

Fast 3D tracking with GPUs for analysis of antiproton annihilations in emulsion detectors

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Fast 3D particle tracking has been a challenge in particle physics for a long time. In particular, the data rate from emulsion detectors is recently about 10-100 TB/day from one microscope. Real-time 3D volume processing and track reconstruction of such a huge data need a large amount of computation, in which the GPU technology plays an essential role. A fast 4π solid angle particle tracking based on GPU technology has been developed for the reconstruction of antiproton annihilations. The results in speed are compared between the multithread CPU processing and the multi-GPU one. By employing multiple GPUs, about two orders of magnitude faster processing has been achieved with an excellent tracking performance in comparison with a single-thread CPU processing.

1 Introduction

The reconstruction of particle trajectory (or *tracking*) is one of the fundamental subjects in experimental particle physics. Thanks to the development of detector technology, particle detectors are tend to employ more and more detector elements and to use higher dimensional data. The importance of 3D volume data processing is getting higher. Since 3D tracking requires a few orders of magnitude larger computation than 2D tracking, it has been essential to solve the computing issue with available computing resources.

Emulsion detector is one of the most classic detectors, however, physicists have attacked to establish the fast 3D volume processing with this detector since many decades.

The basic detector element of emulsion detector is a silver bromide crystal with a typical diameter of 200 nm. The crystals are uniformly distributed in the gelatin medium. An emulsion volume of 1 cc (\simeq an emulsion film of 100 cm²) consists of about 10^{14} crystals and each crystal works as an independent particle detector. The position resolution of emulsion detector is as good as 50 nm.

In the past, the readout of 10^{14} detectors and the reconstruction of the 3D tracks in emulsion detectors were impossible because of lack of technologies. Due to the difficulty of automation, the analysis had relied on human check on manual microscopes. Efforts to develop automated scanning system has started in late 70's. In order to read out the 3D information stored in emulsion films, scanning microscopes take tomographic images by moving focal plane, and then the tomographic images are processed in real-time manner. This is illustrated in Fig. 1. The scanning speed progressed many orders of magnitudes after several generations [1, 2, 3].

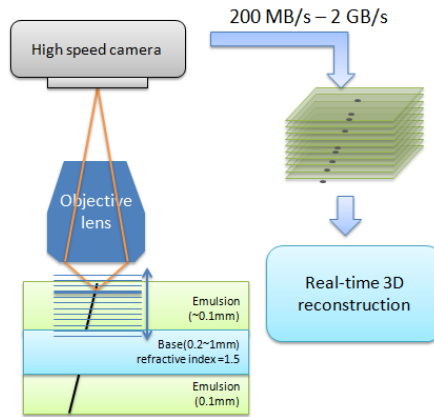


Figure 1: Schematic of scanning microscopes

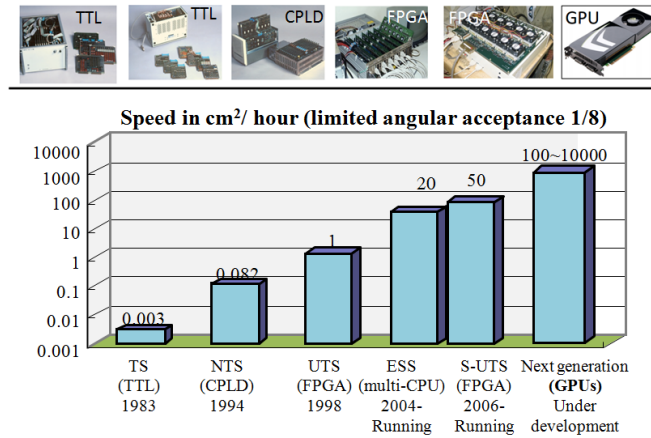


Figure 2: Evolution of scanning speed

The progress of speed in an unit of surface area scanned per hour is shown in Fig. 2, which features the different computing solutions available at those time. The data rate from camera is recently reached to of the order of 1 GBytes/s. To reconstruct 3D tracks in this amount of data, a powerful computing solution is mandatory.

GPU (Graphic Processing Unit) has been developed for the graphics, namely games. Yet, it is recently opened for general purpose computing. A GPU has a number of processors of the order of thousand and it can process tasks in parallel with the processors (parallel processing). An application of GPUs is highly efficient as a computing solution for the case that the algorithm can be parallelized, such as image processing or tracking.

