

On Programming and Biomolecular Computation

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Abstract. In spite of widespread discussion about connections between biology and computation, one question seems notable by its absence: **Where are the programs?** We propose a model of computation that is at the same time biologically plausible: its functioning is defined by a relatively small set of chemical-like reaction rules; programmable (by programs reminiscent of low-level computer machine code); uniform: new "hardware" is not needed to solve new problems; universal: stored-program: data are the same as programs, and so are executable, compilable and interpretable. The model is strongly Turing complete: a universal algorithm exists, able to execute any program, and not asymptotically inefficient.

The model has been designed and implemented (for now in silico on a conventional computer). We hope to open new perspectives on just how to specify computation at the biological level.; and to provide a top-down approach to biomolecular computation.

(Joint work with Jakob Grue Simonsen, Lars Hartmann, Søren Vrist.)

While this talk is not directly about metacomputation, programming languages will be visible in the model and the way it is developed. It is a modest updating of a META 2010 talk *Programming in Biomolecular Computation*.

The topic may be interesting to META; and it is interesting to me since the feedback received so far has mainly been from people responding to the biological-modeling aspect (e.g., questions such as "are cells deterministic enough", "how would you implement it on a Petri dish", etc.).

This talk has much to do with interpreters and (very) finite-state program execution mechanisms, hopefully leading to some connections between

- Program specialisation and specialisation of biological cells (e.g., zygotes, embryo,...)
- Self-application as in Futamura compared with biological self-reproduction

The topic is a bit wild, and as yet not many people have picked up on the ideas. However I think there is a potential, and it will be interesting to hear the metacomputation community's viewpoints .

References

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