



NIH BACKGROUND

National Institutes of Health

Bioinformatics and Computational Biology

Biology has always been a haven for microscopes, test tubes, and Petri dishes, but this conventional picture of the field is expanding rapidly. Sophisticated techniques adapted from physics, chemistry, and engineering enable scientists to use computers and robots to separate molecules in solution, read genetic information, reveal the three-dimensional shapes of natural molecules like proteins, and take pictures of the brain in action. All of these techniques generate large amounts of data, and biology is changing fast into a science of information management.

Today's biomedical researcher routinely generates an amount of data that would fill multiple compact discs, each containing billions of bytes of data. (A byte is approximately the amount of information contained in an individual letter of type on this page.) There is no way to manage these data by hand. What researchers need are computer programs and other tools to evaluate, combine, and visualize these data. In some cases, these tools will greatly benefit from the awesome strength of supercomputers or the combined power of many smaller machines in a coordinated way but, in other cases, these tools will be used on modern personal computers and workstations.

By embarking on the Bioinformatics and Computational Biology initiatives, the NIH Roadmap is paving a future "information superhighway" dedicated to advancing medical research. A central focus of the effort will be a set of National Centers for Biomedical Computing.

As the Centers begin to generate the software and data management tools to serve as fundamental building blocks for 21st century medical research, individual scientists will be funded to work together with the centers. "Big science" and "small science" will work hand-in-hand to advance all of biomedical research. Through these efforts, researchers will be able to share data gathered from large experiments. The best minds will be able to work together effectively to tackle unsolved mysteries, such as the role of heredity in individuals' different responses to medicines and the complex interplay of genetic and environmental factors in common diseases such as Alzheimer's disease, heart disease, cancer, and diabetes.

The Bioinformatics and Computational Biology initiatives will create a national software engineering system. Through a computer-based grid, biologists, chemists, physicists, computer scientists, and physicians anywhere in the country will be able to share and analyze data using a common set of software tools. Developers of the project envision that the system will resemble that of the integrated software packages for office tools installed on most home computers today, in which information can be traded seamlessly between software such as spreadsheets, word-processing and e-mail programs.

The URL for the NIH Roadmap web site is nihroadmap.nih.gov. For more information on the Bioinformatics and Computational Biology initiatives, contact Eric Jakobsson, Ph.D., National Institute of General Medical Sciences, (301) 451-6446, jakobse@mail.nih.gov. Further information about NIH can be found at its Web site: www.nih.gov.