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Thinking postgenomics

Defining knowledge as the ability to predict consequences, the fifth 'After the Genome' (ATG) workshop* was meant to foster a "short-lived think tank to suggest experimental and computational methods that will eventually lead to a quantitative and predictive understanding of biological function". Assuming the availability of genomic sequence, challenges include identifying genes, predicting the proteins they encode, determining when and where genes and proteins are expressed and how they interact, and how these expression and interaction profiles change in response to environmental signals. A group of approximately 80 academic and industrial biologists, computer scientists, physicists, mathematicians and policy makers spent four days discussing these tasks, seemingly less awed by the challenge to make biology computable than by the beauty of the Grand Teton Mountains.

Realizing that bottlenecks exist in measurement and data analysis, participants discussed strategies for systematic information-gathering on genes and proteins, how to improve pattern recognition algorithms, and ways of analysing large data sets efficiently without the need for supercomputers. Whereas such interdisciplinary interactions may have seemed radical (or, with hindsight, visionary) five years ago at the first ATG meeting, they are now widely embraced. Public funding is geared towards interdisciplinary approaches, many universities are developing functional genomics institutes or computational biology centres, and biology curricula are being frantically re-written to emphasize mathematics and computer science. So is there a continued need for a post-genomic think tank? Recognizing the need for interdisciplinary collaboration is only the first step in getting scientists with different expertise to talk with and learn from each other, and workshops such as this one provide a welcome forum. The term 'think tank' implies a somewhat unconventional selection of participants and topics. Thanks to the organizers, the meeting did not disappoint on this score: some less obvious, but not necessarily less relevant, topics were also discussed.

Chris Adami (California Institute of Technology) and Richard Lenski (Michigan State University) reported on their efforts to take the concept of model organisms into the realm of virtual reality. They have generated digital organisms that live on a computer hard disk and compete for central processing units. Analysis of digital organisms has the advantage that all relevant data can be recorded without errors. Observing these self-replicating computer programs evolving and adapting to

*After the Genome V, Jackson Hole, Wyoming, October 6–10, 1999.

defined environments *in silico*, Adami and Lenski have studied genome complexity, robustness and genetic interactions (*Nature* **400**, 661–664; 1999). Do the results from such an artificial system have relevance to 'real' biology? If the goal is to understand complex biological systems, can we really learn from simple ones? There is no question that the study of viruses, bacteria or yeast has taught us a great deal about basic molecular biology and genetics, and that we have much to learn from model organisms, digital or other. The challenge is to use this knowledge to devise strategies to learn about the complexity of more complicated organisms without getting stuck on simple paradigms that are irrelevant to complex systems. Take the related example of monogenic versus complex traits, where it is debatable whether knowledge of the former is helping or hampering dissection of the latter.

Several other presentations focused on the description and communication of complex biology. At present, most biologists use natural language, two-dimensional graphics, and text- and graphic-oriented web interfaces. Max Egenhofer (University of Maine) described the acquisition, modelling and use of spatial information in geographic information systems and proposed the application of spatial concepts to the modelling and analysis of genome sequence and mapping data. David Soll (University of Iowa) has developed software that allows the observation of crawling cells on a surface (http://www.uiowa.edu/~keck/). He persuasively argued that visualization is essential to understanding complex movements and described his vision of being able to walk into a virtual cell and observe metabolism and mobility from within. Jumping from a virtual cell to a virtual world, Bruce Damer (The Contact Consortium; http://www.ccon.org/) described the 'Cambrian explosion' of virtual worlds on the Internet and demonstrated that there is more to virtual space than two-dimensional web pages. Scientists should be aware of the possibility to create and use multidimensional digital worlds to exchange information, and to educate students and the public (see, for example, http://www.ccon.org/vlearn/index.html).

The success of the workshop depends on the extent to which it will result in action by its participants and others. ATG must find ways to communicate its ideas among and beyond its members, and to influence policy makers and the larger community. The group's web site (http://atgx.org; currently under development) is a first step in that direction.

Ringing in the changes

This issue marks a divergence in the evolution of *Correspondence* published by *Nature Genetics*. Rather than publishing a single section in which both scientific and general correspondences appear side by side (as has been the case until now), each type of contribution is housed in a section of its own. *Brief Communications* report peer-reviewed primary research and represent preliminary but intriguing advances on the current literature, whereas *Correspondence* provides a venue for comment from the community. On page 387, for example, is a correspondence by Passarge *et al.* on appropriate use of the routinely abused word 'synteny'. *Nature Genetics* seeks to promote discussion of issues relevant to genetic and genomic research and invites insightful, provocative and polemical correspondence. It also aims to provide its readers with information on useful and publicly available resources, descriptions of which will appear as *Correspondences*, subject to peer review. See, for example, a description of a database of gene tags obtained by serial analysis of gene expression by Velculescu *et al.* (also on page 387). Only resources that offer a substantive advantage over those described in the literature will be considered.