 s    | 109×                         |
| Desktop: CPU + GPU | 1.14 mins     | 0.45 s    | 152×                         |
| Server: CPU + GPU  | 8.13 s         | 0.38 s    | 21×                          |
Table 2 Reconstruction computation time \(T\) to reconstruct a 512 \(\times\) 512 \(\times\) 128 voxel volume with seeding density \(N_{ppp}\) = 0.1 on a desktop (specs reported in Table 1) machine

| Hardware    | Algorithm          | \(T\) [min] |
|-------------|--------------------|-------------|
| CPU only    | MFG-MART, 5 iterations | 2.06        |
| CPU only    | HF method          | 0.068       |
| CPU + GPU   | HF method          | 0.0075      |

single 512 \(\times\) 512 \(\times\) 128 voxels volume. Regardless of whether a GPU is used or not, it can be seen that the HF method significantly improves computation time and the use of a GPU improves computation time by another order of magnitude.

To compare the preformance of the HF method with tomographic reconstruction, the authors ran tomographic reconstruction simulations using their own extension of the code developed by Clark (2012) written in FORTRAN and MATLAB. Table 2 shows the time to reconstruct a 512 \(\times\) 512 \(\times\) 128 voxel volume with seeding density \(N_{ppp}\) of 0.1 using both the HF method and MFG-MART based tomographic reconstruction. As shown in Table 2, the best SA reconstruction case (desktop with off-the-shelf GPU) translates to a 270\times improvement over tomographic reconstruction.

Similar to the HF method-based SA reconstruction, the time taken for tomographic reconstruction for constant \(N_{ppp}\) grows linearly with volume depth. It must be noted that tomographic reconstruction time also grows with \(N_{ppp}\), whereas SA reconstruction time is independent of \(N_{ppp}\). Moreover, the timing results shown in Tables 1 and 2 are obtained using 32 bit floating point images. For perspective, consider an experiment conducted using high-speed cameras with seeding density \(N_{ppp}\) of 0.1, reconstructed volume size of 2048 \(\times\) 2048 \(\times\) 512 voxels and 1000 time frames of interest. Tomographic volume reconstruction of all frames would take about 90 days, as opposed to the HF method (with GPU) which would take 8 h. Therefore, the presented technique can make the volume reconstruction time insignificant compared to the time taken by cross-correlation.

3 Conclusion

This paper shows that the HF method-based SA imaging can reconstruct volumes in a significantly shorter time as compared to the time taken by algorithms used in tomographic techniques. Such an increase in computation speed can allow researchers to process over two orders of magnitude more data than that which can be practically processed currently, thus moving closer to real-time implementations of high-speed 3D PIV in highly unsteady fluids applications.

Additionally, since the HF method is a projection technique, it can be used to simplify mapping functions for tomographic reconstruction to reduce computational complexity and eliminate the need for volume self-calibration for a setup calibrated using refractive bundle adjustment.

All code used in this study has been released under the Open Source Flow Visualization (OpenFV, openfV.org) library which also includes support for tomographic reconstruction and window deformation PIV. The authors encourage other researchers to use the library and contribute improvements and features to help facilitate free and open access to software in the PIV and flow visualization community.

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