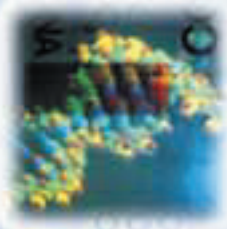
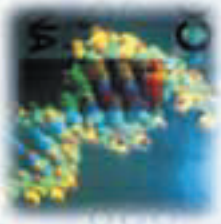


Keynote Address

Raynard S. Kington, M.D., Ph.D.

In his opening remarks, Dr. Kington explains how eRA enables NIH to keep pace with the growing volume of information it needs to manage and to communicate efficiently within the NIH and with those outside. He urges NIH staff to embrace the new eRA system and to actively participate in refining it. Although HHS has not yet made an official announcement, it is clear that eRA will become the grants administration system for the entire Department. Therefore, NIHers are the pioneers whose willingness to use eRA effectively will have great resonance among the HHS granting-making agencies.



Introduction to the Program Module

Carlos Caban, Ph.D., and Bud Erickson

The Program Module (PGM) is a new Web-based eRA application that processes both transactions and reports. It was released in pilot mode in April, 2003. The purpose of the PGM pilot is to provide a central place where Program Officials (POs) can accomplish their grant-related work, including (1) getting information quickly on a grant's status using the SEARCH feature; (2) quickly accessing assigned grants and related documents using MY PORTFOLIO, which automatically distributes and updates assigned grants across the grant cycle tabs; (3) allowing the PO to monitor relevant portfolio workload at each stage of the grant cycle (Pre-Submission, Pending SRG, Pre-Council, Post Council, Pending Type 5s, and Post Award); (4) enabling Program approval for Pre-Award and Progress Reports requirements while in MY PORTFOLIO; (5) accessing reports and exporting lists to EXCEL from each portfolio; and (5) linking to other eRA modules such as Quickview, Commons, ECB and QVR. The July release and future updates will be available to all POs.

Systems Biology: A New Paradigm in Biological Research?

Ronald N. Germain, M.D., Ph.D.

For the past several decades, biological research has been in a “deconstructive” mode. Most studies sought to isolate and investigate individual players in biochemical pathways or cell biological processes. Many investigators dedicated their work to discovering new genes/molecules to add to the existing inventory of “parts” that make up living entities, from single-cell bacteria to man.

With the availability of this information and the development of increasingly powerful tools for global analysis of gene and protein expression (chips/arrays), a “constructionist” bias has begun to creep into biology. There is a growing desire to put the pieces back together and achieve a deeper understanding of how they interact in time and space to make a cell or collection of cells work. This attempt to develop a true understanding of how living beings are “engineered” so that the emergent properties of the assembled parts serve the necessary biological functions is known generically as “systems biology.” In its simplest form, this is an attempt to develop robust quantitative and predictive models of biological function based on a global understanding of how large numbers of small pieces relate to one another in networks and circuits.

Major advances in systems biology are not likely to come from small, single-PI laboratories. Rather, larger teams comprising expert biologists, computer programmers, mathematicians, engineers, chemists, and others are needed to collect and assemble the vast amount of data into predictive models of biological behavior. This means that new types of research support, suitable for large, interdisciplinary groups working on long-term projects, will be needed. New schemes will be necessary to attract those in the physical sciences, math, and engineering into active collaborations with biologists and for training new generations of biologists in quantitative mathematical and computer skills. These and related issues that affect future program development and management will be highlighted during this presentation.

Future Directions

Steve Hausman, Ph.D.

The presentation on future directions is intended to provide a broad perspective of the manner in which computer-related technology has developed, beginning with a brief discourse on the history of how we came to use paper up to a discussion of the most current computer technology and new developments that may come to fruition within a few years. Dr. Hausman also will explain how business practices have changed to accommodate these technological innovations.





Science Administration in the Age of Systems Biology
NIH and Knowledge Management

Richard Morris, Ph.D.

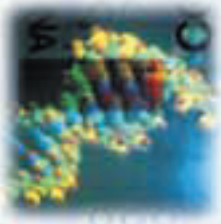
This presentation provides a vision for the NIH “Institute of the Future” and discusses how a diverse family of computer applications, referred to as “knowledge management,” can help achieve this vision by permitting major improvements in scientific administration.

Scientific data management at the local level will become increasingly important for biomedical discovery. Emerging bottlenecks must be addressed if the benefits of systems biology through genomics and proteomics are to be fully realized. Science administrators can improve the situation by applying advanced information technologies to facilitate data sharing, support executive decision making, streamline core business processes, and extract additional value from stored knowledge assets.

This presentation explains how the NIH eRA Project is exploring ways that specific knowledge management applications can deliver these benefits in (a) grant reviewer selection, (b) identification and screening of external reviewers, (c) assignment of applications to NIH institutes and centers, and (d) the high-level analysis of trend data for executive decision-making. Given the high volume of services provided by eRA to the NIH community, these measures promise to have a positive effect on NIH operations, while enabling NIH to better support the advancement of science.







The NIH eRA Commons and E-Grants

Paul Markovitz and David Wright

The NIH eRA Commons is a Web interface where NIH and the grantee community will be able to conduct their extramural research administration business electronically. Since its deployment last October, approximately 180 grantee organizations, representing 60 percent of all funded institutions, have registered for the new NIH eRA Commons system. Paul and David will discuss how the extramural community is reacting to eRA initiatives, and specifically, to the NIH eRA Commons applications currently in production or pilot mode. Paul and David also will speak about the effect of the new NIH eRA Commons system on how the NIH and its grantees do business.

In addition, the presentation will address the issues involved with coordinating eRA efforts with the federal E-Grants initiative. By late summer, NIH plans to accept a limited number of electronic, competitive R01 grant applications (eCGAPs) as XML data streams. NIH is meeting regularly with the E-Grant team and will participate in E-Grant pilot testing this summer.

A First Look at the Web Query Tool

Sherry Zucker

This presentation is a preview of a planned Web-based query tool called “Web QT.” Web QT is being designed as a J2EE application that will replace QuickView, ICSTORe, and, in time, other eRA/IMPAC II query tools.

During the requirements gathering phase for Web QT, eRA staff performed a comparison of all existing IMPAC II and related query tools to identify the features and functionality of each interface. Web QT will have a basic, expanded, and advanced interface for different levels of users. The new tool will combine a variety of search parameters and features with powerful document retrieval and data export capabilities. It will be built on a new “query engine” that will serve as the basis for query and hitlist functionality in all eRA software applications.

The first version of Web QT will serve as a pilot for user input and suggestions. This release is planned for July 2003.