

SEMINARIUM INSTYTUTOWE

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Sala 200

Protein-based computation substrate for parallel combinatorial optimization

Dmytro Shchyrba

Politechnika Wrocławska

Abstract

The NC (Nick's Class)* complexity class is commonly viewed as the "tractable" class for parallel algorithms, just as P (Polynomial time) is for sequential computing. While perceived as simpler from an algorithmic perspective, the scale of parallel computing infrastructure it demands often keeps it intractable or at least highly expensive in practice. An alternative classical computation substrate, based on amyloid peptide proteins, is being developed, fit for the cheap production of parallel processors, albeit with the cost of high latency.

This lecture will discuss:

1. A range of commercially significant problems in the NC complexity class.
2. The properties of amyloid peptide proteins that make them suitable for combinatorial optimization and, specifically, for NC-class problems.
3. Potential approaches to chip-circuit design and construction.
4. Technological and knowledge-based bottlenecks;
5. Advantages and disadvantages compared to other computation models and substrates.
6. Relevant challenges in algorithmic design and problem mapping onto the substrate.

* "Nick's Class" is the set of decision problems decidable in polylogarithmic time on a parallel computer with a polynomial number of processors. Thus, a problem with input size n is in **NC** if there exist constants c and k such that it can be solved in time $O((\log n)^c)$ using $O(n^k)$ parallel processors. Stephen Cook coined the name "Nick's class" after Nick Pippenger, who had done extensive research on circuits with polylogarithmic depth and polynomial size (*after Wikipedia*).