



## KEYNOTE LECTURE

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# The future of bioinformatics

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### Abstract

It is clear that computers will play a key role in the biology of the future. Even now, it is virtually impossible to keep track of the key proteins, their names and associated gene names, physical constants (e.g. binding constants, reaction constants, etc.), and known physical and genetic interactions without computational assistance. In this sense, computers act as an auxiliary brain, allowing one to keep track of thousands of complex molecules and their interactions. With the advent of gene expression array technology, many experiments are simply impossible without this computer assistance. In the future, as we seek to integrate the reductionist description of life provided by genomic sequencing into complex and sophisticated models of living systems, computers will play an increasingly important role in both analyzing data and generating experimentally testable hypotheses.

The future of bioinformatics is thus being driven by potent technological and scientific forces. On the technological side, new experimental technologies such as microarrays, protein arrays, high-throughput expression and three-dimensional structure determination prove rapidly increasing amounts of detailed experimental information on a genomic scale. On the computational side, faster computers, ubiquitous computing systems, high-speed networks provide a powerful but rapidly changing environment of potentially immense power. The challenges we face are enormous: How do we create stable data resources when both the science and computational technology change rapidly? How do we integrate and synthesize information from many disparate subdisciplines, each with their own vocabulary and viewpoint? How do we "liberate" the scientific literature so that it can be incorporated into electronic resources? How do we take advantage of advances in computing and networking to build the international infrastructure needed to support a complete understanding of biological systems.

The seeds to the solutions of these problems exist, at least partially, today. These solutions emphasize ubiquitous high-speed computation, database interoperation, federation, and integration, and the development of research networks that capture scientific knowledge rather than just the ABCs of genomic sequence. I will discuss a number of these solutions, with examples from existing resources, as well as areas where solutions do not currently exist with a view to defining what bioinformatics and biology will look like in the future.