LIFESCIENCES

For decades, biologists' principal tools included human and animal specimens, petri dishes, and microscopes of ever increasing sophistication. During the past decade, however, computers have transformed the discipline. Wet lab processes that took weeks to complete are giving way to digital research done in silico. Notebooks with jotted comments, measurements, and drawings have been supplemented by computers that can easily store terabytes of genetic and chemical data and by a worldwide Web that provides researchers with a plethora of data sources, computation tools, and annotation. Supercomputing is making it possible to develop new knowledge with previous unimagined mathematical exactness. Supporting this "New Biology" and its voracious appetite for data is one of the largest, most demanding and yet the most exciting challenges facing IT today.

This new biology depends upon the world of bioinformatics—a branch of computing concerned with the acquisition, storage, analysis of biological data and modeling of biological processes. Once an obscure part of computer science, bioinformatics has become a linchpin of biology's rapid progress. In the quest for speed and new insights into the nature of life, bioinformatics offers a new breed of biologists unparalleled throughput and efficiency through mathematical modeling. It also seems to be the only practical method of making sense of information from an ever-increasing deluge of data.

Biology, through the art of bioinformatics, has become one of the biggest users (and abusers) of computing power, demanding petaflops (thousands of trillions of floating-point operations per second) of supercomputing power, and terabytes (trillions of bytes) of storage. Bioinformatics encompasses a spectrum of technologies, including computer architecture (e.g., workstations, servers, storage, supercomputers and the like), networks, local and wide-area computational grids, storage and data lifecycle-management systems, databases, knowledge management and collaboration tools, as well as the life-science equipment needed to handle biological samples. Most of these requirements rely on, and in the case of storage, even drive the current state-of-the art in high performance computing.

Unlike conventional IT where there is a consistent, even predictable pattern of demand and requirements (e.g. year end closing of financials), Life Sciences research provides continually changing challenges and the requirement for IT is to be able to respond to a broad and dynamic set of requirements (a.k.a. unreasonable) based on specific needs often driven by the output of a previous day's computational results. A standard bioinformatics IT infrastructure does not exist, and if it did it, would be replaced tomorrow as the answers to yesterday's questions lead to new questions, new algorithms, new tools, ever more data and even more computing. The solution to this challenge does not lie in today's advanced technologies, high-performance networks or supercomputing. It lies in high performance people in a high performance team who can communicate with a diverse set of researchers .
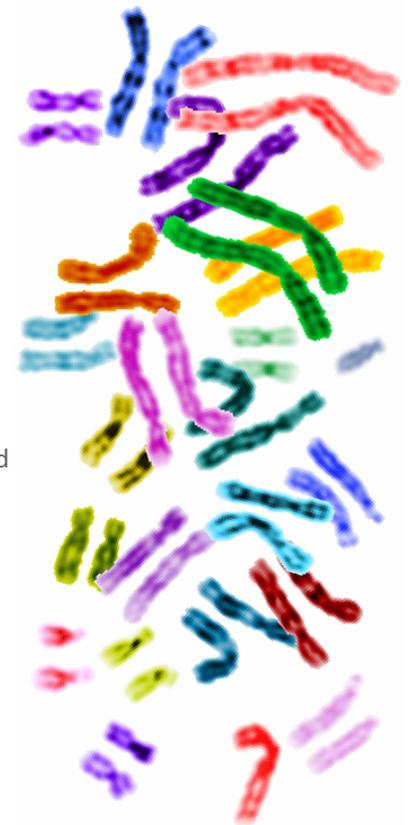
NMCAC
5700 W. University Boulevard. SE Suite 320 • Albuquerque, NM 87106
505-553-5546 • www.nmcac.net
info@nmcac.net

New Mexico Computing Applications Center