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### ISCB NEWSLETTER July 30, 1999 - Vol. 2 #6

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**BURROUGHS WELLCOME FUND INNOVATION AWARDS IN FUNCTIONAL GENOMICS**
Genomic sequencing and structural mapping projects for many organisms, including human beings, are nearing completion. The next and greater scientific challenge will be to define not only the functions of genes but also how they interact within the context of the whole organism. The Burroughs Wellcome Fund has developed a new program--Innovation Awards in Functional Genomics--to draw new and exciting ideas into this emerging field. The goal of this program is to accelerate the integration of the vast amount of genomic sequence and expression data being generated into functional and clinically relevant information that will yield insights into mechanisms of human disease. Awards are offered in two areas:

1. Animal model development.
   Awards are intended to stimulate the development of innovative animal systems (primarily vertebrate) that capitalize on the availability of significant genomic sequence data to model complex human genetic traits, or phenotypes, and disease. Collaborative proposals linking geneticists working on a particular model system and clinicians investigating therapeutic approaches to related clinical phenotypes are encouraged.
2. Computational methods development. Awards are intended to stimulate the development of new theoretical and mathematical models for extracting meaningful information from genomic sequence and expression data, as well as for synthesizing the structural and functional data coming from different gene expression networks and model systems. Collaborative proposals encompassing experimental validation of theoretical models are encouraged.

BWF has committed $3 million to support from eight to 20 awards. Two levels of awards are offered in each targeted area: $400,000 over a period of up to four years (generally more appropriate for proposals involving animal models) and $200,000 over a period of up to four years (generally more appropriate for proposals involving computational methods). Awards are open to individual candidates or small groups of collaborators. Candidates must have a Ph.D., M.D., or D.V.M. degree and hold a tenure-track faculty appointment at the assistant, associate, or full professor level. Proposals should focus on the modeling of complex multigenic traits, rather than on determining the functions of individual genes. Awards are not intended to support ongoing research. The application deadline for the 2000 award series is December 1, 1999. For application materials, contact BWF at Post Office Box 13901, Research Triangle Park, NC 27709-3901, or by telephone at 919/991-5100. Information about the Fund's award programs also is available by sending an e-mail message to *mailback@bwfund.org* (type the word "menu" on the subject line for a list of programs) and by visiting BWF's website at *http://www.bwfund.org*.
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ACEDB '2000ACEDB '2000
An upcoming meeting of users, curators and developers of the 'A *Caenorhabiditis elegans* Database" genomic database management system? This workshop/conference will be held in early April '2000 as a satellite meeting to the HUGO HGM in Vancouver, BC, Canada. See the URL: *http://www.sanger.ac.uk/Info/Events/Acedb2000*

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## ST**ANFORD DEPT OF COMPUTER SCIENCE, SCIENTIFIC COMPUTING FACULTY POSITION**

STANFORD UNIVERSITY
Department of Computer Science
Faculty Opening
The Computer Science Department of Stanford University invites applications for a tenure-track faculty position from candidates with expertise in the areas of continuous and discrete modeling, numerical analysis, or high-performance scientific computing. Candidates are expected to have an excellent background in Applied Mathematics and Computer Science, and to be actively involved in the development of computational tools in relation to application areas such as (but not restricted to) biocomputation, imaging, physical simulation, data mining, and statistical learning. Higher priority will be given to the overall innovation and promise of the candidate's work than to contributions to any of these specific topics. Applicants should have a Ph.D. in a relevant field. The successful candidate will be expected to teach courses, both in scientific computing and in related subjects, at the graduate and undergraduate levels, and to build and lead a team of graduate students in Ph.D. research. The appointment will be made at the level of an Assistant Professor. The position is available immediately. Further information about the Computer Science Department http://www-cs.stanford.edu.
Applications should include a *curriculum vitÊ*, statements of research and teaching interests and the names of at least four references. The application should be sent to:
*Professor Rajeev Motwani, Search Committee Chairman*
*C/O Laura Kenny*
*Computer Science Department*
*Stanford University*
*Gates 2B*
*Stanford, CA 94305-9025*
Applications will be accepted until March 15, 2000 or until the position is filled. Stanford University is an equal opportunity employer and welcomes applications from women and minority candidates.

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## GENOME DIVERSITY AND BIOINFORMATICS CONFERENCE 1999

The Biochemistry Department at the University of Otago, New Zealand, will host this international conference late this year (Nov 28th-Dec 2nd 1999). The conference will be the 14th annual FAOBMB conference and the annual NZSBMB meeting. Closing date for abstracts and early registration is 31st August. Morning plenary sessions will include genomics, genetic modification of plants and animals, human health, bioinformatics and biodiversity. Specific themes will be explored further in afternoon parallel sessions. There will also be presentations on biochemical education with an emphasis on genomics and bioinformatics teaching. There will also be a trade show and poster sessions. More detail is available at our website *(http://biochem.otago.ac.nz:800/FAOBMB)*. International speakers will be led by Craig Venter (TIGR). The impressive line up of confirmed speakers include: Chuck Kurland, Sweden, Microbial genomes; Grant Sutherland, Australia, Human genomics; Yusuke Nakamura, Japan, Cancer genomics; Susan Cory, Australia, Cell Biology; Peter Langridge, Australia, Plant Breeding; Yueh Wei, Taiwan, Cell Biology, Genomics, Aroha Mead, New Zealand, Cutural diversity, Mike Carson, New Zealand, Tree Genomics; Gil Hung Nam, Korea, Plant Development. Key Bioinformatics Speakers: Mark Boguski, NCBI, United States of America, DNA bioinformatics; Johannes Sandbrink, Netherlands, Genomics; Minoru Kanehisa, KEGG, Japan, Microbial Bioinformatics; Dr Tan Tin Wee, Bioinformatics Institute, Singapore. The conference is aimed at scientists and students in the Biochemistry, Genetics and Genomics fields.
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