

Big genome — big science?



Cover of the human genome issue of *Nature*, February 15th 2001

As this issue of *Nature Cell Biology* goes to press, the first draft sequences and maps of the human genome are being published in *Nature* and *Science*. It is the first vertebrate genome, and the largest ever, to be sequenced, and its elucidation has been hailed as an historical scientific achievement, not only because of its sheer scale, but also because of the extraordinary impact it will have, in time, on medicine and on our understanding of human evolution, physiology and disease. Contrary to the unfortunate choice of emphasis by some journalists — with ill-informed headlines such as “Revealed: the secret of human behaviour” — the sequence of the human genome has of course not changed our views on the ‘nature versus nurture’ debate. But to ultimately answer complex questions in biology, whether involving the principles of behaviour and cognition or at the level of understanding the workings of a cell or an organism in its entirety, post-genomic biological research is developing towards what is now often referred to as ‘systems biology’ — seeking to appreciate insights within their broader context (see *Nature* 409, 758–760; 2001). The availability of the human genome sequence is likely to further this development.

As the detailed knowledge of how individual molecules function and interact grows, molecular cell biologists aspire to place this information into a more global picture of cell function. Recent years have therefore seen a surge of ‘big science’, involving high-throughput analyses. Unbiased micro-array studies, for example, are often mere starting points for classical cell-biological studies, and have advanced our understanding of cellular processes by putting changes in gene expression into an overall context, as well as by providing clues as to which might be the most interesting molecules to study. Likewise, proteomic approaches, including large-scale mass spectrometry, and high-throughput inhibitor screens will continue to provide valuable and unprecedented leads in cell biology.

Although the potential of such post-genomic strategies to speed up and expand the scope of scientific discovery makes this an immensely exciting time for biological research, it also highlights an old concern: will this trend towards ‘big science’ exacerbate the gap between ‘the haves’ — those laboratories, institutes and companies with vast resources, facilities and funding — and ‘the have-nots’? Will small laboratories that cannot afford to use high-throughput methods be left behind? Although it seems wise not to ignore the promises of large-scale analyses, it is clear that they cannot replace, but must rather complement, ‘small science’ and traditional approaches to elucidate the detailed functions of individual molecules and their interactions. The latter, perhaps even more than the former, must continue to draw from innovative, imaginative ideas and strategies, driven by gifted individuals with a passion for science.

The results of ‘big science’, the post-genomic flood of data, begs the urgent question as to how this information can be dealt with in a sensible way. For many molecular cell biologists, the answer is that the field is ripe for computational approaches. Indeed, this month in Lenox, Massachusetts, the First International Symposium on Computational Cell Biology will recognize that “the formulation of hypotheses based on complex experimental data is often impossible without the construction of computational models. Computational cell biology is an emerging discipline that responds to the need for computational methods to analyse and organise the abundance of experimental data on the structure and function of the cell” (<http://caboy.uchc.edu/conference/>). It will be interesting in years to come to see how researchers will embrace computational biology, and how big and small science will work hand in hand, bringing previously disparate disciplines together in search of the ‘big picture’. As has been pointed out so many times, this really is only the beginning of the post-genomic era. □