

**Message  
from the  
Vice President,  
Life Sciences  
Solutions**

It is unusual for a technology revolution in one industry to be made possible by advances in another. However, this is exactly the situation in the world of biotechnology, where information technology has become the engine of experimental biology. This trend is evident in genomics, proteomics, structural biology, and emerging areas associated with the study of metabolic regulation.

High-performance computing, data management software, and the Internet are now making possible the large-scale industrialization of many aspects of biomedical research. The basic steps of identifying, purifying, and cloning a gene, followed by purification and characterization of the proteins coded for by that gene, have been automated and streamlined to a degree that no one could have predicted just ten years ago. Many of these advances are directly related to the availability of new software products that enable high-speed acquisition and analysis of data as well as new algorithms for searching, matching, and aligning information.

Superimposed on this trend has been a rapid evolution in the design of large-scale computing infrastructure. Such improvements coupled with explosive growth in the quantity of available bioinformatic data are driving a migration from *in vivo* (observations of real life), to *in vitro* (test tube experimentation), to “in silico” (experimentation by computer simulation). It is this migration to “in silico” research that promises to allow the greatest advance of our time the launch of molecular-based medicine and the first true understanding of the molecular basis of life.

With this view in mind, we are pleased to present this special edition of the *IBM Systems Journal*.



Caroline A. Kovac