Can biological phenomena be understood by humans?

Despite the increasingly successful collaboration between physics and biology, there are contexts in which their styles and philosophies can diverge. Nowhere more so than in ‘understanding’.

Laughlin worries that in the post-genome era, biologists will be too busy accumulating facts and modelling them to seek simplification and underlying principles. The fact-gathering tendency is apparent not just in structural genomics, but also in functional genomics (where the aim is to identify the role of each gene in the genome) and proteomics (with a similar aim for each protein in the cell or organism). Evidently, there are enough facts to keep biologists busy gathering them for decades, so when will they have time to think?

In defence of modelling

One answer, conveyed forcefully at the conference by Klaus Schulten (for protein-structure studies) and David Botstein (for genomics), is that modelling aids thinking, by helping to generate hypotheses. Where a theoretical physicist might gain intuition from pencil and paper, a structural biologist may need molecular dynamics simulations. (And, to be fair, physicists who work on complex systems are themselves no strangers to computer modelling.) The microarrays that are becoming the workhorses of genomics can produce a million data points in a single study; even a physicist, argued Botstein, would find it hard to make sense of these data as a table of numbers. So it makes sense to use the computer to put the data in some kind of order before trying to think about them. The ordering may be driven by a hypothesis — for example, one might look for evidence of a periodic cell cycle in the transcription of genes — but in the absence of a hypothesis, the data themselves may suggest a pattern.

Although one structural biologist went so far as to proclaim that “we have to free ourselves from the hypothesis-driven approach”, even he admitted that it would be nice to find some underlying simplicity. But he and others expressed the view that a search for unifying principles would be premature — that it will first be necessary for biology to go through a stage of fact accumulation and pattern recognition.

But what if it’s not just a ‘stage’? Is it possible that the parts will be enumerated and the functions found, and still there will be no simplification? Fortunately, enlightenment can come in different forms — not just in the elegant simplicity of a physicist’s theory, but also in the more utilitarian guise of an engineer’s analysis. As Hartwell et al. have argued in the recent supplement Impacts of Foreseeable Science (Nature 402, suppl. C47–C52; 1999), molecular and cell biology may have more in common with engineering and computer science than with the basic sciences; for example, the kind of modelling needed to understand the complex intracellular networks that underlie most biological functions comes straight from engineering control theory.

As shown by two papers in last week’s issue (see Nature 403, 335–338, 339–342; 2000), it is becoming possible not just to analyse naturally occurring networks in this spirit, but also to design and build biological networks to implement desired functions. That, surely, is a kind of understanding worth having, and one that theoretical physicists can recognize as progress of a sort.