On the other hand, emulsion detectors are intensively used in the field of antimatter physics, especially in the measurement of gravity for antimatter and matter-antimatter annihilation in the AEGIS experiment [4, 5, 6]. In such experimental conditions, the products from the annihilation vertex are emitted isotropically as shown in Fig. 3. However, the conventional

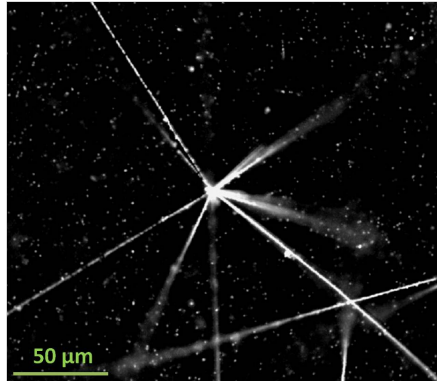


Figure 3: An antiproton annihilation vertex observed in the emulsion detector.

algorithms used in the systems in Fig. 2 reconstruct tracks in limited angular space of $\tan\theta < 0.5$ (θ - angle from the normal of emulsion surface) or, in other word, only 1/8 of full angular space. Thus, a new tracking algorithm which covers full angular space is awaited to achieve a high detection efficiency of antiproton annihilations.

A new algorithm is recently proposed and realized in [7] with a computing solution with GPUs, which is the basis of this article. In this paper, we shortly recall the main feature of the algorithm and report updated results.

2 Tracking algorithm and GPU implementation

The scanning microscope takes a set of tomographic images of 40 layers (*a view*) through an emulsion layer of 50-micron thick as illustrated in Fig. 1. An image size is 1280×1024 pixels, corresponding to $300 \mu m \times 250 \mu m$. Fig. 4 shows the flow of data processing to obtain 3D position of grains. The volume data (a) is filtered in 3D (b) and then grains in the view are recognized in 3D (c).

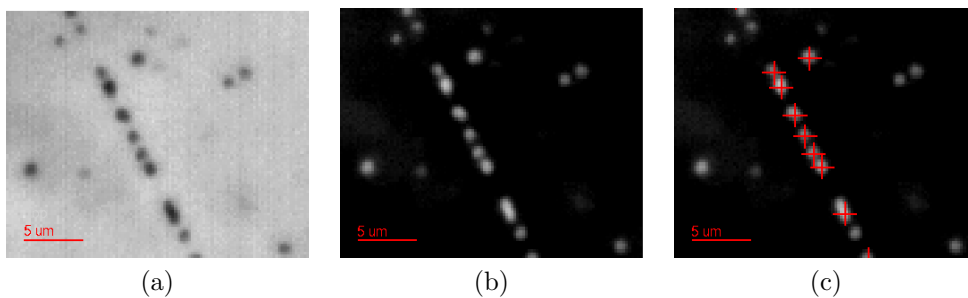


Figure 4: Processing of images. (a) Raw data image. (b) 3D-filtered image. (c) Recognized 3D grains marked with a red cross.

Any two combinations of grains in a limited volume define lines (or *seeds*) by connecting the two grains (Fig. 5 (a)). A cylinder along each seeds is defined and the number of grains in

the cylinder is evaluated (Fig. 5 (b)). If the number of grains is bigger than a preset threshold (e.g. 5 grains), the seed is classified as a tracks. The algorithm can cover all angular acceptance with this seed formation.

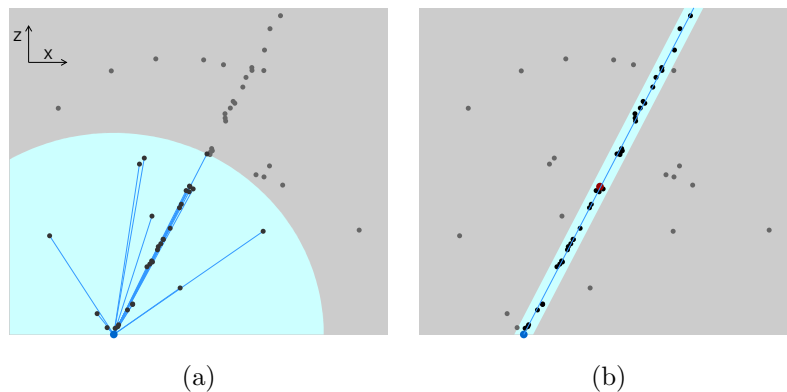


Figure 5: Schematic of tracking algorithm. (a) For each grain (for example, the blue dot), seeds for a track (blue lines) are defined by looping for grains within a given distance. (b) For each seed (blue line formed by blue and red dots), the number of grains along the seed is counted. If the number of grains is larger than a preset threshold, one can define it as a track.

The 3D volume processing (Fig. 4) and the processing of seeds (Fig.5 (b)) account for a large part of computation time, however, they can be highly parallelized. These parts of algorithm are implemented with the GPU programming.

The further detail of the algorithm can be found in [7].

