Editorial

This special, joint issue of *Nucleic Acids Research* and *Computer Applications in the Biosciences* contains more than sixty papers that report progress in the application of computers to molecular biology research. The papers describe algorithms, programs and systems that support research on DNA, RNA and protein structure, function, similarity and design. The *Nucleic Acids Research* volume contains contributions concerning complete systems and research strategies, computer-aided biological discoveries, and the national biological sequence data and computing resources. The *CABIOS* volume comprises manuscripts describing significant new algorithms, programs and exciting discoveries that these new developments make possible. These volumes complement each other, and will serve as a valuable resource to the molecular biology computing community.

This joint issue is timely. Molecular biology computing (molecular biology, genetic engineering, protein engineering, sequence data management and analysis) is rapidly expanding. New developments and critical current issues must be formally communicated to permit international peer review, notification and discussion. Previous special issues of *Nucleic Acids Research* (*The application of computers to research on nucleic acids*, Volumes I–III) helped bridge the information gap during the period when formal mechanisms for publication in this field were limited. Molecular biology computing has matured and outstripped the 'informational effectiveness' of a bi-annual special issue, however.

This joint issue is designed to draw the field together and prepare for an orderly transition from bi-annual updates to continuous communication of computer applications in molecular biology. We believe the scientific community will benefit more in the future from routine, continuing publication. We hope the present peer-reviewed joint issue will provide the foundation for the transition to routine scholarly communication of molecular biology algorithms and computer applications in a regular, specialized, literature resource: *CABIOS*.

We thank all authors and referees for their efforts, and look forward to serving all of you in the future.

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