Postscript: Building Blocks of a Computing Revolution

Discussion thus far has been largely about the role of computer science and computing in transforming, even revolutionising science. There also exists the distinct possibility that the opposite could occur as a consequence: that such advances in science, especially biology and chemistry, could create the building blocks of a fundamental revolution in computing.

Computers as we know them excel at the tasks they were conceived for. Yet, increasingly, one can envision applications of information processing for which the established computing technology is unsuitable. Bioimmersive computing devices that would operate within a living organism, or even inside a living cell, are an example [37]. Their realisation requires a complete information processing architecture smaller than a single transistor. No fundamental limit stands in the way of such a technology, as is amply demonstrated by the sophisticated intracellular information processing found in organisms. Similarly, in the area of robotics, real-time processing of complex data streams in a low-power, tiny, lightweight unit is at present out of reach – yet a broad range of social insects (such as ants) illustrate what would be possible by such robots given an appropriate technology.

Information processing is essential for biological systems, both to maintain their intricate organisation and to compete with rival life forms. Consequently, even the simplest organisms evolved enviable capabilities to tackle computationally difficult challenges. The principles of natural information processing methods are yet to be fully understood, but progress in the biosciences continually unveils more detail. What is known already informs the development of molecular computing concepts [59].

Today's computers have been designed to follow strictly a formalism imposed independent of their physical implementation. The properties of the materials that implement the computation are hidden by careful engineering. Albeit convenient for programming, this is an inefficient use of the computing substrate resulting in relatively large computing devices which are based on vast networks of identical, fast and simple switches. In contrast, the course of computation in nature's molecular computers is directly driven by the physicochemical properties of the materials that implement the computation.

The unique properties of macromolecules in particular afford the possibility of highly integrated information processors. Macromolecules are large enough to possess specific shapes, yet small enough to explore each other by diffusion. Short-range additive forces allow them to overcome entropy at relatively high temperature to self-assemble in selective combinations. Another important property of macromolecules is their conformational dynamics, i.e. their ability to change shape, and as a consequence function, in response to their local physicochemical environment. Through these largely stochastic processes, macromolecules provide much more powerful components than conventional silicon architectures [60]. The combinatorial building block principle for assembling specialised macromolecules offers an inexhaustible set of basic functions.

Two substantial challenges need to be overcome for exploiting the potential of a molecular information technology. First, computational concepts tailored to the

physics of macromolecules need to be worked out. Second, methods to orchestrate the structure and interaction of ensembles of molecules have to be developed. The magnitude of these challenges, however, is matched by the opportunities that will be laid open through the resulting technology. Exploratory research into both aspects is well under way. Indeed, a first step towards an 'intelligent drug' that would determine the disease state of a cell from within and act accordingly has already been tested in the laboratory. Ongoing research along this line may eventually lead to the integration of artificial control structures into cells with broad potential for applications in medicine and environmental sensing.

The change of computing substrate may also necessitate a change in the underlying model of computation. The von Neumann architecture, which underlies all past and present programmable electronic computers, is not relevant to computers made of biomolecules. Fortunately, the plethora of abstract computing devices explored within theoretical computer science has ample models to choose from. Specifically, the Turing machine, which stands at the foundation of theoretical computer science, has many similarities to molecular machines of the living cell: its unbounded tape resembles information encoding molecules such as DNA, RNA and even proteins, and its local processing operation resembles polymerases and the ribosome much more than an electronic computer. Indeed, it has served as inspiration for many theoretical and experimental molecular computing systems.

The new computer revolution will complement and extend, not overthrow, established methods. Enabling a wide range of novel uses for information processing, it will lead to materials, components and devices capable of responding with life-like adaptability to their environment.

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