© 2013 FIZ Karlsruhe

io-port 06097639

Zou, Dan; Dou, Yong; Xia, Fei

Optimization schemes and performance evaluation of Smith – waterman algorithm on CPU, GPU and FPGA.

Concurrency Comput. Pract. Exp. 24, No. 14, 1625-1644 (2012).

Summary: With fierce competition between CPU and graphics processing unit (GPU) platforms, performance evaluation has become the focus of various sectors. In this paper, we take a well-known algorithm in the field of biosequence matching and database searching, the Smith – Waterman (S-W) algorithm as an example, and demonstrate approaches that fully exploit its performance potentials on CPU, GPU, and field-programmable gate array (FPGA) computing platforms. For CPU platforms, we perform two optimizations, single instruction, multiple data and multithread, with compiler options, to gain over 70×speedups over naive CPU versions on quad-core CPU platforms. For GPU platforms, we propose the combination of coalesced global memory accesses, shared memory tiles, and loop unfolding, achieving 50×speedups over initial GPU versions on an NVIDIA GeForce GTX 470 card. Experimental results show that the GPU GTX 470 gains 12×speedups, instead of 100×reported by some studies, over Intel quadcore CPU Q9400, under the same manufacturing technology and both with fully optimized schemes. In addition, for FPGA platforms, we customize a linear systolic array for the S-W algorithm in a 45-nm FPGA chip from Xilinx (XC6VLX760), with up to 1024 processing elements. Under only 133 MHz clock rate, the FPGA platform reaches the highest performance and becomes the most power-efficient platform, using only 25 W compared with 190 W of the GPU GTX 470.

Keywords: biosequence DB searching; the Smith; waterman algorithm; code performance tuning; GPU; FPGA
doi:10.1002/cpe.1913