

Genomics Comes to Cell Biology

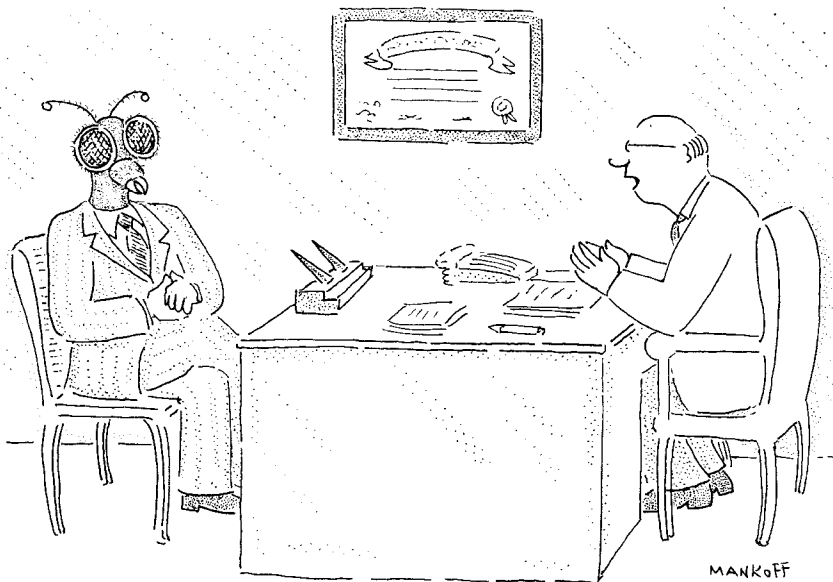
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With the completion of the genomic sequences of *S. cerevisiae*, *C. elegans*, *D. melanogaster*, and shortly, *H. sapiens*, in a sense the frontier has been officially closed on four of the most widely used and extensively studied species on earth. It is obvious that the closing of this frontier will open many new ones, creating directions and experimental opportunities for biologists and biomedical scientists for decades to come. However, the actual nature of these directions and opportunities remains uncertain.

In the popular press, and indeed in scientific weeklies, great attention has been paid to many exciting new opportunities. Most of these, however, involve the use of high throughput sequencing, expression, or proteomic data to gain quantitative pictures of how pathways, cells, and organisms work. In the extreme, these methods will feed in to computational strategies, which in principle might allow us to deconstruct and then integrate every aspect of cellular and organismal existence without ever again having to touch a pipette or culture dish.

As one who is convinced that every hand-held gadget seen in *Star Trek* episodes will someday be developed in reality, I am both intrigued and excited by the prospect of being able to conduct my research from the confines of my computer screen (although I will miss my lab group immensely!). Nevertheless, it will be quite some time, if ever, that computational methods will replace "conventional" laboratory work. Despite the popular clamor over the impact of The Genome Project, the completion of various genomes per se represents a somewhat limited achievement in



"We think it has something to do with your genome."

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biological terms. The value of the genomic information derives largely from cellular and functional context. The provision of that context begins by the process of "annotation," in which the multitude of open reading frames identified in various genomic sequences are named and grouped into homology units. The annotation process is then itself supplemented by speculation as to what the existence of these predicted proteins and homology groups might mean for normal or pathological cell function.

It is understandable why there is such attention focussed on the completion of genomic sequences. However, it is not too early to begin redirecting that attention away from genomics and toward cell biology. The

types of functional insights generated by the array of assays and experimental systems developed by cell biologists worldwide do not exist to annotate the genome. On the contrary, the genome exists to assist us in our efforts to understand the biology of molecules, cells, and tissues. The faster this is realized in the public debate over what to do in the rapidly approaching "post-genomic era," the more likely the general field of cell biology will be understood as holding the key for unlocking, in the near term, the promise of The Genome Project. Certainly, new techniques and strategies must be developed to allow cell biologists to better capitalize on genomic information, but they should be techniques and strategies tailored

to individual cell biological problems, rather than contributions to a computational database of the future.

This special issue of *The Journal of Cell Biology* hopes, in part, to facilitate the coming of genomics to cell biology. This issue contains a series of 11 articles authored by many of the individuals who participated in the Celera-sponsored *Drosophila* genome annotation project earlier this year. Although their initial findings were published as very brief summaries last Spring in *Science*, *The JCB* offered, and most accepted, the opportunity to provide a more complete account of how the *Drosophila* ge-

nome has or will alter current and future concepts in cell biology. You will find an array of exciting articles on topics ranging from adhesion proteins to transcriptional regulators, from cytoskeletal motors to signaling molecules. You will also learn of the discovery of predicted pathways not previously thought to exist in *Drosophila*. For example, detailed homology analysis has suggested that flies express homologues of important disease-related proteins, such as dystrophin. Although dystrophin has long been known to be a protein defective in human muscular dystrophy, its precise function has remained elusive.

Now that we know that dystrophin and several of its presumptive interacting proteins exist in *Drosophila*, one can contemplate entirely new approaches to this important problem.

Special thanks for the production of this issue must go to Karen Dell, JCB Reviews Editor, who worked together with Editorial Assistant Sati Motieram, Managing Editor Mike Rossner, and Editor Louis Reichardt. JCB board member Larry Goldstein deserves particular credit for having conceived the original idea, one which we will endeavor to repeat in the future.

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