FastFlow: multicore and GPGPU programming made easy

University of Torino & University of Pisa, Italy * http://sourceforge.net/projects/mc-fastflow * Open source software under LGPLv3

Motivation
The whole computer hardware industry embraced parallel platforms, such as multicore, GPGPUs, and cloud. For these platforms, the extreme optimisation of sequential algorithms is no longer enough to squeeze the real machine power. In the long term writing parallel programs ought to be as efficient, portable, and correct as it has been to write programs for sequential computers. To date, however, the parallel programming drill does not embrace much more than low-level communication libraries. In the hierarchy of abstractions, it is only slightly above toggling absolute bandwidth into the front panel of the machine. By definition, the raison d’être for parallel computing is high performance, but speed-up need not be the only measure. Human productivity, total cost and time to solution are equally, if not more important.

Material and methods
FastFlow is a C++ parallel programming framework advocating high-level, pattern-based parallel programming. It chiefly supports streaming and data parallelism, targeting heterogeneous platforms composed of clusters of shared-memory platforms, possibly equipped with computing accelerators. The FastFlow run-time support efficiently support fine grain parallelism via non-blocking multi-threading with lock-less synchronisations; zero-copy network messaging; asynchronous GPGPU offloading.

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Signal filtering
A high-performance filter for real-time video denoising. The filter is composed of two phases: detection (e.g. classical median filter) and correction. The filter achieve very good restoration quality, comparable to jpeg compression. Unlike traditional methods, the correction phase is based on a variational method and succeeds to restore also extremely noisy images (up to 90% of noisy pixels). FastFlow provided seamless portability to CUDA boards (e.g. NVidia K-40). This work has been presented at Nvidia GTC 2014.

DNA alignment (Bowtie2 & BWA)
Bowtie2 and BWA are among the fastest and most used alignment tools for genome analysis in bioinformatics. In the FastFlow porting, the concurrency structure has been redesigned passing from a pool of thread accessing shared data to a Farm/Master-Worker equipped with automatic memory affinity scheduling. The FastFlow port differs from the sequential C++ implementation, the graph exploration loop has been parallelised by using the ParallelFor pattern provided by FastFlow, that permitted to improve the performance with minimum effort.

FastFlow architecture

Performance
Like other high-level programming frameworks, such as Intel TBB, OpenMP, Hadoop, FastFlow simplifies the design and engineering of portable parallel applications. However, it has a clear edge in terms of expressiveness and performance with respect to other parallel programming frameworks in specific application scenarios, including, inter alia:

- fine-grain parallelism
- streaming applications
- coupled usage of GPU and multi-core
- memory-bound problems
- recursive, graph-oriented algorithms
- high-frequency problems

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