

DNA Computing

at the First International Conference on

Unconventional Models of Computation, Auckland, January 5 – 9, 1998

The conference, (perfectly) organized by the Centre for Discrete Mathematics and Theoretical Computer Science of the University of Auckland in cooperation with the Santa Fe Institute (chair: C. S. Calude), was mainly devoted to DNA Computing and Quantum Computing (several papers not in these areas have dealt with various models of computation aiming in general to compute beyond the Turing machines). Carefully shuffled, the communications and the invited lectures in the two areas have (almost explicitly) scientifically competed, leading to a meeting of a very high level, with the number of questions per presentation often making necessary the intervention of the session chairman for interrupting the discussion.

In the order of the programme, the DNA Computing was the main topic of the following communications: M. H. Butler, R. C. Paton, P. H. Leng: Unconventional approaches to biologically inspired computing; Gh. Păun: Distributed architectures in DNA Computing based on splicing. Limiting the size of components; M. Amos, S. Wilson, D. A. Hodgson, G. Owenson, A. Gibbons: Practical implementation of DNA computations (invited lecture); G. Alford: Explicitly constructing universal extended H systems; R. Freund, V. Mihalache: Molecular computations on circular and linear strings; A. Salomaa: Turing, Watson-Crick and Lindenmayer. Aspects of DNA complementarity (invited lecture); J. H. Reif: Paradigms for biomolecular computation (invited lecture); M. Oghihara, A. Ray: The minimum DNA Computation model and its computational power; A. Mateescu: Splicing on routes. A framework of DNA Computation.

Although a panel discussion was organized at the end of the meeting, trying to forecast the future of the two much promising but slowly developing unconventional models of computation, no convincing answer has been drawn. The basic shortcomings are common: the errors and the scalability (J. Reif). For DNA Computing, it seems that the first problem, rather difficult in this moment (M. Amos et al), can be soon satisfactorily solved (A. Ray), but the amount of DNA necessary to solve a problem of “commercial size” seems to remain for a while prohibitive. Instead, the theoretical developments motivated by DNA Computing (this is the case also for Quantum Computing) are ... brilliant (R. Freund, V. Mihalache, A. Mateescu, Gh. Păun, A. Salomaa). However, the question “why should we consider such sophisticated new computing methods which produce probabilistic solutions, while we have good enough probabilistic algorithms of a classic type ?” (C. Calude) was answered (in my opinion, unconvincing yet) by “because there are problems which cannot be formulated in classic terms”. Another question (this time, a bad one: premature and non-scientific in essence), only once openly formulated, but implicitly addressed by many speakers, was: “what is more realistic, Quantum Computing or DNA Computing ?” The reader can imagine a full range of answers. I quote here (approximately) what A. Ray (ironically) said: “Because I know a lot about DNA and almost nothing about Quantum Mechanics, I suppose that Quantum Computing is more realistic...” I would add: let’s consider again this question at the twentieth UMC Conference...

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