

Haralick's Texture Features Computation Accelerated by GPUs for Biological Applications

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Abstract: In biological applications, features are extracted from microscopy images of cells and are used for automated classification. Usually, a huge number of images have to be analyzed so that computing the features takes several weeks or months. Hence, there is a demand to speed up the computation by orders of magnitude.

This paper presents the speedup of the computation of co-occurrence matrices and Haralick Texture Features, as used for analyzing images of cells, by general-purpose graphic processing units (GPU).

First we analyze the features and found computational similarities between them. Common intermediate results are shown in a dependency graph and the optimal computational order is derived to avoid costly double computation. Further we group the features in functional steps and parallelize the computation. The matrices needed during the parallelization exceeds the GPU memory. We devised a compression of the matrices with advantages for linear accesses as required by the GPU.

New GPUs include more cores (240 stream processors) and several new capabilities (namely, computing capability v1.3). With the new capabilities we further parallelize the computation of the matrices.

The computing time of the features for one image with around 200 cells is compared to the original software version, an optimized software version and a CUDA version with computing capability v1.0. With the latest CUDA version with capability v1.3 we have a speedup of 321 compared to the original CPU version and of 29 compared to the optimized CPU version. This is an improvement of 1.5 times to the previous CUDA version.

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