3 Performance test

The performance of tracking, especially in terms of speed, is compared between the CPUs programming and the GPUs programming. The code is written with C++ and with NVIDIA CUDA libraries (version 5.5) [8] combined with CERN ROOT libraries [9]. A dedicated processing server (Linux Mint 15) equipped with a recent CPU (i7-3930K, 3.2 GHz, 6 cores, 12 logical processors) with 3 state-of-the-art GPUs (NVIDIA GEFORCE TITAN, 837 MHz, 2688 cores, 6.144 GBytes on-board memory [10]) and with a fast memory (DDR3-2400) has been tested for our purpose.

Obtained tracking time is summarized in Table 1 for a single CPU thread case, with and without a GPU. The performance is also checked in two different samples that have different number of grains in the view. "Cosmic sample" was exposed to cosmic rays and it has about 5,000 grains per view. As underlined, the image filtering is the most dominant process for this case. On the other hand "Antiproton sample" was exposed to the antiproton beam at CERN AD and has about 11,000 grains per view. In this case the 3D tracking process holds the major processing time. For both cases, the processing time is remarkably accelerated by implementing GPU-based computing by factors of 40 and 26, respectively.

A multithread programming was then implemented on the basis of the single CPU thread programming. Each CPU thread is linked to one of the three GPU devices. One can use all the

Process	Cosmic sample (few grains)			Antiproton sample (more grains)		
	CPU-based (s/view)	GPU-based (s/view)	Gain	CPU-based (s/view)	GPU-based (s/view)	Gain
Image filtering	<u>3.388</u>	0.051	× 66	3.396	0.051	× 66
3D grain recognition	0.157	0.012	× 13	0.181	0.023	× 13
3D tracking	0.274	0.033	× 8.3	<u>6.999</u>	0.330	× 21
Total processing time	3.819	0.096	× 40	10.576	0.404	× 26

Table 1: Processing time between the CPU-based and the GPU-based programs with a single CPU thread.

GPUs by running several CPU-threads simultaneously. The result is shown in Figure 6. The processing speed (or frequency) is almost proportional to the number of GPUs. The dashed lines shows a fitted tendency with the formula given in the figure. It is well understandable by taking account the overhead time in the process. The frequency can reach up to 15 Hz, which is far enough for the data taking limitation of 5 Hz with the conventional mechanical hardware for [3]. The gain in time for the antiproton sample between the single CPU thread process (0.096 Hz) and the multi-GPU process (8.7 Hz, 3 GPU and 15 CPU threads) is calculated to be 91.

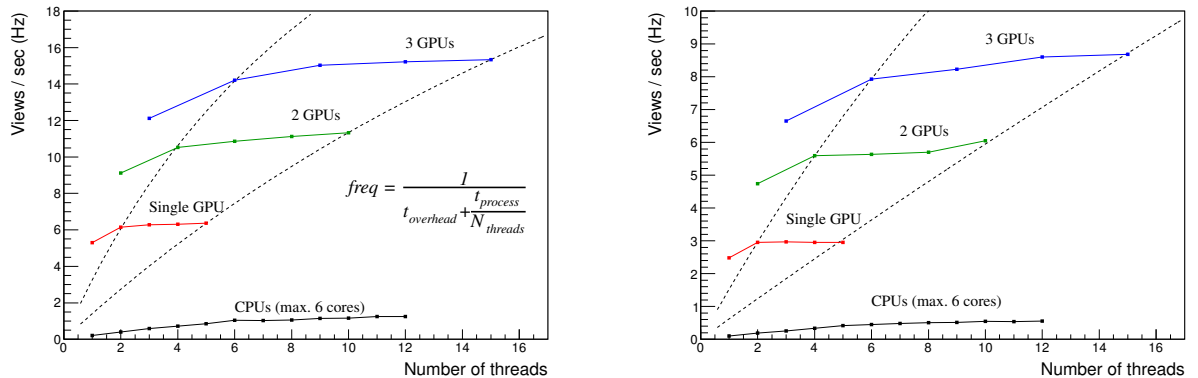


Figure 6: Comparison of scanning speed as a number of views processed per sec, as a function of number of threads. Left: cosmic-ray sample (less grains), right: antiproton sample (more grains).

4 Summary

Fast 3D particle full-angle tracking has been for a long time a challenge when using nuclear emulsion detectors as high accuracy 3D tracking devices. Advances in the GPU technology have opened the way for the actual realization of real-time fast processing.

The proposed algorithm with full angular acceptance, required for the analysis of antiproton interactions, needs a large computing power compared to the conventional algorithms with a

narrower angular acceptance. Nevertheless, the processing speed reached to maximum 15 Hz, which is sufficiently high for the current data taking limitation of 5 Hz.

This new tracking algorithm can be employed by any applications using nuclear emulsion detectors which needs a fast 4π tracking, as the AEGIS experiment at CERN which needs a high detection efficiency for antiproton annihilations.

The development of tracking system will further be extended for the next generation data acquisition system which has about 2 GBytes/s output data rate (currently 0.25 GBytes/s).

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