OPTIMAL SCHEDULING AND MINIMUM RESOURCE CHARACTERIZATION OF BIOCHEMICAL ANALYSES ON DIGITAL MICROFLUIDIC SYSTEMS

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Digital microfluidic systems (DMFS) are an emerging class of lab-on-a-chip systems that manipulate individual droplets of chemicals on a planar array of electrodes. The biochemical analyses are performed by repeatedly moving, mixing, and splitting droplets on the electrodes. This thesis presents algorithms for optimized operations and design of DMFS biochips.

This thesis focuses on two issues: minimizing the completion time of biochemical analyses by exploiting the parallelism among the operations, and identifying the minimum resource requirements of biochemical analyses, towards the design of cost and space-efficient biochips. ***Minimizing the completion time***: We find the lower bound of the mixing completion time according to the tree structure of input analyses, and calculate the minimum number of mixers M_{min} required to achieve the lower bound. We present a scheduling algorithm for the case with a specified number of mixers no greater than M_{min}, and prove it is optimal to minimize the mixing completion time. These are the first results that use the analysis tree structure for optimal scheduling design of biochemical analyses on DMFS. ***Minimizing the resource requirements***: We focus on determining the minimum resources based on the tree structure of the chemical analysis and use it to design (or select) the smallest chip for a given analysis. We present an algorithm to compute, for a given number of mixers, the minimum number of storage units for an input analysis using its tree structure, and design a corresponding scheduling algorithm to perform the analysis. We define the M-depth of the analysis tree to be the minimum number of storage units with M mixers. We characterize the variation of the M-depth of a tree with M, and use it to calculate the minimum total *size* (the number of electrodes) of mixers and storage units. We prove that we can always construct the smallest chip for an arbitrary analysis using one mixer and $f(1)$ storage units where $f(1)$ is the 1-depth of the biochemical analysis tree. These are the first results on the least resource requirements of DMFS for biochemical analyses, and can be used for the design and selection of chips for arbitrary biochemical analyses.