

High Performance Framework for the rapid analysis of Tissue Microarrays

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Tissue Microarrays (TMAs) represent a high throughput technology for biomarker discovery and are being used extensively by research laboratories worldwide. However the need for visual interpretation and manual scoring represents a significant bottleneck and so there is an urgent need for an automated solution. Using specialised scanning hardware, tissue samples can be digitised to produce diagnostic quality digital images (virtual slides) providing enormous opportunities for fully automated TMA analysis. This study investigated the development of a High Performance Cluster (HPC) for parallel processing of TMA cores to allow the high throughput analysis of TMAs. A number of clusters were investigated including several Hewlett Packard benchmarking clusters based in the USA. The framework was built on a 256 processor cluster, programmed using HP Message Passing Interface (MPI) and based on the manager/worker model where a manager processor is responsible for dividing the workload amongst worker processors. Each worker extracts a core from the virtual slide, analyses the core and stores the result in a TMA Data Exchange Specification compliant database. This cycle is performed until all cores have been processed, significantly speeding up analysis. A number of image processing libraries have been developed to run inside the framework and preliminary tests show a significant speedup (159x) when using a HPC, making the high throughput automated analysis of TMAs possible for the first time. This combination of TMAs, virtual microscopy, high performance computing and machine vision represents a powerful combination which will underpin high throughput biomarker discovery in tissue-based research.