

# Multitreading and GPU Computing in Matlab for Acceleration of Hot-Spot Detection in Brain Tumour Virtual Slides

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## Abstract

Analysis of the whole slide images of immunohistochemically stained brain tumour specimens is demanding algorithmically and computationally. For the detection of maximal proliferation regions of a brain tumour, called a hot-spot, the mathematical morphology methods, textural descriptions, classifiers and penalty function are used. The whole slide image, even in the reduced resolution, needs a dozen of minutes for full analysis. So, the acceleration of that process is necessary. The platform for a computation task is composed with the dual processor unit of Intel Xeon EC-2650 2.60GHz supported by the two Tesla K40m GPU devices. The original sequential algorithm written in Matlab for the hot-spot detection [1] was parallelized based on the Parallel Computing Toolbox [2] for the division of computations between CPU and GPU. In order to compare computing times virtual slides from 3Dhistech Panoramic Flash II scanner of various sizes were used. When the sequential analysis needs a dozen to two dozens of minutes, only a parallelization on CPU gives approximately a triple time reduction. The proper division of computation tasks between CPU and GPU resulted in the decrease of computational time of ten times on average. The proper allocation of computational tasks between CPU and GPU gives possibilities of high acceleration of virtual slide analysis in pathomorphological practice. The type, complexity, and support of various data transformation is crucial to planning and data management. This study was supported by the National Centre for Research and Development, Poland (grant PBS2/A9/21/2013).

## References

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