

UNIVERSITÄT

HEIDELBERG

EXZELLENZUNIVERSITÄT

Haralick's Texture Features Computations Accelerated by GPUs in Biological Applications







Abstract

This poster presents the speedup of the computation of co-occurrence matrices (co-matrices) and Haralick Texture Features (features), as used for analyzing microscope images of biological cells, by general-purpose graphics processing units (GPUs).

In a pipeline of automated image analysis algorithms the feature computation is the most costly computing part. The computing time of the algorithm without acceleration amounts to several months. Hence, a massive speedup is required.

Analyzing the features results in a graph showing the orientations are generated. Altogether, the features of 8 analysis. dependency of the feature computations on intermediate cells can be computed in parallel, requiring the calculation

results and on other features. With the dependency graph the optimal order of the feature computation could be determined which saved costly double computations. Analysation of co-matrices showed that they are sparsely filled, and for a highly parallel approach they consume too much memory. We reduced the size of a full co-matrix by removing all rows and columns filled with zeros. This and a speedup of 46 was obtained compared to an reduction strategy allowed us to keep up to two hundred co-matrices in the memory of an ordinary graphics card with direct memory access. For each single cell image 20 co-matrices with different research application in the field of biological image

Initialisation po	rt	
Function 0A	generate index / gray level lookup tables	
Function OR	clear co-occurrence matrices	
Function OC	compute co-occurrence matrices	
Function 0D	normalize co-occurrence matrices	
Part 1, read from	m co-occurrence matrices	
Function 1A	compute f1	
Function 1B	compute f5	
Function 1C	compute f6	
Function 1D	compute P	Ha
Function 1E	compute P x-y	for
Function 1F	compute Px+y	
Part 2, read from	m P	
Function 2A	compute mean	
Function 2B	compute var	
Function 2C	compute H	
Part 3 read from	$\mathbf{P}[\mathbf{x}_{-\mathbf{v}}]$	
$\frac{1}{1}$	compute f?	
Function 3R	compute f11	
Function 3C	compute MacPlx-v	
Function 3D	compute f10	
Part 4, read from	m Px+y	
Function 4A	compute f6	
Function 4B	compute f8	
Function 4C	compute f7	
Dart 5 road from	m co occurrence matrix	
Function $5A$	compute Pii and f3	
Function 5R	compute f/	
Function 50		

References

(1) N. Harder, B. Neumann, M. Held, U. Liebel, H. Erfle, J. Ellenberg, R. Eils, and K. Rohr, "Automated recognition of mitotic patterns in fluorescence microscopy images of human cells", Proc. IEEE Internat. Symposium on Biomedical Imaging: From Nano to Macro (ISBI'06), Arlington/VA, USA, April 6-9, 2006, 1016-1019 (2) C. Conrad, H. Erfle, P. Warnat, N. Daigle, T. Lörch, J. Ellenberg, R. Pepperkok, and R. Eils, "Automatic identification of subcellular phenotypes on human cell arrays," Genome Research, vol. 14, pp. 130-1136, 2004. (3) R. M. Haralick and K. Shanmugam, "Computer Classification of Reservoir Sandstones," IEEE Transactions on Geoscience Electronics, vol. 11, pp. 171-177, 1973 (4) R. M. Haralick, "Statistical and structural approaches to texture," *Proceedings of the IEEE*, vol. 67, pp. 786-804, 1979. (5) S. Theodoridis and K. Koutroumbas, Pattern Recognition Third Edition. San Diego, CA, USA: Academic Press An imprint of Elsevier, 2006. (6) Gipp, M., G. Marcus, N. Harder, A. Suratanee, K. Rohr, R. König, and R. Männer. 2009. Haralick's Texture Features Computed by GPUs for Biological Applications. IAENG International Journal of Computer Science, Volume 36 Issue 1. Newswood Limited, International Association of Engineers, London, 17 February. (7) NVIDIA CUDA Programming Guid Version 2.1

M. Gipp², G. Marcus², N. Harder¹, A. Suratanee¹, K. Rohr¹, R. König¹, R. Männer² ¹Dept. Bioinformatics and Functional Genomics, BIOQUANT, IPMB, and DKFZ, University of Heidelberg ²Institute for Computer Engineering, ZiTi, University of Heidelberg markus.gipp@ziti.uni-heidelberg.de

computing architecture of the GPUs. optimized software version.

ne of automated image analysis. oscope, multi cell image, segment image, feature values, classification)











ck Texture Features (Features) we used and simplified mmetrical Co-Matrices

$$\begin{aligned} &= \sum_{i=1}^{N_g} \sum_{j=1}^{N_g} P_{(i,j)}^2 & f_7 = \sum_{k=0}^{2N_g-2} (k - f_6)^2 P_{x+y}(k) \\ &= \sum_{k=0}^{N_g-1} k^2 \left(\sum_{i=1}^{N_g} \sum_{j=1}^{N_g} P_{(i,j)} \right)^{|i-j| = k} f_8 = -\sum_{k=0}^{2N_g-2} P_{x+y}(k) \log[P_{x+y}(k)] \\ &= \frac{1}{\sigma^2} \sum_{i=1}^{N_g} \sum_{j=1}^{N_g} (ij) P_{(i,j)} - \mu^2 & f_9 = -\sum_{i=1}^{N_g} \sum_{j=1}^{N_g} P_{(i,j)} \log[P_{(i,j)}] \\ &= \sum_{i=1}^{N_g} \sum_{j=1}^{N_g} (i - \mu)^2 P_{(i,j)} & f_{10} = \sum_{k=0}^{N_g-1} \left[P_{|x-y|}(k) (k - \sum_{l=0}^{N_g-1} l P_{|x-y|}(k))^2 \right] \\ &= \int_{i=1}^{N_g} \sum_{j=1}^{N_g} \frac{P_{(i,j)}}{1 + (i - j)^2} & f_{12} = \frac{f_9 - HXY1}{H} \\ &= \sum_{k=0}^{2N_g-2} k P_{x+y}(k) & f_{13} = \sqrt{1 - \exp[-2|HXY2 - f_9|]} \end{aligned}$$





loop over all cells, C cells in parallel			
generate matrices, C*AD in parallel			
compute intermediate results and features for all matrices C*AD in parallel			
store feature values			
clean matrices			

mentations of the algorithm with seed up factors					
	Computing time (s)	Factor to 1.	Factor to 2.		
rithm	2378	1x	-		

version 214 11x 1x	-
GTX) 11.1 214x 19x	1x
280) 6.6 360x 32x 1	.7x
(280) 4.65 511x 46x 2	.4x